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<p>(21) International Application Number: PCT/US98/14679</p> <p>(22) International Filing Date: 15 July 1998 (15.07.98)</p> <p>(30) Priority Data:</p> <table style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 30%;">08/896,164</td> <td style="width: 40%;">17 July 1997 (17.07.97)</td> <td style="width: 30%;">US</td> </tr> <tr> <td>60/061,599</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>60/061,765</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>08/948,705</td> <td>10 October 1997 (10.10.97)</td> <td>US</td> </tr> <tr> <td>9721697.2</td> <td>11 October 1997 (11.10.97)</td> <td>GB</td> </tr> <tr> <td>09/102,322</td> <td>22 June 1998 (22.06.98)</td> <td>US</td> </tr> </table> <p>(71) Applicant (for all designated States except US): LUDWIG INSTITUTE FOR CANCER RESEARCH [CH/US]; 605 Third Avenue, New York, NY 10158 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): OLD, Lloyd, J. [US/US]; 1345 Avenue of the Americas, New York, NY 10105 (US). SCANLAN, Matthew, J. [US/US]; 1275 York Avenue, New York, NY 10021 (US). STOCKERT, Elisabeth [US/US]; 1275 York Avenue, New York, NY 10021 (US). GURE, Ali [US/US]; 1275 York Avenue, New York, NY 10021 (US). CHEN, Yao-Tseng [-/US]; The New York Hospital-Cornell Medical Center, Dept. of Pathology, 525 East 68th Street, New York, NY 10021 (US). GOUT, Ivan</p>			08/896,164	17 July 1997 (17.07.97)	US	60/061,599	10 October 1997 (10.10.97)	US	60/061,765	10 October 1997 (10.10.97)	US	08/948,705	10 October 1997 (10.10.97)	US	9721697.2	11 October 1997 (11.10.97)	GB	09/102,322	22 June 1998 (22.06.98)	US									
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<p>(57) Abstract</p> <p>Various molecules associated with cancer are disclosed. The invention also discloses diagnostic and therapeutic methods based upon these molecules.</p>																													

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CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

Field of the Invention

The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with breast cancer. The invention also relates to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules, polypeptides coded for by such molecules and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic contexts.

Background of the Invention

The mechanism by which T cells recognize foreign materials has been implicated in cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been described. In many instances, the antigens recognized by these clones have been characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL clones which recognize the antigen-expressing cells can be isolated and propagated. While this approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera are used to identify immunogenic protein antigens expressed in cancer cells by screening expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified have been found to have elicited a high-titer humoral immune response in the patients from which the antisera were obtained. Such a high-titer IgG response implies helper T cell recognition of the detected antigen. These tumor antigens can then be screened for the presence of MHC/HLA class I and class II motifs and reactivity with CTLs.

The invention is elaborated upon in the disclosure which follows.

Summary of the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those
5 molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of
10 conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments
15 thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be
20 used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a
25 plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such
30 combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses,

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer.

- 5 Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

15 In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1

- 20 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the presence of the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

5 In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional
10 variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer
15 associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five
20 different polypeptides, each representing a different human cancer associated antigen or functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

25 According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other
30 embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter .composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

5 The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another
10 embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated
15 nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the
isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

20 In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA
25 binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA
30 Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

5 The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a sequence of
10 contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1, (2) complements of (1), and (3) fragments of (1) and (2).

 In one embodiment the sequence of contiguous nucleotides is selected from the group
15 consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2) at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical
20 to the sequence Group 1.

 In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides
25 and every integer length therebetween.

 In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

 Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

30 According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an
5 expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the
10 isolated nucleic acid molecules the invention, described above, is provided. These include PP Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a human antibody.

The invention includes in another aspect an isolated fragment of a human cancer
15 associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length
20 to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from
25 the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

30 According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent,

which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by
5 the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected
10 host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC
15 molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to
20 render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated
25 antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the
30 step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (i) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter
5 includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a
NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the
10 complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents
which bind thereto, and so on in the preparation of medicaments. A particular medicament is for
15 treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal
cancer, colon cancer, prostate cancer or gastric cancer.

Detailed Description of the Invention

In the above summary and in the ensuing description, lists of sequences are provided.
20 The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the
25 sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the
30 coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not known that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

"Nucleic Acid Sequences"

NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

5 (d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by a an autologous antibody or lymphocyte.

10

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor,

15 (b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

20 NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human
25 breast cancer associated antigen precursor.

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

30 NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

5 NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

10 NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

15

NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

20 NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

25 NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

30

Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

PP Group 2. Polypeptides encoded by NA Group 2

PP Group 3. Polypeptides encoded by NA Group 3.

PP Group 4. Polypeptides encoded by NA Group 4.

PP Group 5. Polypeptides encoded by NA Group 5.

5 PP Group 6. Polypeptides encoded by NA Group 6.

PP Group 7. Polypeptides encoded by NA Group 7.

PP Group 8. Polypeptides encoded by NA Group 8.

PP Group 9. Polypeptides encoded by NA Group 9.

PP Group 10. Polypeptides encoded by NA Group 10.

10 PP Group 11. Polypeptides encoded by NA Group 11.

PP Group 12. Polypeptides encoded by NA Group 12.

PP Group 13. Polypeptides encoded by NA Group 13.

PP Group 14. Polypeptides encoded by NA Group 14.

PP Group 15. Polypeptides encoded by NA Group 15.

15 PP Group 16. Polypeptides encoded by NA Group 16.

PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH₂PO₄(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

30 There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to

manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by
5 isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide
10 identity and/or at least 65% amino acid identity and in still other instances will share at least 60% nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (<ftp://ncbi.nlm.nih.gov/pub/>). Exemplary tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov>. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained
15 using the MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect
20 the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences
25 presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs:[31, 33 and 34], which were found to react with allogeneic breast
30 cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674.

- 5 The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of
10 diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of
15 diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those,
20 which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

- The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of
25 encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA,
30 CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique.

Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all

that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.,* Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generate individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990). for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient (for examples of this, see the Examples below).

Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

Immunol. 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

5 In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the
10 vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a
15 cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

20 As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of
25 one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby,
30 inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions.

Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5'-end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

5 In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which
10 (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters,

15 alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamides, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other
20 than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding
25 breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense
30 oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term

"pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a "vector" may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g., β -galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be "operably" joined

when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as

a-TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 α , which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and partial

proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed
5 recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune
recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

10 A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others
15 will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or
20 fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family
25 members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated
30 antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant

polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino

acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c)

K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amato and Drijfhout (D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described

elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant

negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) *The Experimental Foundations of Modern Immunology* Wiley & Sons, Inc., New York; Roitt, I. (1991) *Essential Immunology*, 7th Ed., Blackwell Scientific Publications, Oxford). The

pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')₂ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for F(ab')₂, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

human or non-human sequences; chimeric F(ab')₂ fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer

associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- α , lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34⁺ hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the
10 immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by a
15 subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International
20 Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are
25 other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL
30 clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of β_2 -

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio of 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The
5 tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-
10 1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

15 The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences; in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing
20 screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the
25 invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies
30 this approach, showing the use of transfected cells expressing HPV E7 peptides in a therapeutic

regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. Immunol.*, 154:5637-5648 (1995). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., *J Immunol*, 139:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations.

The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory

5 interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory
10 interaction, Fenton et al., *J. Immunother*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS,
15 Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to
20 enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

25 A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding
30 partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these
5 prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include
keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The
10 expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of
15 nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346, and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and
20 returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and
25 targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of
30 viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 71:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene

5 Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the
10 surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-CaPO₄ precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic
15 acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or
20 incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule.

Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate
25 uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art.

Such systems even permit oral delivery of nucleic acids.

30 When administered, the therapeutic compositions of the present invention can be

administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

5 The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of skill in the art. Generally, such systems should utilize components which will not significantly
10 impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue
15 experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

20 The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to
25 diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and
30 weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100 μ g, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen or variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response.

Adjuvants may enhance the immunological response by providing a reservoir of antigen

(extracellularly or within macrophages), activating macrophages and stimulating specific sets of

lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants

include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after

purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins

including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria*

extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17,

QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete

Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils

such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the

invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986).

Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term

"pharmaceutically acceptable" means a non-toxic material that does not interfere with the

effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-
5 acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-
10 acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or
15 inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

20 The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and
25 may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

30 Compositions suitable for oral administration may be presented as discrete units, such as

capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

Examples

Example 1: Preparation of breast cancer cDNA expression libraries

Step 1: Purification of total RNA from tumors.

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

Step 2: Purification of mRNA.

A Dynabeads mRNA isolation kit (Dyna, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

Step 3: cDNA synthesis.

cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTTTT-Xba 1 site

Step 4: Ligation into the TriplEx vector arms.

The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

Step 6: Titering and amplification of generated libraries was performed according to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene)

according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	1.8×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	3.5×10^6 pfu	Invasive Ductal Carcinoma, Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	2.3×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	1.1×10^6 pfu	Invasive Ductal Carcinoma, Grade II
HBR257	2.5×10^6 pfu	Invasive Ductal Carcinoma, Grade II
HBR297	4.0×10^6 pfu	Ductal Carcinoma, Grade II
HBR248	1.0×10^6 pfu	Invasive Ductal Carcinoma with Vascular Permeation, Grade III

HBR271	2.5×10^6 pfu	Medullary Carcinoma
HBR263	10.0×10^6 pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No
5 serum-positive clones were found by screening HBR271 library.

Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at -70°C prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH
10 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDM) and stored at 4°C . Library screening was performed as described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of 4×10^3
15 10^3 per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at 37°C . Membranes were then blocked with 5% NFDM. As an alternative to the generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3'-
20 diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium
25 chloride/5-bromo-4-chloro-3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of 5×10^5 recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

Example 3: DNA Sequencing

- 5 Phage cDNA clones were converted to pBKCMV phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer) automated DNA sequencer. The sequences of the clones were compared with sequences in
- 10 GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
LONY-Br-1	L34543	LONY-Br-23	AA262134; U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

The mRNA expression pattern of selected cDNA clones was determined by RT-PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 µg poly A⁺ RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed ³²P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen-Clone mRNA sizes

5	Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
	LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
	LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
	LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
	LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
10	LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
	LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
	LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
	LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
	LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
15	LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
	LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
	LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
	LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
	LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
20	LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
	LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

Example 6: Isolation of gastric and prostate clones

A stomach cancer cDNA library was established, using standard techniques, then the library
 25 was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium
 thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7
 30 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by
 passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of 2.5×10^6 , 1.1×10^6 , and 1.7×10^6 cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C . A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of human antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'-diamino benzidine tetrachloride, and 0.015% H_2O_2 , in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C . The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02% Na_3N . The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five times. The samples were then diluted to 50 ml, and kept at -80°C , until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to compare signals to each other. All were positive. Table 5, which follows, summarizes some of this

work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOS:627-634 (gelsolin, zinc finger protein family, variant zinc finger-motif protein goliath and homeodomain proteins); have not been identified in humans previously, although there are related molecules found in other species. Finally, with reference to Table 5, the last four moieties, i.e., prepro- α collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642. The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOS:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

Example 7: Isolation and analysis of colon clones

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus obtained was then purified to isolate all poly A⁺ RNA, using commercially available products designed for this purpose.

The poly A⁺ RNA was then converted into cDNA, and ligated into λ ZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples.

A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g., Ace et al, Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into λZAP. All libraries were amplified, prior to immunoscreening.

Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had *E. coli* Y1090 lysates coupled thereto, and then lysates from bacteriophage infected *E. coli* BNN97 lysates. Final serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of 4×10^3 phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described *supra*. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. The positive clones were then rescreened, using allogeneic serum, following the same method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-). Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ-ID NO: 544/545 (NY-CO-8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as well as other sequences identified via the preceding examples was determined. To do this, RT-PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

5 In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

10 Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA⁺ RNA were analyzed from these samples, using random, ³²P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 15 68°C, for 30 minutes each time.

SEQ ID NOS:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554 (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found 20 in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

25 The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

30 It is reported above that fourteen clones reacted with subsets of serum from both normal

and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophilins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosomal protein. The molecule set forth in SEQ ID NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with *Drosophila* homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

5	SEQ ID NO:	Normal Sera Reactivity	Tumor Sera Reactivity
	580	2/16	2/16
	582	2/16	3/16
10	584	2/16	2/16
	586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

15

Table 8: RT-PCR analysis of colon SEREX clones

	normal tissue	SEQ ID NO.:550	SEQ ID NO.:552	SEQ ID NO.:558	SEQ ID NO.:560
20	kidney	+	Negative	Negative	Negative
	colon	+	Negative	Negative	Negative
	small		Negative	Negative	Negative
	intest.	+	Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
25	stomach	+	Negative	Negative	Negative
	testis	+	Negative	Negative	Negative
	pancreas	+	Negative	Negative	Negative
	lung	+	Negative	Negative	Negative
	liver	+	Negative	Negative	Negative
30	heart	+	Negative	Negative	Negative
	fetal		Negative	Negative	Negative
	brain	+	Negative	Negative	Negative
	mammary		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
35	bladder	+	Negative	Negative	Negative
	adrenal		Negative	Negative	Negative
	gland	+	Negative	Negative	Negative
	uterus	Negative	Negative	Negative	Negative
	skeletal		Negative	Negative	Negative
40	muscle	Negative	Negative	Negative	Negative
	PBL	Negative	Negative	Negative	Negative
	placenta	Negative	Negative	Negative	Negative

	spleen	Negative	Negative	Negative	Negative
	thymus	Negative	Negative	Negative	Negative
	esophagus	Negative	Negative	Negative	Negative
	<u>Tumor Tissue</u>				
5-	renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
	colon primary tumors (10)	+ (10/10)	+ (10/10)	+(10/10)	Negative
10	colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
	breast cancer (6)	+ (3/6)	Negative	Negative	Negative
15	lung cancer (6)	+ (6/6)	Negative	Negative	Negative
	gastric cancer (1)	+	+	+	Not tested
	<u>colon cancer cell lines</u>				
	colo 205	+	+	+	Negative
	HT29	+	+	Negative	Negative
20	HCT15	Negative	Negative	Negative	Negative

Example 8: Isolation and analysis of additional clones

For the establishment of a cDNA library from human tissue total RNA was obtained from 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above. The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into λ ZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library resulted in 1.8×10^6 recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was 10^{11} plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.

In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic λ phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

5 *E. coli* bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of $OD_{600} = 1.0$, the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

10 A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with 10^6 λ ZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

15 To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in
20 accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of $4-5 \times 10^3$ plaque forming units (pfu) per plate in LB-medium with
25 isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk
30 power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made it possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of 1.8×10^6 recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by in vivo excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the λ ZAPII phage vectors and used for the transfection of *E. coli* SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J. *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad. Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as clone HOM-RCC-313). The Northern blot analysis demonstrated that the mRNA of clone HOM-

RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above, allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme *EcoRI*, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into *E. coli* of strain BL21 as described (Spindler et al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with *E. coli* and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum. Reactivity was detected at dilutions of 1: >100,000.

Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of 8×10^5 clones were screened with autologous serum, and 4.5×10^3 clones were screened with three different allogeneic sera. Twenty three clones, representing seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocellular carcinoma libraries were studied in the same way, a total of 1.5×10^6 clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galactin-9 was expressed only in a small, subpopulation of dendritic cells.

Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microtubules. It was found that both restin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microtubule systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 of 5 meningioma tumor samples were found to express the gene.

Example 9: Isolation and analysis of lung cancer clones

A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a λ ZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci USA*. 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc γ secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an ^{32}P -labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5' end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Dracopoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5 μl RT product in a final volume of 25 μl , with 2 μCi of $\alpha^{32}\text{P}$ -dCTP (~3000 Ci/mmol, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1 μl of the mixture was diluted with 5 μl of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

5 Identification of Immunoreactive cDNA clones

A cDNA expression library of 1.42×10^7 primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and 8×10^5 phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A. Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-binding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpolished). Ubiquitously expressed.
NY-LU-3	Annexin 1X [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin 1X are found in multiple autoimmune diseases. ubiquitously expressed.

NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retina, multiple sclerosis, etc.
NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding arsa component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.

et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identify with reported expressed sequence tags (EST), likely representing cDNA products derived from the same genes. These ESTs were derived from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

NY-LU-12 is on TSG locus of chromosome 3p21.

The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the TSG locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res.* 56: 2487-92 (1996)]). Our analysis of LUCA15 revealed the presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res.* 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies.

The predominant cDNA form (SEQ ID No:707), excluding the poly A tail, is of 3591bp in length.

5 An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

Comparison with the g16 sequence verified that these two are identical genes and mapped NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the
10 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the
15 two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the
20 longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

Additional cDNA variants of NY-LU-12

25 In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

30 Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D).

Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

Features of NY-LU-12 and its putative gene product

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs, rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3' end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), LU15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition.

This possibility was explored using DNA sequencing and single-strand-conformational polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous normal lung tissue, and no mutations were found when compared to Lu15-251.

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of SSCP analysis is shown in Fig. 5.

Serological response to NY-LU-12 in lung cancer patient

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

Example 10: Expression analysis of additional cancer associated nucleic acids

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only in testis, which was then investigated by RT-PCR analysis as described above.

The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone-1 Testis; GenBank accession number M60094) was identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

H1R1: GCTTCGTGTAGATTTAGGAATC (bp 344-366 of H1T)

Table 10: RT-PCR analysis

	<u>Normal Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	mammary gland	-	-
	liver	-	-
15	small intestine	-	-
	brain	-	+/- (very weak)
	lung	-	-
	fetal brain	-	-
	placenta	+	+
20	kidney	-	-
	skeletal muscle	-	-
	pancreas	-	-
	adrenal gland	-	-
	heart	-	-
25	thymus	-	-
	uterus	-	-
	prostate	-	+/- (very weak)
	spleen	-	-
	Testis	+	+

	<u>Tumor Tissue</u>	<u>BRDT</u>	<u>H1T</u>
	Colon	0/6	0/6
35	Breast	0/6	6/6+
	Melanoma	0/12	3/12+
	Lung	8/26+	4/26+
	Renal	0/2	0/2
	Ovary	0/2	0/2
40	Esophageal	0/1	0/1

Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was expressed only in normal testis and possibly in placenta. The expression analysis of H1T revealed that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples expressed H1T. H1T was expressed in normal testis and possibly in placenta and brain.

Example 11: allogeneic serotyping

To confirm the cancer associated expression of SEREX clones, allogenic sera screening of gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a control for expression of the clones in non-gastric cancer. The screening procedure used was as described above for the SEREX screening, except for the absorption of anti-bacterial and anti-bacteriophage antibodies. The modifications were as follows.

Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep Chromatography Column, Hercules, CA, USA) containing 0.5 ml Sepharose-4B cross linked to E. coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc, Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and bacteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic typing, an equal numbers of positive phage and negative phage were mixed and plated and processed by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients

Sequence		Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
Gene/Clone	Number			
RPB-J H-2K binding factor		SM1	6/12	6/16
5 Telomeric repeat binding protein		SM1	1/12	0/16
Ser/Thr protein kinase		SM1	1/12	0/16
SRY interacting protein-1		SM1	2/12	1/16
10 Sterol carrier protein X		SM1	2/12	0/16
Archain		SM1	1/12	1/16
HEM-1		SM1	2/12	1/16
Id-1 helix-loop-helix protein		SM1	1/12	0/16
15 helix-loop-helix transcription factor		SM1	1/12	0/16
Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
20 M phase phosphoprotein I		SM1,SS1	8/12	5/16
Lysal tRNA synthase		SM1	1/12	0/16
Gelsolin		SM1	4/12	0/16
Zinc finger protein		SM1	1/12	1/16
Goliath		SM1	2/12	1/16
25 zhx-1		SM1	1/12	1/16
SG24		SM1,SS1, KM	5/12	0/16
SG132		SM1	3/12	0/16
S553		SM1	7/12	7/16
S134		SM1	3/12	0/16
30 S328		SM1	2/12	1/16
S365		SM1, KM	2/12	0/16

	FKBP25		KM, SS1	5/12	0/16
	Pros-27		KM, CK	3/12	1/16
	BS4		KM	1/12	1/16
	GnRH-II		KM	1/12	0/16
5	CTBP		KM	1/12	0/16
	ETF		KM	3/12	1/16
	KIAA0438		KM	1/12	5/16
	KIAA0367		KM	4/12	3/16
	APK1		KM	2/12	0/16
10	IPP		KM	1/12	0/16
	Tropomyosin		KM	1/12	0/16
	p63		KM	1/12	0/16
	KIAA0181		KM	1/12	0/16
	KIAA0349		KM	1/12	0/16
15	RPB1		KM	5/12	9/15
	PPIM		KM	1/12	-
	EB virus		KM	3/12	-
	G.KM073		KM	6/12	-
	G.KM403		KM	1/12	-
20	KM192		KM	1/12	-
	KM294		KM	1/12	-
	KM362		KM	1/12	-
	KM031		KM	1/12	-
	KM081		KM	3/12	-
25	KM201		KM	1/12	-
	KM1496		KM	1/12	-
	KM334		KM	1/12	-
	KM313		KM	1/12	-
	E-cad/Y		CK	1/12	0/16
30	IPBP		SS1	1/4	-
	OS-9		SS1	1/4	-

Kinesin light chain		SS1	1/4	-
---------------------	--	-----	-----	---

The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

10 **Example 12: Preparation of recombinant cancer associated antigens**

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

Example 13: Preparation of antibodies to cancer associated antigens

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

Example 14: Expression of cancer associated antigens in cancers of similar and different origin.

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

Example 15: HLA typing of patients positive for cancer associated antigen

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

5

Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in

10 Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (see, e.g., Parker et al., *J. Immunol.* 152:163, 1994; D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpennig (PCT/US96/03182)).

20 The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

30 Table 12: Identification of HLA binding peptides in lung SEREX clones

		amino acids of	
HLA	peptide	NY-LU-12 protein	SEQ ID NO
5	A1 NVEE-HSFSY	67 - 75	713
	PVDP-NILDY	287 - 295	714
	DTDY-RSMEY	398 - 406	715
10	A2 SLLE-DAIGC	506 - 514	716
	TLMI-QDKEV	521 - 529	717
	YVSSLDWFYC	533 - 542	718
	VIVEVLEPYV	671 - 680	719
	KLTD-WNKLA	948 - 956	720
	QLSDLHKQNL	975 - 984	721
	KQSEQELAYL	991 - 1000	722
	KLVDKEDIDT	1042 - 1051	723
15	VMFA-RYKEL	1114 - 1122	724
20	A3 QMFG-YGQSK	417 - 425	725
	GMPVKNLQLK	481 - 490	726
	GLPE-EEEIK	823 - 831	727
	LLCRRQFPNK	958 - 967	728
25	A24 EYRD-VDHRL	405 - 413	729
	GYVC-VEFSL	499 - 507	730
	DYGY-VCVEF	497 - 505	731
	WYCKRCKANI	540 - 549	732
	TYPQPQKTSI	574 - 583	733
	IYRSTPPEVI	663 - 672	734
	HYYQ-GKKYF	754 - 762	735
	VYVP-QDPGL	816 - 824	736
30	B7 WNRDYPPPPL	26 - 35	737
	MPPV-DPNIL	285 - 293	738
	TARD-AQRDL	432 - 440	739
	GPSEEKPSRL	448 - 457	740
	TPPEVIVEVL	667 - 676	741
	RVMFARYKEL	1113 - 1122	742
40	B44 REMG-SCMEF	272 - 280	743
	EEQSSDAGLF	376 - 385	744
	KEYN-TGYDY	490 - 498	745
	TEAKQELITY	566 - 575	746
	VEALRVVKIL	710 - 719	747
	GEYG-GDSYD	906 - 914	748
	LERREREGKF	1000 - 1009	749

B52	RQDGESKTIM	650 - 659	750
	TPPEVIVEVL	667 - 676	751
	YGFIDLD SHV	701 - 710	752
	RQFP-NKEVL	962 - 970	753

5

NY-LU-12B (variant B)

10	A1	NVEE-HSFSY	121 - 129	754
		PVDP-NILDY	341 - 349	755
		DTDY-RSMEY	452 - 460	756

	A2	WQSA-RFYYL	41 - 49	757
		SLLE-DAIGC	560 - 568	758
15		TLMI-QDKEV	575 - 583	759
		YVSSLDFWYC	587 - 596	760
		VIVEVLEPYV	725 - 734	761
		KLTD-WNKLA	1002 - 1010	762
		QLSDLHKQNL	1029 - 1038	763
20		KQSEQELAYL	1045 - 1054	764
		KLVDKEDIDT	1096 - 1105	765
		VMFA-RYKEL	1168 - 1176	766

25	A3	QMFG-YGQSK	471 - 479	767
		GMPVKNLQLK	535 - 544	768
		GLPE-BEEIK	877 - 885	769
		LLCRRQFPNK	1012 - 1021	770

30	A24	YYLN-ATDVL	47 - 55	771
		FYYLNATDVL	46 - 55	772
		EYRD-VDHRL	459 - 467	773
		GYVC-VEFSL	553 - 561	774
		DYGY-VCVEF	551 - 559	775
		WYCKRCKANI	594 - 603	776
35		TYPQPQKTSI	628 - 637	777
		IYRSTPPEVI	717 - 726	778
		HYYQ-GKKYF	808 - 816	779
		VYVP-QDPGL	870 - 878	780

40	B7	WNRDYPPPPL	80 - 89	781
		MPPV-DPNIL	339 - 347	782
		TARD-AQRDL	486 - 494	783
		GPSEEKPSRL	502 - 511	784
		TPPEVIVEVL	721 - 730	785
45		RVMFARYKEL	1167 - 1176	786

5	B44	SEAWSSNEKF	59 - 68	787
		REMG-SCMEF	326 - 334	788
		EEQSSDAGLF	430 - 439	789
		KEYN-TGYDY	544 - 552	790
		TEAKQELITY	620 - 629	791
		VEALRVVKIL	764 - 773	792
		GEYG-GDSY	960 - 968	793
10		LERREREGKF	1054 - 1063	794
	B52	RQDGESKTIM	704 - 713	795
		TPPEVIVEVL	721 - 730	796
		YGFIDLDSHV	755 - 764	797
		RQFP-NKEVL	1016 - 1024	798

15 Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen

20 To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching

25 the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (see, e.g., Knuth et al., *Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230,

30 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by ⁵¹Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or ⁵¹Cr release as above.

5 Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

10 A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

15

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

20

All references disclosed herein are incorporated by reference in their entirety.

We claim:

TABLE 1

SEQ ID NO. 1:

5 U72994, AC004022, Z68323, AE001160, L34078, AF064863, AC002132, U60440, X66494, N21242, AA678312, W86762, R01605, AA782843, AA275156, W41927, AA874648, AA571241, AA562747, W10480, AA451301, AA866631, AA466667, AA999057, AI029140.

10 SEQ ID NO. 2:

AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648, AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648.

15

SEQ ID NO. 3:

X98371, AL009008, L31790, Z83220, X92946, AC003975, AF008916, U80460, X75544, X66732, X95275, X52177, X07976, AC004451, Z74307, AB000878, AL009179, AF038667, 20 Z78544, Z48008, U23486, J05096, AB000882, Z30213, L11593, U18530, L27325, AC005191, M99579, AA130270, AA158245, AA903098, AI018453, AA436455, AA980593, AA172479, AA637487, AA116588, AA426854, AA050404, AA390025, AI006618, AI048382, C85944, AA673480, AI006510, AA823338, AA413694, W35075, AA015033, AA413584, W29693, AA637069, AA619839, AA125149, AA039004, AA674696, AA871138, AA414747, 25 AA198099, C91478, F071359, AA925957, AA820054, H16496, AI043756, AA892435, AA893551, AA818669, AA892785, AA944026, D33919, N96570, F19798, AI045451, AA800662, D65187, AA944025, AA925731, AA892314, AA945449.

30 SEQ ID NO. 4:

AA900930, AA925665.

35 SEQ ID NO. 5:

U58105, Z81485, Z54236, Z48584, U61375, M55267, M59856, X51942, U77302, Z48621, AF032455, Z11866, AB013392, L32792, AA871997, AA084083, AA130829, AA083063, AA666290, N38894, D54459, T28921, AA806015, AA512059, AI043087, AI042894, 40 AA968324, AA238493, AA237462, AI042885, AI046424, AI035670, AA269430, AA250621, AI035540, AA260613, AA106870, AA238658, AA106134, AI042683, AA105958, AA144007, AA986558, AA457910, AA389400, AA673056, AA153254, AA754678, AI021109, AA390813, C36687, T41571, AI011183, AI013356, AI011739, AI030260, AA924384, C44421.

45

SEQ ID NO. 6:

AF036717, U91327, AF036718, U56248, Z48795, Z99290, M30697, U58204, M24417, AF022983, M33581, AC004619, H64641, AA477478, AA369676, AA088359, AA057574,

- AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527, AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204, AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395, AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787, 5 AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

SEQ ID NO. 7:

- 10 X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750, X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008, D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337, X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880, AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916, 15 AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461, AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410, AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615, AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

20

SEQ ID NO. 8:

- U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506, M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054, 25 AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309, AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611, AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258, AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075, N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161, 30 AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148, AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792, AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516, AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779, AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483, 35 C64685, AA851367, C91730, AA143899, T23399.

SEQ ID NO. 9:

- 40 AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241, AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846, AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802, AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761, C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390, 45 AA848674, AA924440, T15031, AA451569, H35524.

SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

5

SEQ ID NO. 11:

AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647, 10 AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274, 15 AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, A175818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956, 20 AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

U72994, AC004022, AF043493, U43252, U43251, U81830, U58105, U68242, Z93242, AL009029, M29872, U12980, M81118, M30471, Z56258, AF012943, AC004080, AC002563, AF024533, AF002991, Z63771, AP000042, AF064863, U80017, AC004087, Z55235, L05920, AA508139, N90748, AA450240, AA948158, AA828938, AA165115, AI003312, AA436633, AA419100, AA743442, AA961990, AA885286, AA861312, T84801, AI040166, AA494115, 30 AA652324, AA181105, AA095541, R59256, AA503712, AA700364, AA603821, T60326, AA779097, AI023884, AA603785, H79111, W39526, AA506607, W94361, N66078, R01605, H22694, W86762, W99303, AA745640, AA678312, AA431870, W41927, AA874648, C92734, C23102, C53080, C91168, D65098, C32959, C50029, M80125, C34452, C83862, C24659, T21473, AA874720, C06696, W43071, AI043300, C53907. 35

SEQ ID NO. 13:

X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051, 40 X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713, 45 H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619,
 5 Z45284, H14105, R84666, AA090321, AA350108, W52840, R48497, R13097, T66255,
 W44467, AA247676, AA198489, AA388175, AA261453, AA237111, AA790730, AA162394,
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10 SEQ ID NO. 15:

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25 SEQ ID NO. 16:

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40 SEQ ID NO. 17:

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SEQ ID NO. 19:

- AE000500, AF030178, X66784, Z49405, M69106, M27174, X55037, AF004104, X78560, U51281, L17405, M10122, AC003106, X55122, X05553, AC002368, AF004101, U77066, U77456, X58072, AA481578, AA280143, AA481271, AA280144, AA736516, AA780050, AA359089, R82883, AA355987, AA571000, AA563168, AA738653, AA620225, AA855746, AA572293, AA530645, W40812, AA690944, AA839456, X61848, AA525648, AA944854,

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SEQ ID NO. 21:

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SEQ ID NO. 22:

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SEQ ID NO. 25:

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SEQ ID NO. 26:

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SEQ ID NO. 27:

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35 SEQ ID NO. 28:

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5 SEQ ID NO. 29:

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SEQ ID NO. 101:

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SEQ ID NO. 103:

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SEQ ID NO. 109:

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SEQ ID NO. 119:

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SEQ ID NO. 121:

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SEQ ID NO. 125:

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SEQ ID NO. 127:

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SEQ ID NO. 131:

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SEQ ID NO. 135:

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SEQ ID NO. 137:

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SEQ ID NO. 139:

40 M24603, X02596, Y00661, M15025, X06418, U07000, X52829, M19730, M30829, X52831, M30832, X14676, X52828, X52830, S72479, L02935, M64437, M17542, L19704, U01147, X07537, X14677, X14675, M17541, M17543, M19695, X76485, AF023460, X89600, U19759, AF039083, X71790, AC004679, AC002076, AF035456, M99565, Z72005, Z79997, AL021154, 45 Z98259, AC003108, L13706, AF018254, M69197, U67228, Z75887, U14661, M84472, AC005200, AC001228, AC004761, Z95124, AC002540, Z79699, AE000926, U43572, U51281, D82351, AB013379, U34879, AC002425, AC004598, AA338585, AA333142, AA126116, H55543, H55721, R54267, H55614, H55699, H55545, AA744741, AA772917, H29052, AA573543, T16608, AA773472, AA775416, AA601919, AA470534, AA351521,

AI015318, AA351163, AA486365, AA470985, AA565376, AA344993, R92629, AA553555, AA740903,

AA090392, H94289, AA457592, AI033503, T69709, R94066, AA040853, AA065296,

AA349058, AA703759, T05287, H86075, AA043080, AA669995, AA737864, AA726753,

5 AA727154, AA546638, AA222375, AA671227, AA032828, W14856, W33789, AA874531, AA982359, AA965843, AA965737, AA800560, AI035042, AA941796, AA390686, AA735566, AA802030, C74658, AA246925, AA803435, C27952, AA944566, AA817514, C83561, AA978443, C24959, C82705, C72516, H34014, AA712916, AA820781, D21893, D15866.

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SEQ ID NO. 141:

S45630, AF007162, X95383, AF029793, M55534, X60351, S77138, S77142, S74229, X60352,

M63170, M24906, M28638, J03849, M12016, M73741, U04320, M12014, M24092, L08078,

15 S53164, U26661, M12015, M25770, U16124, X87114, D29960, X14789, X85205, M17247, U05569, U66584, M26142, U47921, U47922, V01219, X95382, AP000007, AE000869, AB009529, AF062537, D10457, S37449, X59541, AA742442, AA704135, AA211774, N35834, AA482745, AA211607, N28898.

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SEQ ID NO. 143:

U78082, L78810, U14573, AC004068, U07561, M98511, AC004673, AA613346, AA953216, AA305926, H92800, R98218, AA629543, AA297666, AA302982, AA429481, AA126005,

25 AA837225, AA856961, AA946848, F13749, AA847704, AA833896, AA621381, AA833875, AA459962, H22141, N73060, AA491955, H28477, AA224463, AA708753, AA152253, AI028510, AA483606, AA992126, T54783, AA715075, AA568204, AA715173, N64587, AA570740, AA984258, AA904211, H94979, AA085410, AA599352, AA488620, AA574442, AI049845, AA593471, AA393830, AA610509, AA297145, AA113272, AA835889, AA655005,

30 AA689351, R93919, AA613761, AA550989, AA303054, H07953, AA713815, AA827490, AA865262, AA461308, H73550, AA657835, AA362349, H82679, AA378682, AA577755, AA663472, AA490602, AA857673, AA347114, AI049630, AA086150, AI017251, AA877992, AA084609, AI050760, AA808998, AA503258, AA613138, AA603156, AA513293, R97934, AA610233, AA654874, AA501867, AA604831, N22058, AA492114, T50676, AA757426,

35 AA584482, AA789192, AI004591, T50694, AA862227, AA594145, AA728911, AA847499, AA159978, AA534204.

SEQ ID NO. 145:

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Z69030, L42375, U37352, D26445, U38192, U38191, U37770, U38190, U37353, U59418, L76702.

45 SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873, L07874.

SEQ ID NO. 149:

U07158, X85784, AJ000541, U76832, L20821, AC003089, AC004504, AF049236, L40609, AF053765, L14677, Z94056, Z18277, AE001073, U85969, X79283, AJ223473, AA632339, AA732931, AA610556, AA973899, AA598896, AA531553, AA826535, AI000209, AA290836, AA642711, AA085920, W22275, D20744, UMGS017, AA487868, AA487869, AA085919, 682 AA833281, AA619252, C77541, AA691960, AA763615, AA164051, AA259589, AA060475, AA254185, AA666705, AA272597, AA152985, AI011416, AA850008, H33152, AA941811.

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SEQ ID NO. 151:

M13451, X03445, X03444, M13452, X66870, X76297, X14170, X99257, D14850, D13181, L12399.

15

SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

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SEQ ID NO. 155:

X54859, Z86000, AC003043, X77738, X77737, L35930, AC003084, AC000111, M89651, AP000031, U67588, X03991, AC004660, AL010261, V01515, M86251, L29376, Z71417, L78442, U00921, AC004692, AC003698, AE000742, Z49128, Z73417, Z71418, AA424638, AA442084, AA805748, AA835489, AA713576, AA502343, AA765949, AA812332, AA831755, AA417718, AA776946, AA152295, AA731660, R48791, AA150237, N51650, N52616, N52586, AA533556, AA305755, AA760877, AA729913, AA731659, AA910594, AA904521, AA372550, R48898, N50390, R08712, H83343, AA417867, AA090407, AA009846, AA927286, AA678135, AI033148, AI041408, AA235113, AA398662, M62215, W27276, AA885767, AA460155, AA742433, R19908, AA040696, AA555240, AA043160, AA292844, R53160, AA536080, N70013, N35921, N70096, AA277029, AA560610, AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892, C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855, AI021808, AI009216, D68214, AA220863, D70434.

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SEQ ID NO. 157:

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U43195, U58512, U61266, D89493, U36909.

SEQ ID NO. 159:

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AF069442, AF001295, M13820, M10081, AB010077, AA491075, AA446881, AA588390, AA479958, N20112, R86178, R97894, T64868, W68074, AA365195, AA928749, AI037069, AA882303, AA791693, AA822133, AI037224, AA404165, AI036575, AA499662, AA864136, AA561223, AA183703, AA647218, AA792208, W48100, D40621, AJ225487, AA294595,

02866, H35041, AA944944, AA597316, D26977, D68334, AA685934, W88345, AA964819.

SEQ ID NO. 161:

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K01546, AE000468, X95549, AC004014, Z81584, L19201, X94244, X06932, U39479, X13301, AC000386, U80847, X86737, U39478, AA883211, AA610050, AA774254, AA280736, AA926725, AA459300, N55370, AA233666, H90342, T66839, H91250, AA856968, R92873, AI034196, AI014787, AA910410, AA088535, AA230765, AA467238, 10 AA397279, AA420226, AA396042, AA200070, AA165873, AA762534, AA067133, AA065429, AA185092, AA572057, AA111387, AA175824, AA881071, AA571692, AA104279, AA733670, AI008804, D86670, C67200, D41938, AA141467, D35894, AI001643, AA957220, T37355, T18792, D47809, W21723, AA898504, AA951903, AA661025, AA949796, AA990685, AA661449, AA948837, R04787, D16046, AA439636, AA246769, 15 AA978829, D43523, T02021, AA803212, D22651, AA201227, AA694728, AA891643, D23309, AA820831, D41871, W21774, D16065.

SEQ ID NO. 163:

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X15183, AF028832, D87666, J04633, L33676, X07270, U94395, M27024, M30627, X16857, X07265, M36830, M30626, AA669137, AA725103, AA890496, AA314095, AA554815, AA313331, AA730100, AA214035, AA876412, AA121630, AA314010, AA927532, AA968674, AA679253, N66271, AA558907, AA309988, AA587079, AA075436, AA160964, 25 AA205657, AA214083, AA130903, AA917032, AA149623, AA857523, AA889843, AA305037, AA491055, W73240, AA255644, W73295, AA765431, AA178947, N66409, AA074895, AA306976, AA075052, AA075387, AA130892, AA857443, AA405942, AA629891, AA152004, AA129550, W56527, AA513807, AA703828, AA223171, C75280, AA889155, AA854676, AA773063, AA774999, AA152392, AA307057, AA316954, AA657352, AA522607, AA188113, AA026444, AI003623, AA312717, AA312400, T64299, 30 AA178992, AA228992, AI042136, AA457613, AI032857, AA164461, AA625127, AA807763, AA130815, AA054695, AA937097, W93534, N67875, AA526896, W52802, AA527942, N34251, W28646, AA668543, AA496091, W52511, AA070581, AA306826, AA120908, AA699607, AA086423, N72134, AA630369, AA564649, AA046806, AA666249, AA306893, 35 AA225404, AA127417, AA854951.

SEQ ID NO. 165:

40 M23885, AF047868, AF017732, AB005249, Z83229, AF026483, U97194, Z67884, Z67881, X13481, X07651, AC001226, AC002542, AB002307, AA984684, AA017533, AA306600, AA261957, F08123, R17885, AA282208, H85861, H85836, AA593150, H87276, AA057384, AA243602, AA013399, AA374926, AA721341, R88896, AA021538, AA101740, AA375314, AA090398, H86058, AA984556, AA215816, AA092672, AA034243, AA328017, F11174, 45 AA261777, N40306, W21253, R02386, AA349225, AI038487, H98027, AA385878, AA075431, AA375596, R77638, T73214, AA310841, AA062331, AA919318, AA606883, 373 AA174568, AA790426, AA423321, AA647673, AA109549, AA396473, W16215, AA105538, AA061105, AA066766, AA462773, AA555644, AA499452, AA389523, AA245036, AA475340, AA880992, AA198965, W11981, AA509705, AA237414, AA646230, AA673569,

AA239037, AA672620, AA915168, AA863498, AA123378.

SEQ ID NO. 167:

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Y11251, AF030234, AF043945, L40407.

SEQ ID NO. 169:

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U33822, X61838, AA572230, AA589570, AA929790, AA104830, C81582, AA271190, AA290278, AA543616, AI043207, AA107832, AA958460, AI020992, AA795905, AA277468, AA475069, AA111610, AA389139, AA154163.

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SEQ ID NO. 170:

D32050, D16969, AC004423, S81497.

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SEQ ID NO. 172:

D86982, L07131, M14544, AA296228, AA318436, AA296234, H88394, W26642, AF038251, AA394101, N35855, N56791, N35444, AA147382, AA647547, AA939939, AA895989, AA122437, AA277698, W75741, AI036117, AA980469, AA033178, AI006694, AA980625, AA033190, AA175922, AA172918, AA895209, AA028700, AA416048, AA175247, AA217057, AI045760, R64866, D40836, D41873, AA509279, D40089, AA114361, AA751642, AA848690, AA800525, AA802510, C24001, AA841755, AA882663, D40069, AA433358, D40199, AA958134, AA072494, AI008727, AA618978, AA848687, C21884, AA113662, AA945653, AA660093, C58446, AA908068, AA532100, AA264560, AA426658, AA097169, AA751535.

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SEQ ID NO. 174:

Z81364, AC003033, AE000665, AA570483, AA532739, AA526905, AA725306, AA134415, AA651838, AA481316, AA600310, C04532, AA004615, H20713, AA913640.

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_SEQ ID NO: 176

M14695, X02469, X60012, M14694, X01405, K03199, X60015, X60016, X60011, X60018, X60019, X60014, X60013, X60020, AF021816, X16384, L20442, U48957, U48956, X60010, S83123, X90592, U74486, D49825, X81704, X81705, U43902, AJ001022, D26608, D16460, L37107, AF060514, S77819, X13058, D86070, U50395, U07182, U90328, Y08900, M75144, Y08901, U74487, U48619, K01700, M13872, AF051368, U48616, U48618, X00741, M13874, M13873, X01237, U48617, M22887, X54156, U94788, M13115, U41451, U41452, X01236, K02110, U59757, M22895, M13118, U63714, M22888, M13116, M22894, M13117, U51857, U37120, U62133, U07020, X91793, L07907, U26741, U59758, S78456, L23634, U22145,

X00879, X00881, S77930, S78457, U66066, D63399, U44835, L07908, S57234, D63405, L27630, M22896, U07019, D63404, M13119, X13057, D63402, M75145, D63401, L12046, AA373960, H61357, AA358870, AA928725, H90357, AA302363, R94782, W24142, AA448185, AA004394, AA376121, AA151197, W76037, R82621, AA157426, AA343323, AA301677, AA002978, AA966981, AA839925, AA982800, AA030090, D77246, AA184043, AA142337, AA529242, AA874521, AA048636, AA168688, AA032325, AA881664, AA529082, AA874036, W06121, AA520602, R86591, AA848372, D37535, AA433405, C72790, AI009692, C25990, X91325, D71516.

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SEQ ID NO: 177

X71973, AC004151, L24896, X82679, AF045769, AF045768, U37427, D87896, S80257, L12743, X76009, X76008, AF035264, AC004707, AA633971, AA588533, AA992915, AA399565, AA435883, AA454856, AA877822, AA780281, AA767205, AI016009, AI038211, AA417004, AA400522, AA676416, AA526712, AA431710, AA496292, AI041168, AA451858, AA709014, AA588291, AA758304, AA188597, AA149890, AA815107, AA670145, AA026421, AA468719, R67030, AI024175, AA719171, AA708025, W15350, AA431760, AA887242, AA888171, AA769788, AA948489, N54495, AA453278, AA887529, AI014760, AA287946, AA862377, H44827, W72726, N22715, AA662838, AA187825, AA780142, N70623, AA503741, AA024544, AI023537, AA834970, AA062885, AA991970, AA576623, AA722713, AI014758, AA765436, AA633498, AA507435, C01757, N70601, AA314727, R62311, AI004483, R81700, W60860, AA621104, H51422, N33007, AA046316, H20797, R70369, AA724141, AA694532, H20024, AA627821, AA448392, H93528, AI015880, AA453376, AA977808, AA576363, AA838346, N78626, AA648742, AA305364, H20123, AA024543, AA864931, AA946666, AA417190, W73759, AA815325, AA128171, AA809918, AI039304, AA718260, AA088979, AA403403, W85396, AA222552, AA839828, AA071896, AA109679, AA470211, AA219887, AA816136, W83835, AA064566, AA606943, AA034666, AA270485, AA457957, AA571899, AA050132, AA510431, AI020265, AA590096, W97284, AA691964, W78537, W08051, AA435081, AA020097, W15024, AA008493, AA208204, W53741, AA512604, AA049396, W64741, AA756852, AA048836, AA038639, W14765, W10901, AA920385, AA791715, AA647984, AA690893, W75172, AA184727, AA036383, AA275344, AA619559, AA059803, AA575700, AA967063, W83433, AA203908, AA959416, AA222749, W15727, AA684313, AA286343, AA145935, AA137494, AA272180, AA472719, AA208001, AI006169, AA240906, D19204, AA276329, W59005, AA445679, AA510539, AA222929, AA144725, AA413110, AA268012, AA492769, AA545011, AA204126, W17735, AA516923, AA270092, AA518734, AA475396, AA108883, AA014248, AA221781, AA051598, AA667607, AA048854, AA623999, AA397087, AI006246, AA122798, AA675710, AA462388, AA606840, AA516903, AA407638, AA222968, AA064375, C25916, AA941583, C94734, AI011423, AA893085, AA964072, AA957524, AA963336, AA956783, AI014112, AA894190, C20441, AA231739, D68624, AA964536, AT000114, D22968.

SEQ ID NO: 178

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Z50194, U92983, U44088, AC003101, X72892, AF035444, M32474, AF019953, AC001228, Y15443, AF001294, U12418, X06956, M31176, AF015277, AF002708, R43556, AA088367, AA313553, H92530, AA376262, T09403, AA814143, R75643, AA479005, AA773048, AA507143, AA402127, AA430292, AI015600, AA393069, AA463606, AA885498, AA460759,

- AA398766, R48359, AA426107, AA909990, AI017459, AA076224, N39533, AI026941, AA412699, AA292828, AI024759, AI016910, AA573306, R48386, AA065307, AA774549, AI016070, AA884918, AA431512, AA306051, AA476440, AA292924, AA621059, AA411830, AA405079, AA596171, AA989987, AA472637, AA690249, AA691927, AA792720,
- 5 AA637983, AA020137, AA097337, AA117759, W17615, AA285526, AA111347, AA208823, AA879750, AA413058, W33316, AA161891, W41259, AA511152, AA027481, AA020252, AA033106, AA965045, D41048, AI031042, D48020, AA925258, D40853, AA945674, C19585, AI013412, T15040, AA541011, AA990782, AA851306, AA540938, T23386, AA783863, AA979035, AA951002, AA438957, AA979006, AA978995, AA800046, AA556128, C27411,
- 10 D15562, T20348, AA966363, AA949269, AA785774, AA728671, D16092, N37869, D48782.

SEQ ID NO: 179

- 15 Z50194, U44088, U92983, U12200, AC004147, X82200, Z81527, M63469, Z35494, AC003018, AL021408, M92281, AA576961, AA088194, AA258396, D79238, N27861, AA857168, N35619, N40634, N73008, N21585, AA332511, D56582, D12298, AA641278, Z21892, H92531, AA113084, N76094, N31261, AA227469, AI038845, AA520982, R16910, AA380178, AA238335, AA255056, AA981576, W35008, AA238181, AA739268, AA061742,
- 20 W59335, AA049688, W64993, AA900759, AI009938, AA850887, AA525635, W59849, AA660463, AA841121, N96072, AI044112, C24662, C23675, AA924228, AA841227.

SEQ ID NO: 180

- 25 D87072, U52191, L25270, L29564, L29563, D83144, U73169, AC003036, AC003049, AC004149, Z67744, AC001224, AA215514, AA262849, AA443396, H22815, AA171842, W04162, AA682330, C18753, W01583, AA837306, AA348779, AA492008, AA639340, AA194216, AA371937, AA449692, H09426, AA782728, AA991707, AA085238, AA194029,
- 30 T03226, AA867674, AA009101, AA726511, W90906, AA028401, W54470, AA266581, AA033314, W10534, AA475518, AA606629, AA616625, AA212796, AA184252, W53289, AA240033, AA238131, W98696, AA038374, AA286525, AA265063, AA212145, AA165741, AA146458, AA021970, AA870293, AA790962, AA770919, AA175098, AA080286, W87105, AA125485, AA870257, AA793909, AA673390, AA032500, AA059905, W84293, AA511672,
- 35 W97898, AA881777, AA275041, AA184232, AA178368, W65008, AA734943, AA717871, AA220560, AA184416, AA163885, AA086951, AA032510, AA014341, AA637318, AA239778, AA237322, AA213090, W82825, W70807, AA542256, AA445570, AA444522, AA656978, AA162676, AA051548, AA038373, AA032527, AA840207, AA273185, AA260228, AA051553, W56956, D89319, AI045498, D24681, AA801346, AA962980,
- 40 C71711, AA824977, D69290, AA264695, D68955, C74586, C72683, AA750613, C83111, AA568036, C82978.

SEQ ID NO: 181

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15 SEQ ID NO: 194

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45 SEQ ID NO: 198

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25 SEQ ID NO: 319

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35 SEQ ID NO: 320

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5 - SEQ ID NO: 321

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SEQ ID NO: 506

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20 SEQ ID NO: 507

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35 SEQ ID NO: 508

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45 SEQ ID NO: 514

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20 SEQ ID NO: 532

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 T49620, T49620 ya77g03.s1 Homo sapiens cDNA clone 67732 3'. 452 e-125
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 AA673899, AA673899 vo86g07.r1 Barstead mouse irradiated colon... 583 e-164
 AA797488, AA797488 vw28a05.r1 Soares mouse mammary gland NbMM... 519 e-145
 W71831, W71831 me45b06.r1 Soares mouse embryo NbME13.5 14.5 M... 472 e-131
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 AA036586, AA036586 mi41h08.r1 Soares mouse embryo NbME13.5 14... 42 0.078
 AA207496, AA207496 mv78g02.r1 GuayWoodford Beier mouse kidney... 42 0.078
 AA120433, AA120433 mp82h11.r1 Soares 2NbMT Mus musculus cDNA ... 42 0.078
 W08185, W08185 mb42h02.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.2
 AA065563, AA065563 ml71b06.r1 Stratagene mouse kidney (#93731... 38 1.2
 AA288756, AA288756 mr46h07.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
 AA119334, AA119334 mp80e10.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
 AA163051, AA163051 ms24a10.r1 Stratagene mouse skin (#937313)... 38 1.2
 N28074, N28074 MDB1392R Mouse brain, Stratagene Mus musculus ... 38 1.2
 AA288757, AA288757 mr46h08.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
 AA122857, AA122857 mq06a02.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
 AA617519, AA617519 vj77d05.r1 Knowles Solter mouse blastocyst... 38 1.2

W89420, W89420 mf80b03.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2
 AI047837, AI047837 ud64c11.x1 Sugano mouse liver mlia Mus mus... 38 1.2
 AA840310, AA840310 vw91a10.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA986428, AA986428 ue13b04.x1 Sugano mouse embryo mewa Mus mu... 36 4.8
 W47677, W47677 mc89g07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 AA057996, AA057996 mj56c10.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA183858, AA183858 mo95h01.r1 Stratagene mouse testis (#93730... 36 4.8
 AA212232, AA212232 mu43e08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
 W41067, W41067 mc39a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.8
 AA967594, AA967594 uh01d06.r1 Soares mouse hypothalamus NMHy ... 36 4.8
 AA414093, AA414093 vc64c07.s1 Knowles Solter mouse 2-cell Mus... 36 4.8
 AA123833, AA123833 mp93c03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
 AA432920, AA432920 vd91b11.r1 Soares mouse NbMH Mus musculus ... 36 4.8
 AA874496, AA874496 vx03a08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
 AA000433, AA000433 me76e09.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA023983, AA023983 mh94a07.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
 AA013726, AA013726 mh12e09.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
 AA274648, AA274648 vb08c01.r1 Soares mouse NML Mus musculus c... 36 4.8
 AA140347, AA140347 mq89g06.r1 Stratagene mouse heart (#937316... 36 4.8
 AA499377, AA499377 vi89c07.r1 Stratagene mouse heart (#937316... 36 4.8
 C88747, C88747 Mus musculus early blastocyst cDNA, clone 01B... 36 4.8
 AA726125, AA726125 vu88c06.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA760311, AA760311 vv71c12.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA763007, AA763007 vw60b05.r1 Soares mouse mammary gland NMLM... 36 4.8
 AA929878, AA929878 vz44d03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
 W59064, W59064 md67e10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 AA103519, AA103519 mo24b12.r1 Life Tech mouse embryo 13 5dpc ... 36 4.8
 AA222310, AA222310 my14d08.r1 Barstead mouse heart MPLRB3 Mus... 36 4.8
 W83557, W83557 mf32d02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 AA168631, AA168631 ms33c05.r1 Stratagene mouse skin (#937313)... 36 4.8
 AA960143, AA960143 vw60b05.s1 Soares mouse mammary gland NMLM... 36 4.8
 W34557, W34557 mc58a05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 W98818, W98818 mf94e06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
 AA008527, AA008527 mg85h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA008734, AA008734 mg86h03.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA510568, AA510568 vg33a10.r1 Soares mouse mammary gland NbMM... 36 4.8
 AA672524, AA672524 vo59e11.r1 Soares mouse mammary gland NbMM... 36 4.8
 AA052773, AA052773 mf24h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8
 AA096626, AA096626 mo09h06.r1 Life Tech mouse embryo 10 5dpc ... 36 4.8
 AA124880, AA124880 mp73e06.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
 AA198005, AA198005 mv12b09.r1 GuayWoodford Beier mouse kidney... 36 4.8
 AA624213, AA624213 vm98h06.r1 Knowles Solter mouse blastocyst... 36 4.8
 AA521863, AA521863 vi08b01.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8
 AA692113, AA692113 vt19d03.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8
 W71551, W71551 me39e11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8

AA646501, AA646501 vn12g12.r1 Stratagene mouse heart (#937316... 36 4.8
 AA607056, AA607056 vm95e05.r1 Knowles Solter mouse blastocyst... 36 4.8
 AA163340, AA163340 ms65b10.r1 Stratagene mouse embryonic carc... 36 4.8
 AA110893, AA110893 mm02b04.r1 Stratagene mouse kidney (#93731... 36 4.8

AI030290, AI030290 UI-R-C0-jb-d-01-0-UI.s1 UI-R-C0 Rattus nor... 293 1e-77
 C71833, C71833 Rice cDNA, partial sequence (E0428_1A) 44 0.017
 AA926551, AA926551 TENS1173 T. cruzi epimastigote normalized ... 42 0.069
 AA875699, AA875699 TENU0170 T.cruzi epimastigote normalized c... 42 0.069
 AA567661, AA567661 HL01595.5prime HL Drosophila melanogaster ... 40 0.27
 C74504, C74504 Rice cDNA, partial sequence (E31753_1A) 40 0.27
 AA698333, AA698333 HL04291.5prime HL Drosophila melanogaster ... 38 1.1
 AA441429, AA441429 LD16359.5prime LD Drosophila melanogaster ... 38 1.1
 N68770, N68770 TgESTzy35b12.r1 TgRH Tachyzoite cDNA Toxoplasma... 38 1.1
 AA246440, AA246440 LD05311.5prime LD Drosophila melanogaster ... 38 1.1
 AA801776, AA801776 GM12975.5prime GM Drosophila melanogaster ... 38 1.1
 N69148, N69148 TgESTzy33d10.r1 TgRH Tachyzoite cDNA Toxoplasma... 38 1.1
 AA536484, AA536484 LD17114.5prime LD Drosophila melanogaster ... 38 1.1
 AA392544, AA392544 LD11451.5prime LD Drosophila melanogaster ... 38 1.1
 AA202696, AA202696 LD03182.5prime LD Drosophila melanogaster ... 38 1.1
 AA392367, AA392367 LD11287.5prime LD Drosophila melanogaster ... 38 1.1
 AA264629, AA264629 LD08245.5prime LD Drosophila melanogaster ... 38 1.1
 AA735318, AA735318 LD21104.5prime LD Drosophila melanogaster ... 38 1.1
 AA264558, AA264558 LD08333.5prime LD Drosophila melanogaster ... 38 1.1
 AA536476, AA536476 LD17106.5prime LD Drosophila Embryo Drosop... 38 1.1
 AA957774, AA957774 UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor... 38 1.1
 AA567991, AA567991 HL02092.5prime HL Drosophila melanogaster ... 38 1.1
 AA957876, AA957876 UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor... 38 1.1
 AA892488, AA892488 EST196291 Normalized rat kidney, Bento Soa... 38 1.1
 AA699001, AA699001 HL06668.5prime HL Drosophila melanogaster ... 36 4.3
 C19706, C19706 Rice cDNA, partial sequence (E10809_1A) 36 4.3
 D41773, RICS4574A Rice cDNA, partial sequence (S4574_2A). 36 4.3
 C40680, C40680 C.elegans cDNA clone yk247c4 : 5' end, single... 36 4.3
 AA698625, AA698625 HL05354.5prime HL Drosophila melanogaster ... 36 4.3
 C82819, C82819 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
 D46016, RICS10393A Rice cDNA, partial sequence (S10393_3A). 36 4.3
 AA536314, AA536314 LD16858.5prime LD Drosophila melanogaster ... 36 4.3
 AA801012, AA801012 EST190509 Normalized rat muscle, Bento Soa... 36 4.3
 D46541, RICS11289A Rice cDNA, partial sequence (S11289_1A). 36 4.3
 D47315, RICS12612A Rice cDNA, partial sequence (S12612_1A). 36 4.3
 AA735857, AA735857 GM09977.5prime GM Drosophila melanogaster ... 36 4.3
 AA753921, AA753921 97BS0370 Rice Immature Seed Lambda ZAPII c... 36 4.3
 D47243, RICS12505A Rice cDNA, partial sequence (S12505_1A). 36 4.3
 AA978395, AA978395 LD28411.5prime LD Drosophila melanogaster ... 36 4.3

D15134, RICC0136A	Rice cDNA, partial sequence (C0136A).	36	4.3
D46483, RICS11185A	Rice cDNA, partial sequence (S11185_1A).	36	4.3
D46618, RICS11395A	Rice cDNA, partial sequence (S11395_1A).	36	4.3
D46659, RICS11457A	Rice cDNA, partial sequence (S11457_1A).	36	4.3
D46719, RICS11572A	Rice cDNA, partial sequence (S11572_1A).	36	4.3
D48579, RICS14880A	Rice cDNA, partial sequence (S14880_2A).	36	4.3
AA802334, AA802334	GM04219.5prime GM Drosophila melanogaster ...	36	4.3
D46066, RICS10470A	Rice cDNA, partial sequence (S10470_1A).	36	4.3
D47037, RICS12104A	Rice cDNA, partial sequence (S12104_1A).	36	4.3
D46874, RICS11807A	Rice cDNA, partial sequence (S11807_2A).	36	4.3
D47174, RICS12340A	Rice cDNA, partial sequence (S12340_2A).	36	4.3
T04578, T04578	625 Lambda-PRL2 Arabidopsis thaliana cDNA clon...	36	4.3
C83675, C83675	Oryctolagus cuniculus corneal endothelial cDN...	36	4.3
D47950, RICS13762A	Rice cDNA, partial sequence (S13762_1A).	36	4.3
R90044, R90044	16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	36	4.3
D46994, RICS12013A	Rice cDNA, partial sequence (S12013_2A).	36	4.3
AA440820, AA440820	LD15713.5prime LD Drosophila melanogaster ...	36	4.3
C72089, C72089	Rice cDNA, partial sequence (E0963_1A)	36	4.3
Z84004, SSZ84004	S.scrofa mRNA; expressed sequence tag (5'; ...	36	4.3
D47519, RICS13070A	Rice cDNA, partial sequence (S13070_1A).	36	4.3
C19735, C19735	Rice cDNA, partial sequence (E10858_1A).	36	4.3
D47231, RICS12462A	Rice cDNA, partial sequence (S12462_1A).	36	4.3
D47147, RICS12293A	Rice cDNA, partial sequence (S12293_1A).	36	4.3
AA950198, AA950198	LD30147.5prime LD Drosophila melanogaster ...	36	4.3
Z47624, ATTS4480	A.thaliana transcribed sequence; clone TAI...	36	4.3
D45955, RICS10259A	Rice cDNA, partial sequence (S10259_1A).	36	4.3
D47137, RICS12280A	Rice cDNA, partial sequence (S12280_1A).	36	4.3
D69927, CELK093H2F	C.elegans cDNA clone yk93h2 : 5' end, sin...	36	4.3
AA392275, AA392275	LD11117.5prime LD Drosophila melanogaster ...	36	4.3

SEQ ID NO:546

D87455, D87455	Human mRNA for KIAA0266 gene, complete cds	1164	0.0
Z99129, HS425C14	Human DNA sequence from clone 425C14 on chr...	42	0.20
D90900, D90900	Synechocystis sp. PCC6803 complete genome, 2/...	40	0.80
Z74281, SCYDL233W	S.cerevisiae chromosome IV reading frame O...	38	3.1
AL021528, HS394P21	Homo sapiens DNA sequence from PAC 394P21...	38	3.1
Z49155, HSL83D3	Human DNA from cosmid L83d3, Huntington's Di...	38	3.1
U33761, HSU33761	Human cyclin A/CDK2-associated p45 (Skp2) mR...	38	3.1
AF052832, AF052832	Trypanosoma cruzi CL Brener cosmid 1b21 ch...	38	3.1
Z98600, SPAC20G4	S.pombe chromosome I cosmid c20G4	38	3.1

Y09438, SPHUSPLUS *S.pombe* hus1+ gene 38 3.1
 D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0
 AA824593, AA824593 oc83d10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 670 0.0
 AA954862, AA954862 op20c03.s1 NCI_CGAP_Co12 Homo sapiens cDNA... 581 e-164
 T16360, T16360 NIB1193-Normalized infant brain, Bento Soares ... 517 e-145
 R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143
 AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142
 AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104
 R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103
 AA249614, AA249614 k3041.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65
 AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44
 AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5
 AA992442, AA992442 or85h03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79
 AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035
 W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035
 AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035
 AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2
 AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
 AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2
 AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2
 AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2
 AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2
 AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2
 AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9
 C40718, C40718 C.elegans cDNA clone yk247f9 : 5' end, single... 36 1.9
 AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9
 AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.35
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.35
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.67
 AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.67
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.67
 AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.67
 AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.67
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.67
 AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
 AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.67
 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.67
 AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.67
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.67
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.67
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.67

AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.67
AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
W47466, W47466 zc34h02.r1 Soares senescent-fibroblasts NbHSF... 40 0.67
AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.67
AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.67
AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.67
N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.67
N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.67
AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.67
AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.67
AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.67
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.67
AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.67
AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.67
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.67
AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 2.6
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.6
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.6
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.6
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.6
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.6
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6
H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6
R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.24
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.24
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.24
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.24
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.24
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.24
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.24
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.94
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7

AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.7
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.7
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.7
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.7
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12.5 Mus muscu... 36 3.7
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.7
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.7
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.7
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.7
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.7
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.7

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.053
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.84
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.84
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.84
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.84
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.84
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.84
 AA660819, AA660819 00713 MtrHE Medicago truncatula cDNA 5' ... 38 0.84
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.84
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.84
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.3
 AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.3
 D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.3
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.3
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.3
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.3
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.3
 AA660859, AA660859 00754 MtrHE Medicago truncatula cDNA 5' si... 36 3.3
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.3
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.3
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.3
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.3
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.3

SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34
 U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.34
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 3e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
 AA344913, AA344913 EST50856 Gall-bladder II Homo sapiens cDNA... 337 2e-90
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.16
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.64
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.64
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.64
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.64
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.64
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.64
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.64
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.64
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.64
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.5
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.5
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.5
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.5
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.5
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.23
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.23
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.23
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.23
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.23
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.23
 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.23
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.91
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
 AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.6
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.6
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.6
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.6
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.6
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.6
 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.6
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.6
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.6
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.6
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.6
 AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.6
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.6
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.6
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.6
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.6

 AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.052
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.81
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' ... 38 0.81
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.81
 D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.2
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.2
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.2
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.2

D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.2
 Z32603, ATTS2731 *A. thaliana* transcribed sequence; clone PAP... 36 3.2
 AA785775, AA785775 h4b05a1.f1 *Aspergillus nidulans* 24hr asexu... 36 3.2
 C68472, C68472 *C.elegans* cDNA clone yk305a12 : 5' end, singl... 36 3.2
 AA125602, AA125602 JM00M011.QM3 *Miracidia Sjc* 3/96-Schistosom... 36 3.2
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.2
 Z32602, ATTS2730 *A. thaliana* transcribed sequence; clone PAP... 36 3.2

SEQ ID NO:549

U79271, HSU79271 Human clones 23920 and 23921 mRNA sequence 650 0.0
 AC000395, AC000395 Genomic sequence from Human 9q34, complete... 42 0.28
 AC004636, AC004636 *Homo sapiens* chromosome 5, P1 clone 1268h6... 42 0.28
 M94579, HUMCEL Human carboxyl ester lipase (CEL) gene, comple... 42 0.28
 AC002097, AC002097 *Homo sapiens* chromosome 9q34, clone 246H5,... 42 0.28
 AB006709, AB006709 *Vibrio alginolyticus* rpoN gene for RNA po... 42 0.28
 Z47074, CEK07C10 *Caenorhabditis elegans* cosmid K07C10, compl... 40 1.1
 AC004755, AC004755 *Homo sapiens* chromosome 19, fosmid 37502,... 40 1.1
 Z28051, SCYKL051W *S.cerevisiae* chromosome XI reading frame O... 40 1.1
 AF022655, AF022655 *Homo sapiens* cep250 centrosome associated... 40 1.1
 AB006708, AB006708 *Arabidopsis thaliana* genomic DNA, chromos... 40 1.1
 AF049105, AF049105 *Homo sapiens* centrosomal Nek2-associated p... 40 1.1
 Z28050, SCYKL050C *S.cerevisiae* chromosome XI reading frame O... 40 1.1
 X75781, SCXI286K *S.cerevisiae* chromosome XI (28.6 kb) DNA fo... 40 1.1
 Y16899, DMY16899 *Drosophila melanogaster* mRNA for optomotor-... 38 4.3
 M87854, RATBARK1 *Rattus norvegicus* beta-adrenergic receptor k... 38 4.3
 M74822, RATMHTLL Rat MHC class I TL-like protein gene, comple... 38 4.3
 M80776, HUMBARK1A Human beta-adrenergic receptor kinase 1 mRN... 38 4.3
 D84549, YSACA *Candida tropicalis* DNA for carnitine acetyltra... 38 4.3
 L23127, RATRMCI *Rattus norvegicus* germline MHC class I gene, ... 38 4.3
 AC004257, AC004257 *Homo sapiens* chromosome 19, cosmid R33209,... 38 4.3
 U70850, CELF28F9 *Caenorhabditis elegans* cosmid F28F9 38 4.3
 U88309, CELT23B3 *Caenorhabditis elegans* cosmid T23B3 38 4.3
 X53421, DVCHOS18 *D. virilis* s18, s15, s19, s16 chorion prote... 38 4.3
 D89245, D89245 *Schizosaccharomyces pombe* mRNA, partial cds, ... 38 4.3
 AF009623, AF009623 *Parascaris univalens* PUMA1 (puma1) mRNA, c... 38 4.3
 S48813, S48813 beta-adrenergic receptor kinase [rats, brain, ... 38 4.3
 Z67883, CEK02A4 *Caenorhabditis elegans* cosmid K02A4, complet... 38 4.3
 U90567, GGU90567 *Gallus gallus* glutamine rich protein mRNA, p... 38 4.3
 M98498, BOVEZRINA *Bos taurus* ezrin mRNA, complete cds. 38 4.3
 M34073, MUSMHT10C *Mus musculus* (clone T10-c) MHC class I cell... 38 4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3
 X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3
 U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3
 U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2. 38 4.3

HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0
 AA886109, AA886109 ny44f05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 656 0.0
 AA829894, AA829894 oe51e12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 650 0.0
 AA879456, AA879456 oj91g03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 650 0.0
 AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
 AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
 AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0
 W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
 N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0
 AI033069, AI033069 ow93f02.s1 Soares_fetal_liver_spleen_INFLS... 642 0.0
 AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0
 N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180
 N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180
 H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180
 AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180
 R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178
 AA744290, AA744290 ny51d02.s1 NCI_CGAP_Pr18 Homo sapiens cDNA... 626 e-177
 AI038590, AI038590 ox34e03.s1 Soares_total_fetus_Nb2HF8_9w Ho... 624 e-177
 AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177
 AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176
 AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173
 R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167
 R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167
 H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165
 R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164
 AA910762, AA910762 ol25h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 559 e-157
 AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156
 AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153
 R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151
 H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150
 N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149
 D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129
 H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122
 AA971254, AA971254 op73c08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 442 e-122
 W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118
 AA878973, AA878973 oj26d11.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 389 e-106
 AA715235, AA715235 nv10g01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96
 AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74
 AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69
 AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41
 T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'. 170 2e-40
 N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'. 165 1e-38
 AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18
 AI038890, AI038890 ox84g12.x1 Soares_senescent_fibroblasts_Nb... 40 0.53
 D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08. 38 2.1
 AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1
 AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen INFLS... 38 2.1
 AA742364, AA742364 ny89c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
 AA907234, AA907234 ol03h08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
 T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1
 AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1
 AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1
 W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1
 AI039908, AI039908 ox25f07.x1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
 AA280664, AA280664 zs99f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
 AA973566, AA973566 oo46f09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
 N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'. 38 2.1
 AA995707, AA995707 os29c09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
 AI016407, AI016407 ot72e09.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
 N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'. 38 2.1
 AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
 AA938631, AA938631 oo96f07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
 AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103
 AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44
 AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41
 AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38
 AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10
 AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07
 AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19
 AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19
 AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75
 AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75
 W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75
 AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AI019772, AI019772 ua90h02.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA472253, AA472253 vh10g05.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA230895, AA230895 mw14g07.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.0
 W18052, W18052 mb83g03.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.0
 AA797681, AA797681 vx66c12.r1 Stratagene mouse skin (#937313)... 36 3.0
 W66734, W66734 me26g05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
 AA968020, AA968020 uh07g01.r1 Soares mouse hypothalamus NMHy ... 36 3.0
 AA051644, AA051644 mj55d12.r1 Soares mouse embryo NbME13.5 14... 36 3.0
 AA162797, AA162797 mr29g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA549644, AA549644 vk80f08.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
 AA273295, AA273295 vc01e01.r1 Soares mouse lymph node NbMLN M... 36 3.0
 AA048480, AA048480 mj33d08.r1 Soares mouse embryo NbME13.5 14... 36 3.0
 AA098207, AA098207 mn83d01.r1 Stratagene mouse Tcell 937311 M... 36 3.0
 AA027381, AA027381 mi05c06.r1 Soares mouse placenta 4NbMP13.5... 36 3.0
 AA544474, AA544474 vk33h06.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA416466, AA416466 vd15c09.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
 AA285999, AA285999 vb88h08.r1 Soares mouse 3NbMS Mus-musculus... 36 3.0
 AA175025, AA175025 ms85f06.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA544386, AA544386 vk33f06.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA175557, AA175557 ms96g04.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA711924, AA711924 vu59f09.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA734052, AA734052 vv22c10.r1 Stratagene mouse heart (#937316)... 36 3.0
 W53738, W53738 md12a12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
 AA611837, AA611837 vo82a06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.0
 AA879531, AA879531 vv96f06.r1 Soares mouse mammary gland NbMM... 36 3.0
 AA288625, AA288625 vb23g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
 AA784124, AA784124 d2b06a1.f1 Aspergillus nidulans 24hr asexu... 38 0.67
 AI044911, AI044911 UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor... 36 2.6
 AA550452, AA550452 1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 2.6
 F20017, ATTS6056 A. thaliana transcribed sequence; clone TAP... 36 2.6
 AA786697, AA786697 k5d01a1.f1 Aspergillus nidulans 24hr asexu... 36 2.6
 AA433457, AA433457 SW3ICA2345SK Brugia malayi infective larva... 36 2.6

SEQ ID NO:550

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.20
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.20
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.20
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 0.80

AC004301, AC004301 *Drosophila melanogaster* DNA sequence (P1 D... 40 0.80
 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 40 0.80
 Y14330, HSY14330 *Homo sapiens* partial mRNA for jagged2 protein 38 3.2
 AF003521, AF003521 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2
 AF029778, AF029778 *Homo sapiens* Jagged2 (JAG2) mRNA, complete... 38 3.2
 AF020201, AF020201 *Homo sapiens* Jagged 2 mRNA, complete cds 38 3.2
 Z71523, SCYNL247W *S.cerevisiae* chromosome XIV reading frame ... 38 3.2
 AF029779, AF029779 *Homo sapiens* hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2
 U70049, RNU70049 *Rattus norvegicus* jagged2 precursor gene, pa... 38 3.2
 X96722, SCCHXIVL *S.cerevisiae* DNA region from chromosome XIV... 38 3.2
 AF005938, AF005938 *Cavia porcellus* L-type voltage-dependent c... 38 3.2
 X78972, SBSTRBF *S.blauensis* ISP 5564 genes strB and strF 38 3.2
 X94912, HSPR22 *H.sapiens* Pr22 gene 38 3.2

HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT *Homo sapiens* ... 650 0.0
 AA348243, AA348243 EST54707 Hippocampus I *Homo sapiens* cDNA 5... 513 e-144
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 *Homo sapiens* cDNA ... 363 2e-98
 AA327309, AA327309 EST30621 Colon I *Homo sapiens* cDNA 5' end 353 2e-95
 AA344913, AA344913 EST50856 Gall bladder II *Homo sapiens* cDNA... 337 1e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) *Homo*... 317 1e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) *Homo*... 317 1e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR *Homo sapie*... 42 0.098
 AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 *Homo sapiens* cDNA ... 40 0.39
 AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 *Homo sapien*... 40 0.39
 AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 *Homo sapiens* c... 40 0.39
 AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 40 0.39
 AA824270, AA824270 aj29f01.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 *Homo sapiens* cDNA... 40 0.39
 AA813115, AA813115 aj44d06.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 40 0.39
 AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 *Homo sapiens* cDNA... 40 0.39
 AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 *Homo sapiens* cDNA ... 40 0.39
 AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 *Homo sapien*... 40 0.39
 AA759377, AA759377 ah54a10.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA629243, AA629243 zu77e03.s1 Soares testis NHT *Homo sapiens* ... 40 0.39
 AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 *Homo sapiens* cDNA ... 40 0.39
 AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39

AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.39
 AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.39
 AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.39
 AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.39
 N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.39
 AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.39
 AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.39
 W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.39
 AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.39
 AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.39
 AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
 AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
 W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.39
 AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
 AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
 AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
 AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.39
 N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.39
 N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.39
 AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.39
 AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.39
 AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
 R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 1.5
 H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 1.5
 AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 1.5
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 1.5
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 1.5
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 1.5
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 6e-44
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.14
 AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.14

AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA... 40 0.14
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.14
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.14
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.14
 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.14
 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.14
 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.14
 AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.14
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.14
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
 AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.14
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#937313) ... 40 0.14
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.14
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.14
 AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.14
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.55
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
 AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 2.2
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 2.2
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 2.2
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 2.2
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 2.2
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
 AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 2.2
 AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 2.2
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.2
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 2.2
 AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 2.2
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 2.2
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 2.2
 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 2.2
 AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 2.2

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AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031
 AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.48
 AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48
 AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
 AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
 AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48
 AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48
 AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48
 AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48
 AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 1.9
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 1.9
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9
 AA125602, AA125602 JM00M011:QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9
 AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
 AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
 AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
 AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.68
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.68
 AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.68
 AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.68
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.68
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.68
 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.68
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.68
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.68
 AA172158, AA172158 zp29a01.s1 Stratagene-neuroepithelium (#93... 40 0.68
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.7
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.7
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.7
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.7
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.7
 R14449, R14449 yf81h09.r1 Homo sapiens cDNA clone 29034 5'. 38 2.7
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.7

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
 AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
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 AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
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 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
 AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
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 AA250010, AA250010 mz59b12.r1 Soares mouse lymph node NbMLN M... 38 0.97
 AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.97
 AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 0.97
 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.8
 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.8
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 AA103139, AA103139 mol7f05.r1 Life Tech mouse embryo 13 5dpc ... 36 3.8

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 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.8
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 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
 AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.8
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.8
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 AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 3.8
 W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.8
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 AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 3.8
 W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 3.8
 AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 3.8
 AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.8
 AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
 AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.8
 AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 3.8
 AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
 C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.8
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 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.8
 AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
 AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 3.8
 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 3.8
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.8
 AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 3.8
 W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
 AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.8

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055
 AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22
 Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
 AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22
 AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22
 H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22
 AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22
 Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
 AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86
 AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86
 T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86
 AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.4
 AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4
 AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.4
 C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4
 AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4
 Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4
 Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4
 AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4
 AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4
 H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4
 Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4
 D45997, RICS10346A Rice cDNA, partial sequence.(S10346_1A): 36 3.4
 AA125602, AA125602 JM00M011:QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4
 AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.4
 D46069, RICS10475A Rice cDNA, partial sequence.(S10475_1A): 36 3.4

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U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38
 AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38
 U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38
 Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5
 U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5
 U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
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AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
 AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
 AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
 AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
 AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
 AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
 AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.18
 AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72
 N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72
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 R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.72
 AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.72
 AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.72
 AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.72
 AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.72
 AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8
 N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8
 AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.8
 N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8
 AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8
 AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8
 AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.8

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 AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26
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 AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26
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 AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 4.0

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 AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 4.0
 AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 4.0
 AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 4.0
 AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 4.0
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 W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
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 AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 4.0
 AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 4.0
 AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 4.0
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 AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.0
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 AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 4.0
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 AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 4.0
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 W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0
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 AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
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 AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 4.0
 AA591243, AA591243 vml8c04.r1 Knowles Solter mouse blastocyst... 36 4.0

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AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.90
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.6
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.6
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.6
AA785775, AA785775 h4b05a1.fl Aspergillus nidulans 24hr asexu... 36 3.6
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.6
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.6
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.6
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.6
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.6

SEQ ID NO:553

Z99297, HS262D12 Homo sapiens DNA sequence from PAC 262D12 o... 1963 0.0
Z81540, CEF46B3 Caenorhabditis elegans cosmid F46B3, complet... 40 0.89
U67488, U67488 Methanococcus jannaschii section 30 of 150 of ... 38 3.5
AE000786, AE000786 Borrelia burgdorferi plasmid lp28-2, compl... 38 3.5
L02053, OMMGSHT1 Ommastrephes sloani glutathione transferase... 38 3.5
AC004521, ATAC004521 Arabidopsis thaliana chromosome II BAC F... 38 3.5
L41250, DROGPDHN Drosophila nebulosa glycerol-3-phosphate deh... 38 3.5
AE000619, HPAE000619 Helicobacter pylori section 97 of 134 of... 38 3.5
U39720, Mycoplasma genitalium ackA, licA, mucB, rpL10, rpL32... 38 3.5
AC004533, HUAC004533 Homo sapiens Chromosome 16 BAC clone CIT... 38 3.5
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

HUMAN ESTs

W02630, W02630 za52c02.r1 Soares fetal liver spleen 1NFLS Hom... 1009 0.0
AA557183, AA557183 nl74f12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 874 0.0
AA761171, AA761171 nz09e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 866 0.0
AA976975, AA976975 oq26g11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 854 0.0
AA449515, AA449515 zx06b11.r1 Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0
 AA909198, AA909198 ol12d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 831 0.0
 W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0
 W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0
 W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0
 AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0
 H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0
 W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0
 AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0
 AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0
 AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0
 AA662309, AA662309 nu97c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 668 0.0
 W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
 N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176
 N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165
 AA251287, AA251287 zs04c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 583 e-164
 AA971082, AA971082 op70h01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 567 e-160
 W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159
 AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157
 AA729063, AA729063 nw22f08.s1 NCI_CGAP_GCB0 Homo sapiens cDNA... 557 e-157
 AA987313, AA987313 or81h06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 553 e-155
 AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152
 AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148
 N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146
 AA947355, AA947355 od86e12.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 504 e-140
 AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127
 AA742964, AA742964 ny15d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 454 e-126
 AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125
 W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123
 W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121
 AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109
 N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106
 N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104
 AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99
 AA936553, AA936553 on23g11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 361 9e-98
 N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95
 AA834628, AA834628 od98a10.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 341 8e-92
 AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92
 AA909616, AA909616 ol09d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 341 8e-92
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 AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84
 AA911960, AA911960 oh88g08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 317 1e-84
 AA969099, AA969099 op55e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 2e-80
 AA766191, AA766191 oa12g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 5e-53
 AA689312, AA689312 nx05e10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586 zv93e05.r1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
 AA418570, AA418570 zv93e05.s1 Soares NhHMPu S1 Homo sapiens c... 182 5e-44
 AA534939, AA534939 nf82f03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 167 3e-39
 AA888430, AA888430 nw74e05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 167 3e-39
 N50003, N50003 yv24d04.r1 Homo sapiens cDNA clone 243655 5' s... 149 6e-34
 AA535102, AA535102 nf84f06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 135 1e-29
 AA262335, AA262335 zr71g03.s1 Soares NhHMPu S1 Homo sapiens c... 129 6e-28
 AA766681, AA766681 oa34c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 105 9e-21
 AA761492, AA761492 nz27a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 101 1e-19
 AA688350, AA688350 nv15a05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 90 5e-16
 AA347041, AA347041 EST53285 Fetal heart II Homo sapiens cDNA ... 76 8e-12
 T94395, T94395 ye35e02.s1 Homo sapiens cDNA clone 119738 3'... 46 0.007
 AA833565, AA833565 aj46a02.s1 Soares testis NHT Homo sapiens ... 46 0.007
 AA095460, AA095460 l4630.seq.F Fetal heart, Lambda ZAP Expres... 40 0.43
 AA904415, AA904415 ok07e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.43
 AI018800, AI018800 ov32h04.x1 Soares_testis_NHT Homo sapiens ... 38 1.7
 AA631083, AA631083 nq77e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 1.7

AA399772, AA399772 vd70g05.r1 Beddington mouse embryonic regi... 347 5e-94
 AA467106, AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 309 1e-82
 AI046844, AI046844 uh55c11.r1 Soares mouse embryonic stem cel... 208 3e-52
 AA475075, AA475075 vh11g05.r1 Soares mouse mammary gland NbMM... 194 4e-48
 AA646094, AA646094 vs31e06.r1 Stratagene mouse Tcell 937311 M... 186 1e-45
 AA390020, AA390020 vb30e07.r1 Soares mouse lymph node NbMLN M... 170 6e-41
 AA245553, AA245553 my52g04.r1 Barstead mouse pooled organs MP... 170 6e-41
 AA930741, AA930741 vs57b02.r1 Stratagene mouse skin (#937313)... 155 4e-36
 W62610, W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 117 8e-25
 AA239270, AA239270 my40e01.r1 Barstead mouse pooled organs MP... 109 2e-22
 AA015148, AA015148 mh16e01.r1 Soares mouse placenta 4NbMP13.5... 54 1e-05
 AA764095, AA764095 vw09h02.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.61
 AA238570, AA238570 my35h02.r1 Barstead mouse pooled organs MP... 38 0.61
 AA600576, AA600576 vm75f08.r1 Knowles Solter mouse blastocyst... 38 0.61
 AA636273, AA636273 vq76a10.s1 Knowles Solter mouse 2 cell Mus... 36 2.4
 AA051407, AA051407 mj41f08.r1 Soares mouse embryo NbME13.5 14... 36 2.4
 AA823136, AA823136 vw41b03.r1 Soares mouse mammary gland NbMM... 36 2.4
 W83831, W83831 mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
 D77944, MUSC0D06 Mouse embryonal carcinoma F9 cell cDNA, C0D06 36 2.4
 AA915408, AA915408 vz29h04.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.4
 AI047229, AI047229 uh63a09.r1 Soares mouse embryonic stem cel... 36 2.4
 AA271880, AA271880 va73d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
 AA475165, AA475165 vg95f01.r1 Barstead mouse pooled organs MP... 36 2.4
 AA619774, AA619774 vl58a05.s1 Knowles Solter mouse 2 cell Mus... 36 2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
 AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4
 W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
 AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4
 AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
 AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
 AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus musc... 36 2.4
 AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4
 AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14
 F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54
 H91505, H91505 SWMFCA089SK Brugia malayi microfilaria cDNA (S... 36 2.1
 AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1
 AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1
 AI008397, AI008397 EST202848 Normalized rat embryo, Bento Soa... 36 2.1

SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0
 Z46940, HSPRMTNP2 H.sapiens PRM1 gene, PRM2 gene and TNP2 gene 44 0.048
 U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19
 AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19
 AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19
 U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
 Z97343, ATFCA8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75
 L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75
 M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75
 L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75
 J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75
 M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75
 X72711, MMREPCFC M.musculus mRNA for replication factor C, l... 38 3.0
 M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0
 U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0
 AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0
 J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0
 J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0
 X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0
 X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0
 D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0
 Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0
 D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-)-met... 38 3.0
 Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0
 L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0
 U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0
 U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0
 K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0
 Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0
 U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0
 Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

HUMAN ESTs

SEQ ID NO:555

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019
 AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073
 X82638, CSCYTOX C.sordellii cytotoxin gene 42 0.29
 U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29
 X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29
 Z74201, SCYDL153C S.cerevisiae chromosome IV reading-frame O... 42 0.29
 U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29
 Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29
 X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29
 X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29
 L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29
 U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 1.1
 S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1
 U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1
 Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1
 U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 1.1

AF050157, MMHC135G15	Mus musculus major histocompatibility lo...	40	1.1
X58857, SCPH22	S.cerevisiae PPH22 gene for protein phosphat...	40	1.1
X79379, SCPROIS	S.cerevisiae gene for proline isomerase	40	1.1
Z68341, CEF01G4	Caenorhabditis elegans cosmid F01G4, complet...	40	1.1
M17192, MUSHOX1	Mouse homeodomain protein (Hox1.1) mRNA, comp...	40	1.1
U50307, CELF43H9	Caenorhabditis elegans cosmid F43H9.	40	1.1
S73144, S73144	bone sialoprotein [cattle, fetal bone cells, m...	40	1.1
L34569, YSCFPR3A	Saccharomyces cerevisiae (clone pBYNG1) prol...	40	1.1
D78303, D78303	Rattus norvegicus YT521 mRNA for RNA splicing...	40	1.1
X83276, SCDNAIV	S.cerevisiae DNA for ORFs from chromosome IV	40	1.1
U54558, HSU54558	Human translation initiation factor eIF3 p66...	40	1.1
Z50109, CEC09H10	Caenorhabditis elegans cosmid C09H10, compl...	40	1.1
X56983, EAVATP1	E.arvense gene for catalytic 70kDa V-ATPase ...	40	1.1
AB011125, AB011125	Homo sapiens mRNA for KIAA0553 protein, p...	40	1.1
Z46373, SC8248	S.cerevisiae chromosome XIII cosmid 8248	40	1.1
AF039042, CELZK697	Caenorhabditis elegans cosmid ZK697	40	1.1
Z28028, SCYKL028W	S.cerevisiae chromosome XI reading frame O...	40	1.1
AC005266, AC005266	Homo sapiens chromosome 19, cosmid F23465,...	38	4.5
U60822, HSU60822	Human dystrophin (DMD) gene, exons 7, 8 and ...	38	4.5
AJ003141, HVAJ3141	Hordeum vulgare mRNA for stress-related p...	38	4.5
M26250, CRAGAP43	Goldfish (C.auratus) growth-associated prote...	38	4.5
X95267, GGRYR3	G.gallus mRNA for ryanodine receptor type 3	38	4.5
L37092, MUSCDPK	Mus musculus cyclin-dependent kinase homologu...	38	4.5
Z72507, CEF17C11	Caenorhabditis elegans cosmid F17C11, compl...	38	4.5
U29608, DMU29608	Drosophila melanogaster large tumor suppress...	38	4.5
Z49072, CET24A11	Caenorhabditis elegans cosmid T24A11, compl...	38	4.5
M83142, RATBGASTR	Rattus norvegicus beta-galactoside-alpha 2,...	38	4.5
Z20656, HSCAMHCA	Homo sapiens of cardiac alpha-myosin heavy ...	38	4.5
M82937, YSACS2A	Candida albicans chitin synthase 2 (CHS2) gen...	38	4.5
U28888, MMU28888	Mus musculus neurogenic differentiation fact...	38	4.5
S66408, S66408	c-erbB=proto-oncogene {exon 1, promoter} [chic...	38	4.5
AC002396, AC002396	Arabidopsis thaliana chromosome I BAC F3I6...	38	4.5
AE000665, MMAE000665	Mus musculus TCR beta locus from bases 5...	38	4.5
L39837, DROWARTS	Drosophila melanogaster tumor supressor (war...	38	4.5
AG000377, AG000377	Homo sapiens genomic DNA, 21q region, clo...	38	4.5
X05632, HSMHCAG1	Human alpha-MHC gene for myosin heavy chain...	38	4.5
AC002108, AC002108	Genomic sequence from Mouse 4, complete se...	38	4.5
U37219, HSU37219	Human cyclophilin-like protein CyP-60 mRNA, ...	38	4.5
M58633, MUSP58GTA	Mouse p58/GTA protein kinase mRNA, complete...	38	4.5
M25162, HUMMYHC08	Human cardiac alpha-myosin heavy chain (MYH...	38	4.5
Z46259, SCRPD3COS	S.cerevisiae FY1676 RPD3 gene.	38	4.5
U09558, LJU09558	Lactobacillus johnsonii ATCC 11506 insertion...	38	4.5
U66160, MMUSC104	Mus musculus extracellular matrix associated...	38	4.5
Z73126, SCYLL021W	S.cerevisiae chromosome XII reading frame ...	38	4.5
U83981, HSU83981	Homo sapiens apoptosis associated protein (G...	38	4.5

U59897, MRU59897 *Macropus robustus* hypoxanthine phosphoribosy... 38 4.5
 D38256, YSCSCT1 Yeast gene for suppressor of ctr mutation 38 4.5
 X69838, HSG9A *H.sapiens* mRNA for G9a 38 4.5
 X52952, RNCMOSO Rat mRNA for c-mos 38 4.5
 U37221, HSU37221 Human cyclophilin-like protein mRNA, partial... 38 4.5
 X65880, DPRH4OP1 *D.pseudoobscura* rh4 opsin gene, exon 1 38 4.5
 U58971, NTU58971 *Nicotiana tabacum* calmodulin-binding protein... 38 4.5
 Z35773, SCYBL012C *S.cerevisiae* chromosome II reading frame O... 38 4.5
 X67668, MMHMG2 *M.musculus* mRNA for high mobility group 2 pro... 38 4.5
 L81727, HSL81727 *Homo sapiens* (subclone 1_d5 from P1 H69) DNA... 38 4.5

 AL023800, HS833B2 Human DNA sequence *** SEQUENCING IN PROGR... 38 4.5
 X62438, HVPERO *H.vulgare* mRNA for peroxidase 38 4.5
 AC004096, AC004096 Mouse Cosmid ma66a100 from 14D1-D2, comple... 38 4.5
 AL008980, PFSC03050 *Plasmodium falciparum* DNA *** SEQUENCING... 38 4.5
 U64827, MMU64827 *Mus musculus* extracellular matrix associated... 38 4.5
 AC003010, HUAC003010 *Homo sapiens* Chromosome 16 BAC clone CIT... 38 4.5
 AE001002, AE001002 *Archaeoglobus fulgidus* section 105 of 172 ... 38 4.5

 U86662, LEU86662 *Lycopersicon esculentum* VPS41 (tVPS41) mRNA,... 38 4.5
 M20386, CHKEGFR Chicken epidermal growth factor receptor (CER... 38 4.5
 M77637, CHKEGF *Gallus gallus* EGF/TGF-alpha receptor (c-erbB) ... 38 4.5
 U08185, MMU08185 *Mus musculus* BALB/c zinc-finger protein Blim... 38 4.5
 AC004231, AC004231 *Homo sapiens* chromosome 17, clone hRPC.111... 38 4.5
 Z50100, HVC39SAT *H.vulgare* GAA-satellite DNA 38 4.5
 X53731, SCSA2G *S.cerevisiae* SPA2 gene 38 4.5
 U37220, HSU37220 Human cyclophilin-like protein mRNA, partial... 38 4.5
 X97560, SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome... 38 4.5
 AB011479, AB011479 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5
 U89340, LVU89340 *Lytechinus variegatus* Endo16 homolog (LvEndo1... 38 4.5
 U73850, TCU73850 *Trypanosoma cruzi* 29 kDa proteasome subunit ... 38 4.5
 AB006698, AB006698 *Arabidopsis thaliana* genomic DNA, chromos... 38 4.5
 D37888, CYIMYC2 *Cyprinus carpio* c-myc gene for c-Myc, comple... 38 4.5
 AF017349, MMDSGIII 7 *Mus musculus* desmoglein 3 (Dsg3) gene, i... 38 4.5
 X91807, OSTA136 *O.sativa* mRNA for alpha-tubulin (clone OSTA-... 38 4.5
 Z71587, SCYNL311C *S.cerevisiae* chromosome XIV reading frame ... 38 4.5
 AE000742, AE000742 *Aquifex aeolicus* section 74 of 109 of the ... 38 4.5

HUMAN ESTs

AA324311, AA324311 EST27136 Cerebellum II *Homo sapiens* cDNA 5... 593 e-167
 AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 *Homo sapiens* cDNA ... 513 e-143
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 505 e-141
 AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 *Homo sapiens* cDNA ... 502 e-140
 AA412036, AA412036 zt68d09.s1 Soares testis NHT *Homo sapiens* ... 502 e-140
 AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 *Homo sapiens* cDNA ... 502 e-140

AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 502 e-140
 AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 502 e-140
 AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 502 e-140
 R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5' ... 490 e-136
 AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 464 e-128
 AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128
 AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109
 R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3' ... 359 5e-97
 AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84
 R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68
 AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50
 W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20
 W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08
 T65784, T65784 ycl1f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14
 AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14
 AA928679, AA928679 on48e08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 40 0.55
 AA887972, AA887972 nq95g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
 W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55
 AA887862, AA887862 nq99b08.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
 AA554819, AA554819 ni34d08.s1 NCI_CGAP_Lu1 Homo sapiens cDNA ... 40 0.55
 AA557362, AA557362 nl81d12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55
 N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55
 AA552228, AA552228 nk06b04.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 40 0.55
 AI017648, AI017648 ou99b02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA... 40 0.55
 T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55
 AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55
 AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55
 N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55
 AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55
 AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55
 AA731625, AA731625 nw64a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
 AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55
 AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55
 AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55
 R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55
 AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55
 AA633213, AA633213 nq57c06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.55
 W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55
 AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55
 N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55
 N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
 AI041637, AI041637 ox92h08.x1 Soares_senescent_fibroblasts_Nb... 40 0.55
 N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55

AA535094, AA535094 nf84e06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 AA514414, AA514414 nf57d11.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55
 N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55
 AA535811, AA535811 nf93g10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 AA115591, AA115591 zl05g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
 N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55
 AA534433, AA534433 nf80a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55
 AA970859, AA970859 oo81h03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.55
 F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55
 AA810279, AA810279 od14g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
 AA595146, AA595146 nl84b01.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 AA632386, AA632386 np67e06.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55
 AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55
 AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55
 AA156872, AA156872 zl20h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
 AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55
 AA961724, AA961724 or60a10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 40 0.55
 AA551210, AA551210 nj27e09.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 40 0.55
 R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55
 AA938086, AA938086 oj08h08.s1 NCI_CGAP_Mel3 Homo sapiens cDNA... 40 0.55
 AA576021, AA576021 nm57d11.s1 NCI_CGAP_Br3 Homo sapiens cDNA ... 40 0.55
 AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55
 AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
 T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55
 AA632245, AA632245 np67b09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55
 R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55
 AI028447, AI028447 ow08b09.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.55
 AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55
 AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA815223, AA815223 oc05c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
 W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55
 AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA643849, AA643849 np26f07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.55
 AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55
 AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
 AA535972, AA535972 nf95a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
 AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55
 AA866044, AA866044 oh52g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.55
 C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 167 1e-39
AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.78
AA413261, AA413261 ve52f04.r1 Beddington mouse embryonic regi... 38 0.78
AA097645, AA097645 mm36f09.r1 Stratagene mouse skin (#937313)... 38 0.78
AA122578, AA122578 mn25b08.r1 Beddington mouse embryonic regi... 38 0.78
AA122581, AA122581 mn25c08.r1 Beddington mouse embryonic regi... 38 0.78
AA646168, AA646168 vn11e06.r1 Stratagene mouse Tcell 937311 M... 36 3.1
AA200881, AA200881 mu03c09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1
AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 3.1
AA217675, AA217675 mv01b09.r1 Soares mouse lymph node NbMLN M... 36 3.1
AI006387, AI006387 ua71d09.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1
AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 3.1
AA207387, AA207387 mv89a11.r1 GuayWoodford Beier mouse kidney... 36 3.1
AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 3.1
AA123112, AA123112 mn30g01.r1 Beddington mouse embryonic regi... 36 3.1
AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 3.1
AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 3.1
W12171, W12171 ma59a10.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.1
AA208446, AA208446 mv85e01.r1 GuayWoodford Beier mouse kidney... 36 3.1
AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 3.1
AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 3.1
AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 3.1
AA561847, AA561847 vl27a12.r1 Stratagene mouse Tcell 937311 M... 36 3.1
AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 3.1
AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.1
AA052080, AA052080 mf69f12.r1 Soares mouse embryo NbME13.5 14... 36 3.1
AA000646, AA000646 mg23f09.r1 Soares mouse embryo NbME13.5 14... 36 3.1
AA510521, AA510521 vh59a05.r1 Soares mouse mammary gland NbMM... 36 3.1
AI006122, AI006122 ua86h01.r1 Soares mouse mammary gland NbMM... 36 3.1
AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 3.1
W77413, W77413 me64d06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1
AA114809, AA114809 mn17e09.r1 Beddington mouse embryonic regi... 36 3.1
AA793564, AA793564 vn54c05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.1
AA174537, AA174537 mt10f09.r1 Soares mouse 3NbMS Mus musculus... 36 3.1
W62181, W62181 md87d08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.1
AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.1
AA286005, AA286005 va30e05.r1 GuayWoodford Beier mouse kidney... 36 3.1
AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 3.1
AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 3.1

AA519228, AA519228 TgESTzz39h02.s1 TgME49 invivo Bradyzoite c... 44 0.011

AA520185, AA520185	TgESTzz39d03.s1 TgME49 invivo Bradyzoite c...	44	0.011
AA531917, AA531917	TgESTzz48f01.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA519997, AA519997	TgESTzz36h03.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA520811, AA520811	TgESTzz64d05.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA520866, AA520866	TgESTzz68e05.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA519844, AA519844	TgESTzz36c03.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA274295, AA274295	TgESTzz24c11.s1 TgME49 invivo Bradyzoite c...	44	0.011
AA520901, AA520901	TgESTzz65a05.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA519829, AA519829	TgESTzz36a02.r1 TgME49 invivo Bradyzoite c...	44	0.011
AA531839, AA531839	TgESTzz47h05.r1 TgME49 invivo Bradyzoite c...	44	0.011
C70525, C70525	C.elegans cDNA clone yk409g6 : 5' end, single...	44	0.011
AA520235, AA520235	TgESTzz53c06.r1 TgME49 invivo Bradyzoite c...	42	0.044
T42800, T42800	6063 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	42	0.044
R29976, R29976	12581 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	42	0.044
H32045, H32045	EST106774 Rat PC-12 cells, untreated Rattus sp...	40	0.18
AA819924, AA819924	MF5MA171.AE3 S. mansoni female adult Lambd...	40	0.18
H37128, H37128	15257 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	40	0.18
T04367, T04367	414 Lambda-PRL2 Arabidopsis thaliana cDNA clon...	40	0.18
R90528, R90528	16883 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	40	0.18
AA660422, AA660422	00298 MtrHE Medicago truncatula cDNA 5'	40	0.18
U94861, RRU94861	Rattus norvegicus clone HCY3 mRNA sequence	40	0.18
F14275, ATTS5197	A. thaliana transcribed sequence; clone YBY...	38	0.69
W43730, W43730	23107 CD4-16 Arabidopsis thaliana cDNA clone H...	38	0.69
N65025, N65025	20065 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	38	0.69
AI001628, AI001628	EST0210 Tilapia brain cDNA library in pUC1...	38	0.69
H74687, H74687	383 Brassica napus cDNA clone R25R...	38	0.69
AA395597, AA395597	27394 Lambda-PRL2 Arabidopsis thaliana cDN...	38	0.69
AA753070, AA753070	97AS2091 Rice Immature Seed Lambda ZAPII c...	38	0.69
D41274, RICS3647A	Rice cDNA, partial sequence (S3647_1A).	38	0.69
Z25731, ATTS1208	A. thaliana transcribed sequence; clone VCV...	38	0.69
N82780, N82780	TgESTzy34e03.r1 TgRH Tachyzoite cDNA Toxoplas...	38	0.69
AA597822, AA597822	29889 Lambda-PRL2 Arabidopsis thaliana cDN...	38	0.69
AA948906, AA948906	LD27590.5prime LD Drosophila melanogaster ...	38	0.69
AI013695, AI013695	EST208370 Normalized rat spleen, Bento Soa...	38	0.69
AA753263, AA753263	96BS0294 Rice Immature Seed Lambda ZAPII c...	38	0.69
F14402, ATTS5324	A. thaliana transcribed sequence; clone TAP...	36	2.7
T46158, T46158	9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	36	2.7
C91400, C91400	Dictyostelium discoideum slug cDNA, clone SSK169	36	2.7
T46009, T46009	9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	36	2.7
AA440655, AA440655	LD15510.5prime LD Drosophila melanogaster ...	36	2.7
AA559374, AA559374	MU002092.NH3 York-Harrop-lung-A Schistosom...	36	2.7
Z32623, ATTS2751	A. thaliana transcribed sequence; clone YAP...	36	2.7
T43683, T43683	6946 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	36	2.7
AA263535, AA263535	LD06645.5prime LD Drosophila melanogaster ...	36	2.7
C37095, C37095	C.elegans cDNA clone yk482c11 : 3' end, singl...	36	2.7

C57017, C57017 *C.elegans* cDNA clone yk308h9 : 3' end, single... 36 2.7
 C93857, C93857 *Dictyostelium discoideum* slug cDNA, clone SSL794 36 2.7
 C92242, C92242 *Dictyostelium discoideum* slug cDNA, clone SSD283 36 2.7
 Z33976, ATTS3037 *A. thaliana* transcribed sequence; clone YAP... 36 2.7
 R62091, R62091 EST351 *Strongylocentrotus purpuratus* cDNA 5' end. 36 2.7
 AA567455, AA567455 HL01288.5prime HL *Drosophila melanogaster* ... 36 2.7
 C74456, C74456 Rice cDNA, partial sequence (E31357_1A) 36 2.7
 AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7
 C92456, C92456 *Dictyostelium discoideum* slug cDNA, clone SSE569 36 2.7
 T20458, T20458 2466 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7
 R29905, R29905 12510 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7
 M79841, M79841 wEST00378 *Caenorhabditis elegans* cDNA clone CE... 36 2.7
 Z17562, ATTS0136 *A. thaliana* transcribed sequence; clone TAT... 36 2.7
 D71983, CELK084H2R *C.elegans* cDNA clone yk84h2 : 3' end, sin... 36 2.7
 T20404, T20404 2412 Lambda-PRL2 *Arabidopsis thaliana* cDNA clo... 36 2.7
 AI012789, AI012789 EST207240 Normalized rat placenta, Bento S... 36 2.7
 U83048, BTU83048 *Bos taurus* clone 0429 mRNA sequence 36 2.7
 AA660182, AA660182 00022 MtRHE *Medicago truncatula* cDNA 5' si... 36 2.7
 D48514, RICS14740A Rice cDNA, partial sequence (S14740_1A). 36 2.7
 C90110, C90110 *Dictyostelium discoideum* slug cDNA, clone SSI103 36 2.7
 H36880, H36880 15009 Lambda-PRL2 *Arabidopsis thaliana* cDNA cl... 36 2.7
 AA699152, AA699152 HL07807.5prime HL *Drosophila melanogaster* ... 36 2.7
 C11922, C11922 *C.elegans* cDNA clone yk144a11 : 5' end, singl... 36 2.7
 AA816691, AA816691 LD03795.5prime LD *Drosophila melanogaster* ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 *M.musculus* mRNA for exon from unknown gene 22A3 260 5e-67
 Z83760, CICOS41 *Ciona intestinalis* DNA sequence from cosmid ... 40 0.94
 Z75710, CED1081 *Caenorhabditis elegans* cosmid D1081, complet... 40 0.94
 U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94
 X99757, DMDYDTRO *D.melanogaster* mRNA for dystrophin 38 3.7
 U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7
 AC004118, AC004118 *Drosophila melanogaster* (P1 DS06238 (D26))... 38 3.7
 U50313, CELF44C4 *Caenorhabditis elegans* cosmid F44C4. 38 3.7
 AC004503, AC004503 *Homo sapiens* chromosome 5, P1 clone 1354A7... 38 3.7
 M16840, WHTCPA2 Wheat Asp-tRNA gene. 38 3.7
 Y13381, RNAMPH1 *Rattus norvegicus* mRNA for amphiphysin, amph1 38 3.7
 AC002994, AC002994 *Homo sapiens* chromosome 17, clone HRPC987K... 38 3.7
 AB008271, AB008271 *Arabidopsis thaliana* genomic DNA, chromos... 38 3.7
 D49701, ASNNIAD *Aspergillus oryzae* niaD gene for nitrate red... 38 3.7

X59422, HSPLD1 H.sapiens Pl d1 repetitive DNA 38 3.7
Z98555, PFSC03027 Plasmodium falciparum DNA *** SEQUENCING I... 38 3.7

HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0
U56653, HSU56653 Human heat shock inducible mRNA 769 0.0
AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0
AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0

AA314922, AA314922 EST186735 HCC cell line (matatasis to liv... 698 0.0
AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0
H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5'. 624 e-177
AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176
AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170
AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164
AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150

AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150
AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150
AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141
R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5'. 486 e-135
AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134
AA564849, AA564849 nj22c04.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 442 e-122
AA932576, AA932576 oo57g10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 440 e-121
AA876265, AA876265 oi12g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 434 e-120
AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118
U56654, HSU56654 Human heat shock inducible mRNA 426 e-117
AA746600, AA746600 nx18c02.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 406 e-111
AA876346, AA876346 oj24a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 406 e-111
W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110
AI034059, AI034059 ow14h11.x1 Soares_parathyroid_tumor_NbHPA ... 357 2e-96
AA662934, AA662934 nu92d09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 323 2e-86
AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80
AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78
R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5'. 280 3e-73
T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5'. 254 2e-65
AA731264, AA731264 nw57c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
AA768549, AA768549 oa67c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54
T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3'. 198 8e-49
AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49
AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22
R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5'. 58 2e-06
T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5'. 38 1.8
AA595230, AA595230 nl84g02.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 38 1.8

AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0
 AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167
 AI048164, AI048164 ud71b09.y1 Sugano mouse liver mlia Mus mus... 537 e-151
 W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128
 AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69
 AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53
 AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43
 AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32
 AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23
 AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23
 AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15
 AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13
 AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65
 AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6
 AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6
 AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21
 AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15
 C23464, C23464 Jpanese flounder liver cDNA, LE5(10) 72 4e-11
 C23465, C23465 Jpanese flounder liver cDNA, LE5(10) 56 2e-06
 AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57
 AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57
 AA274286, AA274286 TgESTzz24c01.s1 TgME49 invivo Bradyzoite c... 38 0.57
 AA660585, AA660585 00471 MtrHE Medicago truncatula cDNA 5' si... 38 0.57
 L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57
 AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57
 C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3
 C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3
 C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3
 AA542589, AA542589 fa08d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3
 AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3
 AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 AA495181, AA495181 fa04d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
 D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3
 C28238, C28238 Rice cDNA, partial sequence (C60429_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0
 S51239, S51239 calreticulin [Aplysia californica=marine snail... 56 1e-05
 Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.012
 U25723, CPU25723 Cavia porcellus alpha-2B adrenoceptor gene, ... 44 0.047
 AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19
 U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.19

 V01470, ZMZE01 Zea mays gene encoding a zein gene (clone lam... 42 0.19
 U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19
 X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.19
 AE000926, AE000926 Methanobacterium thermoautotrophicum from ... 42 0.19
 AC004135, AC004135 Genomic sequence for Arabidopsis thaliana ... 42 0.19
 AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74
 AF050157, MMHC135G15 Mus musculus major histocompatibility lo... 40 0.74

 AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74
 X07699, MMNUCLEO Mouse nucleolin gene 40 0.74
 X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contai... 40 0.74
 M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74
 M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74
 U15972, MMU15972 Mus musculus homeobox (Hoxa7) gene, complete... 40 0.74
 AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74
 U09820, HSU09820 Human helicase II (RAD54L) mRNA, complete cds. 40 0.74
 AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74
 U26259, MMU26259 Mus musculus C2-H2 zinc finger protein mRNA, ... 40 0.74
 L48363, MUSZFPTR Mus musculus zinc finger protein gene, compl... 40 0.74
 AC003113, AC003113 Arabidopsis thaliana BAC F24O1 chromosome ... 40 0.74
 D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74
 U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74
 U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74
 U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 0.74
 Z48618, SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), ... 40 0.74
 U75653, HSU75653 Human zinc finger helicase (Znf-HX) mRNA, co... 40 0.74
 Z72672, SCYGL150C S.cerevisiae chromosome VII reading frame ... 40 0.74
 Z50109, CEC09H10 Caenorhabditis elegans cosmid C09H10, compl... 40 0.74
 AF013969, AF013969 Mus musculus antigen containing epitope to... 40 0.74
 M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74
 U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74
 M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene, c... 40 0.74
 U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 0.74
 U97085, HSXNP14 Homo sapiens X-linked nuclear protein (ATRX) ... 40 0.74
 L34363, HUMNUCPRO Human X-linked nuclear protein (XNP) gene, ... 40 0.74
 U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 0.74
 U88539, MMU88539 Mus musculus chromatin structural protein ho... 40 0.74
 U07704, HSU07704 Human protein kinase PITSLRE isoform PBETA21... 38 2.9
 U07705, HSU07705 Human protein kinase PITSLRE isoform PBETA22... 38 2.9
 AF019612, AF019612 Homo sapiens S2P mRNA, complete cds 38 2.9
 U04818, HSU04818 Human protein kinase PITSLRE alpha 2-4 mRNA,... 38 2.9
 AB002381, AB002381 Human mRNA for KIAA0383 gene, partial cds 38 2.9
 AB009520, AB009520 Pyrococcus horikoshii OT3 genomic DNA, 13... 38 2.9
 Z83848, HS57A13 Human DNA sequence from PAC 57A13 between ma... 38 2.9
 AC004592, AC004592 Homo sapiens PAC clone DJ0244J05 from 5q31... 38 2.9
 L11710, ZEFZCMYC Brachydanio rerio c-myc oncoprotein mRNA, co... 38 2.9
 D43920, CHKMETASE Chicken mRNA for DNA (cytosine-5-)-methylt... 38 2.9
 U49056, RNU49056 Rattus norvegicus CTD-binding SR-like protei... 38 2.9
 U04824, HSU04824 Human protein kinase PITSLRE alpha 2-1 mRNA,... 38 2.9
 U78045, HSU78045 Human collagenase and stromelysin genes, com... 38 2.9
 U04816, HSU04816 Human protein kinase PITSLRE alpha 2-2 mRNA,... 38 2.9
 U04817, HSU04817 Human protein kinase PITSLRE alpha 2-3 mRNA,... 38 2.9

HUMAN ESTs

AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ... 519 e-145
 AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 513 e-144
 R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740.5' ... 490 e-136
 AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 450 e-124
 AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 402 e-110
 AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 347 1e-93
 AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 347 1e-93
 AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 1e-93
 AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 347 1e-93
 AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 315 4e-84
 AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 299 2e-79
 AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 299 2e-79
 AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 250 2e-64
 R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3' ... 250 2e-64
 W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 3e-20
 W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 6e-09
 AA737681, AA737681 nw63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
 T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.090
 R52021, R52021 yg84h09.r1 Homo sapiens cDNA clone 40181 5' si... 42 0.090
 AA569993, AA569993 nm47h04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 42 0.090
 R50149, R50149 yj61c05.s1 Homo sapiens cDNA clone 153224 3' s... 42 0.090
 R87930, R87930 yo47a11.s1 Homo sapiens cDNA clone 181052 3' s... 42 0.090
 AA812204, AA812204 ob84f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
 AA770224, AA770224 ah82e12.s1 Soares testis NHT Homo sapiens ... 42 0.090

D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36
 AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36
 AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36
 T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36
 AA974278, AA974278 oq14d03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.36
 W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36
 H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36
 AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36
 N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36
 R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36
 CI4370, CI4370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36
 H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36
 AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36
 W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36
 T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36
 AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4
 AA993061, AA993061 ot92h08.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 1.4
 R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4
 H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4
 W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4
 N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4
 AA630851, AA630851 nt57f04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 1.4
 N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4
 AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4
 AA911761, AA911761 og19b01.s1 NCI_CGAP_PNS1 Homo sapiens cDNA... 38 1.4
 AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4
 AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4
 AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4
 F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4
 AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4
 AA908705, AA908705 ol01b09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.4
 AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41
 AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032
 AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032
 AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13
 AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13
 AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13
 AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13
 AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13
 AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037	vc68g03.s1 Knowles Solter mouse 2 cell Mus...	40	0.13
AA596585, AA596585	vm58e12.r1 Stratagene mouse Tcell 937311 M...	38	0.51
AA863563, AA863563	vx05a10.r1 Soares 2NbMT Mus musculus cDNA ...	38	0.51
AA795177, AA795177	vq94g04.r1 Knowles Solter mouse blastocyst...	38	0.51
AA914764, AA914764	vy92h04.r1 Soares mouse mammary gland NbMM...	38	0.51
AA590440, AA590440	vm20c04.r1 Knowles Solter mouse blastocyst...	38	0.51
AA563402, AA563402	vl75d08.r1 Knowles Solter mouse blastocyst...	38	0.51
AA260352, AA260352	va93c10.r1 Soares mouse 3NME12 5 Mus muscu...	38	0.51
AA444734, AA444734	ve75d10.r1 Soares mouse mammary gland NbMM...	38	0.51
C85885, C85885	Mus musculus fertilized egg cDNA 3'-end seque...	38	0.51
AA794590, AA794590	vu78h12.r1 Stratagene mouse skin (#937313)...	38	0.51
AA529643, AA529643	vi38a09.r1 Beddington mouse embryonic regi...	38	0.51
AA607084, AA607084	vm84a09.r1 Knowles Solter mouse blastocyst...	38	0.51
AA636994, AA636994	vn05g06.r1 Knowles Solter mouse blastocyst...	38	0.51
AA675676, AA675676	vr73h08.s1 Knowles Solter mouse 2 cell Mus...	38	0.51
AA163890, AA163890	ms52f09.r1 Life Tech mouse embryo 13 5dpc ...	38	0.51
C80539, C80539	Mus musculus 3.5-dpc blastocyst cDNA 3'-end s...	38	0.51
AA051352, AA051352	mj53a09.r1 Soares mouse embryo NbME13.5 14...	38	0.51
W36885, W36885	mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus...	38	0.51
AA930627, AA930627	vy67c05.r1 Stratagene mouse macrophage (#9...	38	0.51
AA244639, AA244639	mx02g12.r1 Soares mouse NML Mus musculus c...	36	2.0
AA967267, AA967267	vz70e08.r1 Soares mouse mammary gland NbMM...	36	2.0
AI048938, AI048938	uc84h06.y1 Sugano mouse kidney mkia Mus mu...	36	2.0
AA162722, AA162722	mn42b07.r1 Beddington mouse embryonic regi...	36	2.0
AA170036, AA170036	ms52d01.r1 Life Tech mouse embryo 13 5dpc...	36	2.0
AA511382, AA511382	vg14b04.r1 Soares mouse NbMH Mus musculus ...	36	2.0
AA555634, AA555634	vk49f08.r1 Stratagene mouse Tcell 937311 M...	36	2.0
AA212823, AA212823	mw81c07.r1 Soares mouse NML Mus musculus c...	36	2.0
AA606813, AA606813	vm90h12.r1 Knowles Solter mouse blastocyst...	36	2.0
AA591610, AA591610	vk49d08.r1 Stratagene mouse Tcell 937311 M...	36	2.0
AA987039, AA987039	uc74e05.x1 Sugano mouse liver mlia Mus mus...	36	2.0
AA105882, AA105882	ml84h07.r1 Stratagene mouse kidney (#93731...	36	2.0
AA451370, AA451370	vf84h02.r1 Soares mouse mammary gland NbMM...	36	2.0
AA612185, AA612185	vo03d05.r1 Stratagene mouse skin (#937313)...	36	2.0
AA103424, AA103424	mo21e05.r1 Life Tech mouse embryo 13 5dpc ...	36	2.0
AA145817, AA145817	mq68a12.r1 Soares 2NbMT Mus musculus cDNA ...	36	2.0
AA272905, AA272905	va39d01.r1 Soares mouse 3NME12 5 Mus muscu...	36	2.0
AA237313, AA237313	mx17b11.r1 Soares mouse NML Mus musculus c...	36	2.0
AA267119, AA267119	mz74d07.r1 Soares mouse lymph node NbMLN M...	36	2.0
AA106683, AA106683	ml83h06.r1 Stratagene mouse kidney (#93731...	36	2.0
AA125061, AA125061	mq83d10.r1 Stratagene mouse melanoma (#937...	36	2.0
AA655241, AA655241	vq84c07.s1 Knowles Solter mouse 2 cell Mus...	36	2.0
AA512835, AA512835	vg13f11.r1 Soares mouse NbMH Mus musculus ...	36	2.0

C70525, C70525	C.elegans cDNA clone yk409g6 : 5' end, single...	44	0.007
F15112, SSO4D09	S.scrofa mRNA; expressed sequence tag (5'; c...	42	0.029
AA684640, AA684640	EST104989 Rat PC-12 cells, untreated Rattu...	40	0.11
H32045, H32045	EST106774 Rat PC-12 cells, untreated Rattus sp...	40	0.11
AA660422, AA660422	00298 MtRHE Medicago truncatula cDNA 5'	40	0.11
C59696, C59696	C.elegans cDNA clone yk440e1 : 3' end, single...	38	0.45
AI008699, AI008699	EST203150 Normalized rat embryo, Bento Soa...	38	0.45
AA753263, AA753263	96BS0294 Rice Immature Seed Lambda ZAPII c...	38	0.45
T38461, T38461	EST103957 Saccharomyces cerevisiae cDNA 3' end.	38	0.45
C59257, C59257	C.elegans cDNA clone yk386b12 : 3' end, singl...	38	0.45
AA948906, AA948906	LD27590.5prime LD Drosophila melanogaster ...	38	0.45
AI001628, AI001628	EST0210 Tilapia brain cDNA library in pUC1...	38	0.45
H31962, H31962	EST106545 Rat PC-12 cells, untreated Rattus sp...	38	0.45
AA979509, AA979509	LD34118.5prime LD Drosophila melanogaster ...	38	0.45
D41274, RICS3647A	Rice cDNA, partial sequence (S3647_1A).	38	0.45
C58362, C58362	C.elegans cDNA clone yk366a8 : 3' end, single...	38	0.45
C57756, C57756	C.elegans cDNA clone yk298b9 : 3' end, single...	38	0.45
AA753070, AA753070	97AS2091 Rice Immature Seed Lambda ZAPII c...	38	0.45
H74687, H74687	383 Brassica napus cDNA clone R25R.	38	0.45
C10513, C10513	C.elegans cDNA clone yk147e9 : 3' end, single...	38	0.45
C55569, C55569	C.elegans cDNA clone yk191d1 : 3' end, single...	38	0.45
C94819, C94819	Sus scrofa mRNA; expressed sequence tag (5'...	38	0.45
C32982, C32982	C.elegans cDNA clone yk338a12 : 3' end, singl...	38	0.45
AA816691, AA816691	LD03795.5prime LD Drosophila melanogaster ...	36	1.8
AA519844, AA519844	TgESTzz36c03.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA531839, AA531839	TgESTzz47h05.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA660182, AA660182	00022 MtRHE Medicago truncatula cDNA 5' si...	36	1.8
D71983, CELK084H2R	C.elegans cDNA clone yk84h2 : 3' end, sin...	36	1.8
R29905, R29905	12510 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	36	1.8
AA519997, AA519997	TgESTzz36h03.r1 TgME49 invivo Bradyzoite c...	36	1.8
U83048, BTU83048	Bos taurus clone 0429 mRNA sequence	36	1.8
AA440655, AA440655	LD15510.5prime LD Drosophila melanogaster ...	36	1.8
AA559374, AA559374	MU002092.NH3 York-Harrop-lung-A Schistosom...	36	1.8
C93857, C93857	Dictyostelium discoideum slug cDNA, clone SSL794	36	1.8
AA520901, AA520901	TgESTzz65a05.r1 TgME49 invivo Bradyzoite c...	36	1.8
T46158, T46158	9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	36	1.8
AA520866, AA520866	TgESTzz68e05.r1 TgME49 invivo Bradyzoite c...	36	1.8
Z17562, ATTS0136	A. thaliana transcribed sequence; clone TAT...	36	1.8
AA520811, AA520811	TgESTzz64d05.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA567455, AA567455	HL01288.5prime HL Drosophila melanogaster ...	36	1.8
AA519228, AA519228	TgESTzz39h02.s1 TgME49 invivo Bradyzoite c...	36	1.8
AA531917, AA531917	TgESTzz48f01.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA519829, AA519829	TgESTzz36a02.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA520185, AA520185	TgESTzz39d03.s1 TgME49 invivo Bradyzoite c...	36	1.8
C37095, C37095	C.elegans cDNA clone yk482c11 : 3' end, singl...	36	1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8
T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8
AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8
AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092
U50719, MSU50719 Manduca sexta neuroglian mRNA, complete cds 40 0.36
Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36
AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36
X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36
D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36
AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4
AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4
X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene... 38 1.4
X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0
D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0
D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0
H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172
AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166
AA977877, AA977877 oq56d03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 571 e-161
AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159
AA972542, AA972542 oo82e01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 561 e-158
AA954270, AA954270 on72e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 557 e-157
AA740333, AA740333 ob23c02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 557 e-157
AA999722, AA999722 ov04c06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 555 e-156
AA970621, AA970621 op40h08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 551 e-155
AA932930, AA932930 oo04g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 541 e-152
AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152
W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152
AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152
R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3' s... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150
 AI027967, AI027967 ov84d04.x1 Soares_testis_NHT Homo sapiens ... 535 e-150
 AA776717, AA776717 ah49d07.s1 Soares testis NHT Homo sapiens ... 535 e-150
 AI040961, AI040961 ov53d06.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
 AI024835, AI024835 ov35h09.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
 AA740667, AA740667 ob01g12.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 531 e-149
 AA994527, AA994527 ou42h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 531 e-149
 AA932728, AA932728 oo31g06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 529 e-149
 AI001978, AI001978 ot39f03.s1 Soares_testis_NHT Homo sapiens ... 529 e-149
 N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149
 N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148
 AA883578, AA883578 al46b08.s1 Soares NFL T GBC S1 Homo sapien... 527 e-148
 AA890154, AA890154 al53f07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 525 e-147
 AA757222, AA757222 ah56f11.s1 Soares testis NHT Homo sapiens ... 525 e-147
 AA456074, AA456074 aa17b07.s1 Soares NhHMPu S1 Homo sapiens c... 523 e-147
 AA884285, AA884285 am32f04.s1 Soares NFL T GBC S1 Homo sapien... 523 e-147
 AA969436, AA969436 op53e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
 AA952918, AA952918 on55h11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
 AA971938, AA971938 op88b01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
 R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146
 AA865258, AA865258 og87d08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 519 e-146
 AA758323, AA758323 ah65e11.s1 Soares testis NHT Homo sapiens ... 519 e-146
 AA972041, AA972041 op88e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 519 e-146
 R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146
 AA917965, AA917965 om37e04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
 AA505880, AA505880 ni01a09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 517 e-145
 AA906270, AA906270 oj98e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
 AA758549, AA758549 ah70b04.s1 Soares testis NHT Homo sapiens ... 517 e-145
 AA927156, AA927156 om20f05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 515 e-144
 AA976254, AA976254 oo30f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 515 e-144
 R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144
 AA938552, AA938552 oo78g11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 513 e-144
 AA483809, AA483809 ne41c08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 513 e-144
 AA962659, AA962659 or31f10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 511 e-143
 AA724803, AA724803 ai05f02.s1 Soares parathyroid tumor NbHPA ... 511 e-143
 AA410432, AA410432 zv12c09.s1 Soares NhHMPu S1 Homo sapiens c... 511 e-143
 AA775373, AA775373 ad19c07.s1 Soares NhHFB Homo sapiens cDNA ... 511 e-143
 AA758038, AA758038 ah67h09.s1 Soares testis NHT Homo sapiens ... 509 e-143
 AA904368, AA904368 ol15d02.s1 Soares_NFL_T_GBC_S1 Homo sapien... 509 e-143
 AA861386, AA861386 ak37b11.s1 Soares testis NHT Homo sapiens ... 507 e-142
 R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141
 AA843421, AA843421 ak07f11.s1 Soares parathyroid tumor NbHPA ... 504 e-141
 H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141
 N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141
 AA815351, AA815351 ai63g05.s1 Soares testis NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 502 e-140
 H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140
 AA988977, AA988977 or87e11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 500 e-140
 AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140
 AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139
 AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139
 R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139
 H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139
 AA875917, AA875917 oj15a08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 496 e-138
 R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138
 AA970616, AA970616 op40h03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 494 e-138
 AA912408, AA912408 ol23a05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
 AA910051, AA910051 ol40e08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
 AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137
 R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136
 AA954722, AA954722 oo84c12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 488 e-136
 R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136
 R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136
 AA885425, AA885425 am12h09.s1 Soares NFL T GBC S1 Homo sapien... 486 e-136
 AA884231, AA884231 am32a01.s1 Soares NFL T GBC S1 Homo sapien... 484 e-135
 AA885048, AA885048 am11a12.s1 Soares NFL T GBC S1 Homo sapien... 482 e-134
 AA996162, AA996162 os14f10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 482 e-134
 AA748637, AA748637 ny10a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 482 e-134
 AI031908, AI031908 ow47e12.x1 Soares_parathyroid_tumor_NbHPA ... 482 e-134
 AA884703, AA884703 am18e02.s1 Soares NFL T GBC S1 Homo sapien... 480 e-134
 AA928243, AA928243 on87e10.s1 Soares_NFL_T_GBC_S1 Homo sapien... 480 e-134
 AI025986, AI025986 ow03a09.s1 Soares_parathyroid_tumor_NbHPA ... 478 e-133
 AA897637, AA897637 oj72g07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 472 e-131
 AA877346, AA877346 olc07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 472 e-131
 AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131
 AA832163, AA832163 oc91b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 470 e-131
 R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131
 N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128
 R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126
 AA579968, AA579968 ng51c03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 444 e-123
 AA843427, AA843427 ak07g06.s1 Soares parathyroid tumor NbHPA ... 438 e-121
 AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121
 AA835882, AA835882 oc81d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 434 e-120
 AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119
 AA512970, AA512970 nj16b08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 432 e-119
 R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118
 AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114
 H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111
 AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110
 AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103
 AA577436, AA577436 nm96h06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 351 4e-95
 AA516390, AA516390 nf55e03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 6e-94
 AA534533, AA534533 nf80h06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 341 3e-92
 AA541583, AA541583 ni89f05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 311 3e-83
 N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3'. 303 8e-81
 AA905015, AA905015 ok09b08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 8e-81
 AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76
 AA939048, AA939048 op56h04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 256 2e-66
 AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63

 R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61
 AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59
 W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44
 AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44
 AA455577, AA455577 aal7b07.r1 Soares NhHMPu S1 Homo sapiens c... 176 1e-42
 AA583931, AA583931 nn64e04.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 172 2e-41
 AA907332, AA907332 ol22g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 168 3e-40

 R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37
 W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36
 AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30
 AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19
 H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19
 AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18
 AA931370, AA931370 oo03d01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 96 3e-18
 AA501911, AA501911 ng54a08.s1 NCI_CGAP_Li2 Homo sapiens cDNA ... 94 1e-17
 AA548419, AA548419 nj14g09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
 AA588892, AA588892 no23b06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
 AI025228, AI025228 ov40h08.x1 Soares_testis_NHT Homo sapiens ... 76 3e-12
 R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11
 R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06
 N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04
 H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04
 H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011
 N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70
 AA614692, AA614692 np52b10.s1 NCI_CGAP_Br1.1 Homo sapiens cDN... 38 0.70
 H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7
 H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7
 AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7
 AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7
 AA632009, AA632009 np74c07.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 2.7
 H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7
 AI022018, AI022018 ow64d01.x1 Soares_senescent_fibroblasts_Nb... 36 2.7
 AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7
 N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7
 AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65
 AA051612, AA051612 mj52c07.r1 Soares mouse embryo NbME13.5 14... 238 1e-61
 AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst... 234 2e-60
 AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56
 AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56
 AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54
 AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50
 W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48
 AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34
 W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27
 Z31174, MMTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25
 AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12
 AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11
 AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004
 AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99
 AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99
 W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99
 AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99
 AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99
 Z31139, MMTEST427 M.musculus expressed sequence tag MTEST427 36 0.99
 C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9
 AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9
 AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9
 W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9
 AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9
 AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9
 AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9
 AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9
 AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9
 AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9
 AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9
 W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9
 AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9
 AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9

AI043768, AI043768 UI-R-C0-jm-d-11-0-UI.s1 UI-R-C0 Rattus nor... 174 1e-42
 AA531635, AA531635 TgESTzz29b08.r1 TgME49 invivo Bradyzoite c... 38 0.22
 AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22
 AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87
 D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87
 AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87
 AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5
 C20118, C20118 Rice cDNA, partial sequence (E11542_2A) 34 3.5
 AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5
 AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

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U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11
 V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45
 X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45
 U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8
 U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8
 U04101, POU04101 Pleurotus ostreatus D1742, Japan, mating gro... 38 1.8
 AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8
 M18680, HUMRGAPS Homo sapiens 5S-rRNA pseudogene. 38 1.8
 AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8
 AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8
 Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8
 U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8
 U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8
 U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8
 U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8
 U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147
 AA834501, AA834501 of21c02.s1 NCI_CGAP_Kid6 Homo sapiens cDNA... 381 e-104
 W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84
 R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54
 AA761660, AA761660 nz24b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 3e-53
 AA887861, AA887861 nq99b07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 74 2e-11
 AA644044, AA644044 nm20b12.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22
 AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22
 T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86
 AA515882, AA515882 nf67f10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 38 0.86
 AA664812, AA664812 nu69b05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA... 36 3.4
 T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4
 AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4
 AA916894, AA916894 og34g10.s1 NCI_CGAP_Br7 Homo sapiens cDNA ... 36 3.4
 N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4
 AA953544, AA953544 om79g06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 36 3.4
 AA505576, AA505576 nh93f03.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 3.4
 H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4
 AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4
 AA595583, AA595583 nk92c04.s1 NCI_CGAP_Co11 Homo sapiens cDNA... 36 3.4
 AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4
 AA810167, AA810167 ob88a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 36 3.4
 H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4
 W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4
 R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4
 AA514234, AA514234 nf56e10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms
 AA821640, AA821640 vw
 AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001
 T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069
 AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1
 AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1
 AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1
 AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3
 R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3
 AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

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X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

Z50028, X72735, U13072, Z34294, AB002109, X68401, M92840, D88399, Z36238, AF000262, Z46828,

HUMAN ESTs

AA215808, AA215808 zr98b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 1082 0.0
 N75131, N75131 yz29g07.r1 Soares multiple sclerosis 2NbHMSP H... 989 0.0
 AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0
 AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0
 AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0
 AA878521, AA878521 oj19c01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 844 0.0
 AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0
 W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0
 AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0
 N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0
 N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0
 AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0
 AA768023, AA768023 oa60e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 728 0.0
 AA872018, AA872018 oi05f08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 718 0.0
 AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0
 AA814881, AA814881 oa75e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 708 0.0
 R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0
 W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0
 R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0
 D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10... 630 e-179
 AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178
 AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177
 R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176
 AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175
 AA633335, AA633335 nq58h09.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 611 e-173
 AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169
 R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168
 AA872617, AA872617 oi05g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 591 e-167
 H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166
 AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159
 H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153
 AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147
 AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145
 AA297001, AA297001 EST112550 Adipose tissue, white II Homo sa... 502 e-140
 AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139
 AA769090, AA769090 oa74e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 494 e-138
 H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121
 H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120
 AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116
D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113
AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102
AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101
AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101
AA932620, AA932620 oo61h04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 365 4e-99
AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91
AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76
AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71
H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66

R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66
AA229414, AA229414 nc47f12.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 246 3e-63
D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52
AA249061, AA249061 ll4438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40
R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33
R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19
AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081

AA977111, AA977111 oq24c03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.32
AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0
gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0
gb|AA510881|AA510881 wh59c11.r1 Soares mouse mammary gland NbMM... 617 e-175
gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174
gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155
gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153
gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123
gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117
gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108
emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83
gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78
gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76
gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69
gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69
gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62
dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41
gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19
gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12
gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08
gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06
gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04
gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45
 gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8
 gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8

gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161
 gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108
 gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96
 gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90
 gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82
 gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82
 gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73
 gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37
 gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34
 dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10
 gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6
 dbj|C22690|C22690 Rice cDNA, partial sequence (S5274 4A) 36 1.6

gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6
 gb|AA550136|AA550136 1244m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 1.6
 gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6

gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6

gb|AA056876|AA056876 SWMFCA987SK Brugia malayi microfilaria cDN... 36 1.6

gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

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emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10
 gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10
 emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10
 gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
 gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
 dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40
 dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40
 gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40
 emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6
 dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6
 gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6
 emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6
 gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

HUMAN ESTs

gb AA401219 AA401219	zv63a03.r1	Soares total fetus Nb2HF8 9w Ho...	993	0.0
gb H69371 H69371	yu19h09.r1	Homo sapiens cDNA clone 234305 5' s...	44	0.049
gb N62576 N62576	za13d10.s1	Homo sapiens cDNA clone 292435 3' s...	42	0.19
gb W77763 W77763	zd69c06.r1	Soares fetal heart NbHH19W Homo sap...	40	0.77
gb R14832 R14832	yf93g05.r1	Homo sapiens cDNA clone 30203 5'.	40	0.77
gb T90524 T90524	yd40a04.s1	Homo sapiens cDNA clone 110670 3' s...	38	3.0
gb R91887 R91887	yq04c09.r1	Homo sapiens cDNA clone 195952 5'.	38	3.0
gb AA586935 AA586935	nn68h03.s1	NCI_CGAP_Lar1 Homo sapiens cDNA...	38	3.0
gb T46987 T46987	yb12a07.s1	Homo sapiens cDNA clone 70932 3' co...	38	3.0
gb AA853975 AA853975	aj51f09.s1	Soares testis NHT Homo sapiens ...	38	3.0
gb T97059 T97059	ye50e01.r1	Homo sapiens cDNA clone 121176 5'.	38	3.0
gb AA883119 AA883119	am15h02.s1	Soares NFL T GBC S1 Homo sapien...	38	3.0
gb AA860074 AA860074	ak45b06.s1	Soares testis NHT Homo sapiens ...	38	3.0
gb AA889618 AA889618	ak28f06.s1	Soares_testis NHT Homo sapiens ...	38	3.0

gb AA230450 AA230450	mv73c06.r1	Soares mouse 3NME12 5	Mus muscu...	38	1.1
gb AA058041 AA058041	mj58e08.r1	Soares mouse embryo	NbME13.5 14...	38	1.1
gb AA152953 AA152953	mq54a03.r1	Soares 2NbMT	Mus musculus cDNA ...	38	1.1
gb W34414 W34414	ma98b07.r1	Soares mouse p3NMF19.5	Mus musculus...	38	1.1
gb AA465969 AA465969	ve90c06.s1	Knowles Solter mouse 2 cell	Mus...	38	1.1
gb AA261173 AA261173	mz62b11.r1	Soares mouse lymph node	NbMLN M...	38	1.1
gb AA238109 AA238109	mw97b05.r1	Soares mouse NML	Mus musculus c...	38	1.1
dbj C86549 C86549		Mus musculus fertilized egg	cDNA 3'-end seque...	38	1.1
gb AI048677 AI048677	ub29g09.r1	Soares 2NbMT	Mus musculus cDNA ...	38	1.1
dbj D77921 MUSC1A08		Mouse embryonal carcinoma F9 cell	cDNA, C1A08	38	1.1
gb AA396183 AA396183	vb45e04.r1	Soares mouse lymph node	NbMLN M...	38	1.1
gb AA465898 AA465898	vc62f12.s1	Knowles Solter mouse 2 cell	Mus...	36	4.3
gb AA041869 AA041869	mj05b12.r1	Soares mouse embryo	NbME13.5 14...	36	4.3
gb AA637824 AA637824	vr21f11.r1	Barstead mouse myotubes	MPLRB5 ...	36	4.3
gb W82563 W82563	mf05g06.r1	Soares mouse p3NMF19.5	Mus musculus...	36	4.3
gb AA389972 AA389972	vb30e03.r1	Soares mouse lymph node	NbMLN M...	36	4.3
gb AA396253 AA396253	vb45f08.r1	Soares mouse lymph node	NbMLN M...	36	4.3
gb AA920907 AA920907	vy84f04.r1	Stratagene mouse macrophage (#9...		36	4.3
gb AA517166 AA517166	vh98h05.r1	Barstead mouse myotubes	MPLRB5 ...	36	4.3
gb AA433599 AA433599	vf47a05.r1	Soares mouse NbMH	Mus musculus ...	36	4.3
gb AA867252 AA867252	vx25c01.r1	Soares 2NbMT	Mus musculus cDNA ...	36	4.3
dbj C85619 C85619		Mus musculus fertilized egg	cDNA 3'-end seque...	36	4.3
gb AA260277 AA260277	va93g05.r1	Soares mouse 3NME12 5	Mus muscu...	36	4.3
gb AA172548 AA172548	mt04g11.r1	Soares mouse 3NbMS	Mus musculus...	36	4.3
gb AA266879 AA266879	mz96a02.r1	Soares mouse lymph node	NbMLN M...	36	4.3
gb AA473019 AA473019	vd43e06.r1	Barstead	MPLRB1 Mus musculus cD...	36	4.3

gb|R47549|R47549 SW3ICA119SK *Brugia malayi* infective larva cDNA... 40 0.24
 gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated *Rattus* sp... 38 0.96
 gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 *Rattus* nor... 38 0.96
 gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 *Rattus* nor... 38 0.96
 gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96
 gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96
 gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96
 gb|R95272|R95272 SWOvL3CA167SK *Onchocerca volvulus* infective la... 36 3.8
 gb|AA917208|AA917208 ka05f02.s1 *Onchocerca volvulus* infective l... 36 3.8
 dbj|C62023|C62023 *C.elegans* cDNA clone yk249d5 : 5' end, single... 36 3.8

 gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8
 gb|AI043280|AI043280 TENU0920 *T. cruzi* epimastigote normalized ... 36 3.8
 gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8
 gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8
 dbj|C62878|C62878 *C.elegans* cDNA clone yk296d4 : 5' end, single... 36 3.8
 gb|AA915818|AA915818 SWOvL3CA1269SK *Onchocerca volvulus* infecti... 36 3.8
 gb|W00009|W00009 TgESTzy75b07.r1 TgRH Tachyzoite cDNA *Toxoplasm*... 36 3.8

 gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8
 gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 *Rattus* nor... 36 3.8
 gb|H54977|H54977 HHU16a *Sorghum bicolor* cv. TX430 *Sorghum* bicol... 36 3.8

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gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082
 gb|U50197|CELF25E2 *Caenorhabditis elegans* cosmid F25E2. 44 0.082
 dbj|AB007727|AB007727 *Arabidopsis thaliana* genomic DNA, chromos... 44 0.082
 gb|U02562|BSU02562 *Bacillus subtilis* N-acetylglucosaminidase (l... 42 0.32
 dbj|D45048|BACORFX *Bacillus subtilis* gene for beta-N-acetylgluc... 42 0.32
 emb|Z70683|CEF13B12 *Caenorhabditis elegans* cosmid F13B12, compl... 40 1.3
 emb|AL023828|CEY17G7B *Caenorhabditis elegans* cosmid Y17G7B, com... 40 1.3
 gb|U39740|CELZC64 *Caenorhabditis elegans* cosmid ZC64. 40 1.3
 gb|AF006490|AF006490 *Gossypium hirsutum* adenine nucleotide tran... 40 1.3
 emb|AL010170|PFSC03098 *Plasmodium falciparum* DNA *** SEQUENCING... 40 1.3
 gb|U53701|GHU53701 *Gossypium hirsutum* alcohol dehydrogenase 2d ... 40 1.3

HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0
 gb|AA251062|AA251062 zs07c10.r1 NCI_CGAP_GCB1 *Homo sapiens* cDNA... 795 0.0

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0
 gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165
 gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154
 gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148
 gb|AA225705|AA225705 nc10b05.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 515 e-144
 gb|W27883|W27883 39b10 Human retina cDNA randomly primed sublib... 484 e-134
 gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121
 gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119
 gb|AA250933|AA250933 zs07d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 426
 e-117

gb|AA216370|AA216370 nc10b05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 398 e-109
 gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108
 gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108
 gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97
 gb|AA602297|AA602297 np25a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 281 1e-73
 gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66
 gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59
 gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56
 gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55
 dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47
 gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38
 gb|AA642960|AA642960 60f07.s1 NCI_CGAP_Lym3 Homo sapiens cDNA... 147 4e-33
 gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62
 gb|AA521500|AA521500 aa73h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.62
 gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62
 gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4
 dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4
 gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104
 gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93
 gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60
 gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60
 gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44
 gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05
 gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001
 gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001
 gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
 gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004
 gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056

gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88
 gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88
 dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88
 gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88
 gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88
 gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
 gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5
 gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5
 gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5
 emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5

 gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5
 gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5
 gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
 gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5
 gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

 dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78
 gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78
 gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78
 gb|H33464|H33464 EST109494 Rat PC-12 cells, NGF-treated (9 days... 38 0.78
 gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1
 dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1
 gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1
 gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
 gb|N60251|N60251 TgESTzy.11d04.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 3.1
 gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1
 gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1
 gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
 gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1
 gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1
 gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

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gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41
 gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23
 gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23
 gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23
 gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22
 emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21
 gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19
 gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17
 gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15
 gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14

 gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13
 gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13
 emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13
 emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12
 gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12
 gb|G29058|G29058 chicken STS ADL368 76 3e-11
 gb|G29060|G29060 chicken STS ADL352 76 3e-11

 gb|U34048|H DU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11
 gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09
 gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08
 gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06
 gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06
 emb|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06
 gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029
 emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12
 emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12
 gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46
 emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46
 emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46
 emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46
 gb|L13767|STMSEC101A Streptomyces lividans sec101 gene, 5' end p... 42 0.46
 emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8
 gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|J02871|HUMC45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8
 dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8
 gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8
 gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8
 emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8
 gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8
 emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8
 gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0
 gb|AA975279|AA975279 oq36e08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 900 0.0
 gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0
 gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0
 gb|AA632259|AA632259 np67d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 730 0.0
 gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0
 gb|AA515175|AA515175 ng68f10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA... 615 e-174
 gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172
 gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165
 gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165
 gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163
 gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163
 gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157
 gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149
 gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147
 gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139
 gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134
 gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129
 gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125
 gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115
 gb|AA907095|AA907095 ol03b12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 414 e-113
 gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67
 gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55
 gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55
 gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52
 gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47
 gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24
 N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109
 gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105
 gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93
 gb|AA028696|AA028696 mi12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82
 gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62
 gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57
 gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57
 dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57
 gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17
 gb|AA667535|AA667535 vv18b12.r1 Stratagene mouse heart (#937316... 40 0.31
 gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb|AA444814|AA444814 vg50e04.r1 Soares mouse mammary gland NbMM... 38 1.2
 gb|AA763341|AA763341 vw53b12.r1 Soares mouse mammary gland NMLM... 38 1.2
 gb|AA110827|AA110827 mp57a12.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
 gb|AA691932|AA691932 vt06b04.r1 Barstead mouse myotubes MPLRB5 ... 38 1.2
 gb|W77233|W77233 me61f11.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2
 gb|AA072872|AA072872 mm80g08.r1 Stratagene mouse embryonic carc... 38 1.2
 gb|AA980630|AA980630 ua43f05.r1 Soares mouse mammary gland NbMM... 36 4.9
 gb|AA065522|AA065522 ml54d09.r1 Stratagene mouse testis (#93730... 36 4.9
 gb|AA982398|AA982398 uh07b08.r1 Soares mouse hypothalamus NMHy ... 36 4.9
 gb|W62610|W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
 gb|AA286651|AA286651 vb79b02.r1 Soares mouse 3NbME12-5 Mus muscu... 36 4.9
 gb|AA399772|AA399772 vd70g05.r1 Beddington mouse embryonic regi... 36 4.9
 gb|AA510475|AA510475 vg32h08.r1 Soares mouse mammary gland NbMM... 36 4.9
 gb|AA109064|AA109064 ml63g02.r1 Stratagene mouse testis (#93730... 36 4.9
 gb|AA033485|AA033485 mi42c08.r1 Soares mouse embryo NbME13.5 14... 36 4.9
 gb|W57221|W57221 md59g10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
 gb|AA467106|AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 36 4.9
 gb|W97470|W97470 mf95a11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
 gb|AA606917|AA606917 vm91c05.r1 Knowles Solter mouse blastocyst... 36 4.9
 dbj|C78330|C78330 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9
 gb|AA013753|AA013753 mh26h12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9
 gb|AA145240|AA145240 mr12a03.r1 Soares mouse 3NbMS Mus musculus... 36 4.9
 gb|AA245533|AA245533 mx03c11.r1 Soares mouse NML Mus musculus c... 36 4.9
 gb|AA770893|AA770893 vt13a08.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9
 dbj|C79987|C79987 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9
 gb|AA014027|AA014027 mh24a12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9
 dbj|C89051|C89051 Mus musculus early blastocyst cDNA, clone 01B... 36 4.9
 gb|AA058308|AA058308 mj59e09.r1 Soares mouse embryo NbME13.5 14... 36 4.9
 gb|AA673826|AA673826 vu08h10.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9
 gb|AA637080|AA637080 vn07h04.r1 Knowles Solter mouse blastocyst... 36 4.9
 gb|W44292|W44292 mc80c07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9

gb|AA955972|AA955972 UI-R-E1-ff-d-10-0-UI.s1 UI-R-E1 Rattus nor... 159 4e-37
 gb|AA957275|AA957275 UI-R-E1-fq-f-08-0-UI.s1 UI-R-E1 Rattus nor... 157 2e-36
 emb|Z84031|SSZ84031 S.scrofa mRNA; expressed sequence tag (5'; ... 111 9e-23
 gb|AF041408|AF041408 Fragaria x ananassa clone FA110b 96 5e-18
 gb|AA933116|AA933116 SWBmL3SA048T3 Brugia malayi L3 subtracted ... 58 1e-06
 gb|AA933363|AA933363 SWBmL3SA615T3 Brugia malayi L3 subtracted ... 52 7e-05
 gb|AA660164|AA660164 00001 MtrHE Medicago truncatula cDNA 5' si... 50 3e-04
 gb|N37420|N37420 18647 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018
 gb|H35981|H35981 14503 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018
 gb|AA882627|AA882627 TENS0198 T. cruzi epimastigote normalized ... 44 0.018
 gb|AI026481|AI026481 TENU0693 T. cruzi epimastigote normalized ... 42 0.070
 gb|AA946369|AA946369 EST201868 Normalized rat lung, Bento Soare... 42 0.070

gb AI010371 AI010371	EST204822	Normalized rat lung, Bento Soare...	42	0.070
gb AI010257 AI010257	EST204708	Normalized rat lung, Bento Soare...	42	0.070
dbj D39318 RICR3325A		Rice cDNA, partial sequence (R3325_1A).	40	0.28
gb U40140 OSU40140		Oryza sativa clone pFDRRC22 mRNA sequence.	40	0.28
gb AI009132 AI009132	EST203583	Normalized rat embryo, Bento Soa...	40	0.28
dbj D47291 RICS12574A		Rice cDNA, partial sequence (S12574_1A).	40	0.28
dbj D47316 RICS12613A		Rice cDNA, partial sequence (S12613_1A).	40	0.28
gb T42265 T42265	5528	Lambda-PRL2 Arabidopsis thaliana cDNA clo...	40	0.28
dbj D47631 RICS13239A		Rice cDNA, partial sequence (S13239_1A).	40	0.28
gb AI013513 AI013513	EST208188	Normalized rat spleen, Bento Soa...	40	0.28
gb AA751980 AA751980	96AS0896	Rice Immature Seed Lambda ZAPII c...	40	0.28
gb AA660165 AA660165	00002	MtRHE Medicago truncatula cDNA 5' si...	40	0.28
emb Z34868 ATTS3597		A. thaliana transcribed sequence; clone FAF...	40	0.28
dbj D39131 RICR2302A		Rice cDNA, partial sequence (R2302_1A).	40	0.28
gb AA963968 AA963968	UI-R-C0-gs-b-05-0-UI.s1	UI-R-C0 Rattus nor...	40	0.28
gb AA866346 AA866346	UI-R-A0-bm-a-05-0-UI.s1	UI-R-A0 Rattus nor...	40	0.28
gb AI044437 AI044437	UI-R-C1-js-e-06-0-UI.s1	UI-R-C1 Rattus nor...	40	0.28
dbj D41811 RICS4634A		Rice cDNA, partial sequence (S4634_1A).	40	0.28
dbj C19261 C19261		Rice cDNA, partial sequence (E10176_1A)	40	0.28
dbj D48409 RICS14588A		Rice cDNA, partial sequence (S14588_1A).	40	0.28
dbj C26556 C26556		Rice cDNA, partial sequence (C12586_1A)	40	0.28
dbj D47831 RICS13548A		Rice cDNA, partial sequence (S13548_1A).	40	0.28
dbj C72152 C72152		Rice cDNA, partial sequence (E1094_3A)	40	0.28
dbj D46553 RICS11305A		Rice cDNA, partial sequence (S11305_2A).	40	0.28
gb AI028926 AI0289		(and many others of similar score)		

SEQ ID NO:565

emb X68308 OOLPLIP	O.ovis mRNA for lipoprotein lipase	40	1.2
gb AE000660 HUA000660	Homo sapiens T-cell receptor alpha delta...	40	1.2
emb AL022333 HS474I12	Human DNA sequence *** SEQUENCING IN PROG...	38	4.6
emb Z12618 CFTRG	C.fasciculata gene encoding trypanothione redu...	38	4.6
gb M81651 HUMSEMIIB	Human semenogelin II (SEMGII) gene, complet...	38	4.6
gb M96980 HUMMYT1A	Homo sapiens myelin transcription factor 1 (...)	38	4.6
gb U89688 ACU89688	Acanthamoeba castellanii myosin-I binding pr...	38	4.6
gb AC002497 AC002497	Human Cosmid g1940a142 from 7q31.3, comple...	38	4.6
gb M81652 HUMSMNGLN	Homo sapiens semenogelin II mRNA, complete ...	38	4.6
gb M25665 HUMNCF1A	Human neutrophil cytosol factor 1 (NCF-47k) ...	38	4.6
gb M73325 TRFTRPREDC	Crithidia fasciculata trypanothione reduct...	38	4.6
gb M73324 TRFTRPREDB	Crithidia fasciculata trypanothione reduct...	38	4.6
emb X92589 MMSEMIIGN	M.mulatta semenogelin II gene	38	4.6
emb Z47556 HSSG1SG2	H.sapiens genes for semenogelin I and semen...	38	4.6
gb AC004753 AC004753	Homo sapiens chromosome 16, cosmid clone R...	38	4.6
gb M55067 HUMNADPHO	Human 47-kD autosomal chronic granulomatous...	38	4.6

gb|M73323|TRFTRPRED A Crithidia fasciculata trypanothione reduct... 38 4.6

HUMAN ESTs

gb|R11942|R11942 yf54c05.r1 Homo sapiens cDNA clone 25950 5'. 656 0.0
 gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130
 gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94_24 5' ... 133 5e-29
 gb|R37032|R37032 yf54c05.s1 Homo sapiens cDNA clone 25950 3'. 44 0.036
 gb|AA661650|AA661650 nv02h12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA261982|AA261982 zs20d03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA588219|AA588219 no24c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA250891|AA250891 zs06c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA244177|AA244177 nc05a02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 38 2.2
 gb|AA715147|AA715147 nv10d05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA659887|AA659887 nv03a10.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA627890|AA627890 nq70a08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA603596|AA603596 np27b11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA613738|AA613738 np25h09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA715248|AA715248 nv10h06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AI038487|AI038487 ow25d12.x1 Soares_parathyroid_tumor_NbHPA ... 38 2.2
 gb|AA252786|AA252786 zs26f10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA287819|AA287819 zs50h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA564176|AA564176 nj04c08.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA643870|AA643870 np26h07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA280371|AA280371 zt05f07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|R00687|R00687 ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2
 gb|AA587820|AA587820 nj06h05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA588443|AA588443 no22c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA568385|AA568385 nl88f06.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 38 2.2
 gb|AA281831|AA281831 zt06c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2
 gb|AA689530|AA689530 ns66e07.r1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA688300|AA688300 nv14a09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA687962|AA687962 nv13h04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA526586|AA526586 ni96f11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA642589|AA642589 nq73f04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA541594|AA541594 ni89g07.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
 gb|AA278713|AA278713 zs76h02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
 gb|T58661|T58661 ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2
 gb|AA689473|AA689473 ns66e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
 gb|AA459023|AA459023 aa26a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07
 gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2
 gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2
 gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2
 gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2
 gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2
 gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2
 gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8
 gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8
 gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasma... 36 2.8
 gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8
 gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8
 gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8
 gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8

dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044_1A). 36 2.8
 gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8
 gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8
 dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786_1A). 36 2.8
 gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8
 dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612_1A). 36 2.8
 gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8
 dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620_1A). 36 2.8
 gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8
 gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

We claim:

1. A method of determining a position of a mobile station, comprising the steps of: receiving a signal from the mobile station; determining a position of the mobile station based on the received signal; and displaying the determined position on a map.

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

2. The method of claim 1, wherein the agent is selected from the group consisting of

(a)

a nucleotide acid molecule comprising NA group 1 nucleic acid molecules

or a fragment thereof,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules or

a fragment thereof,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules

or a fragment thereof,

(d)

an antibody that binds to an expression product of NA group 1 nucleic

acids,

(e)

an antibody that binds to an expression product of NA group 3 nucleic

acids,

(f)

an antibody that binds to an expression product of NA group 17 nucleic acids,

5

(g)

and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

10

(h)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and

(I)

15

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3.

The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

20

25

4.

The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5.

30

A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

5

the protein,

(ii)

a peptide derived from the protein,

10

(iii)

an antibody which selectively binds the protein or peptide, and

(iv)

cytolytic T cells specific for a complex of the peptide derived from the

15 protein and an MHC molecule,

as a determination of regression, progression or onset of said condition.

6.

The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.

20

7.

The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of

(a)

25

an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii), and

30

(c)

a cell which presents the complex of the peptide and MHC molecule of

(iv).

5

8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group
3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group
15 11 molecule.

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group
12 molecule.

20 13. The method of claim 5, wherein the nucleic acid molecule is a NA Group
13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group
14 molecule.

25

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group
15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group

30 16 molecule.

17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

5 18. A pharmaceutical preparation for a human subject comprising
an agent which when administered to the subject enriches selectively the
presence of complexes of an HLA molecule and a human cancer associated antigen, and
a pharmaceutically acceptable carrier, wherein the human cancer
associated antigen is a fragment of a human cancer associated antigen precursor encoded by a
10 nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises
a plurality of agents, each of which enriches selectively in the subject complexes of an HLA
molecule and a different human cancer associated antigen.

15 20. The pharmaceutical preparation of claim 19, wherein the plurality is at
least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid
20 molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected
from the group consisting of

(1) an isolated polypeptide comprising the human cancer associated
25 antigen, or a functional variant thereof,

(2) an isolated nucleic acid operably linked to a promoter for expressing
the isolated polypeptide, or functional variant thereof,

(3) a host cell expressing the isolated polypeptide, or functional variant
thereof, and

(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an
5 adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell
expressing an isolated polypeptide comprising the human cancer associated antigen or a
functional variant thereof, and wherein the cell is nonproliferative.

10

25. The pharmaceutical preparation of claim 18, wherein the agent is a cell
expressing an isolated polypeptide comprising the human cancer associated antigen or a
functional variant thereof, and wherein the cell expresses an HLA molecule that binds the
polypeptide.

15

26. The pharmaceutical preparation of claim 18, wherein the agent is at least
two, at least three, at least four or at least five different polypeptides, each coding for a different
human cancer associated antigen or functional variant thereof.

20 27. The pharmaceutical preparation of claim 18, wherein the agent is a PP
Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP
Group 3 polypeptide or a PP Group 4 polypeptide.

25

29. The pharmaceutical preparation of claim 25, wherein the cell expresses
one or both of the polypeptide and HLA molecule recombinantly.

30. The pharmaceutical preparation of claim 25, wherein the cell is

30 nonproliferative.

31. A composition comprising
an isolated agent that binds selectively a PP Group 1 polypeptide.

32. The composition of matter of claim 31, wherein the agent binds selectively
5 a PP Group 3 polypeptide.

33. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 11 polypeptide.

10 34. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 12 polypeptide.

35. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 13 polypeptide.

15

36. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 14 polypeptide.

37. The composition of matter of claim 31, wherein the agent binds selectively
20 a PP Group 15 polypeptide.

38. The composition of matter of claim 31, wherein the agent binds selectively
a PP Group 16 polypeptide.

25 39. The composition of claims 31-38, wherein the agent is a plurality of
different agents that bind selectively at least two, at least three, at least four, or at least five
different such polypeptides.

40. The composition of claims 31-38, wherein the agent is an antibody.

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic
5 agent.

43. The composition of matter of claim 42, wherein the conjugate is of the
agent and a therapeutic or diagnostic that is a toxin.

10 44. A pharmaceutical composition comprising an isolated nucleic acid
molecule selected from the group consisting of:

(1)

NA Group 1 molecules, and

15 (2)

NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic
acid molecule comprises a NA Group 3 or NA Group 4 molecule.

20

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic
acid molecule comprises at least two isolated nucleic acid molecules coding for two different
polypeptides, each polypeptide comprising a different human cancer associated antigen.

25 47. The pharmaceutical composition of claims 44-46 further comprising an
expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host
cell recombinantly expressing the isolated nucleic acid molecule.

49. A pharmaceutical composition comprising
an isolated polypeptide comprising a PP Group 1 or a PP Group 2
polypeptide, and
a pharmaceutically acceptable carrier.

5

50. The pharmaceutical composition of claim 49, wherein the isolated
polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

10 51. The pharmaceutical composition of claim 49, wherein the isolated
polypeptide comprises at least two different polypeptides, each comprising a different human
cancer associated antigen.

52. The pharmaceutical composition of claim 49, wherein the isolated
15 polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP
Group 12 polypeptides or HLA binding fragments thereof.

20

54. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

55. The pharmaceutical composition of claim 49, wherein the isolated
25 polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated
polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

30

57. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 16 polypeptides or HLA binding fragments thereof.

58. The pharmaceutical composition of claims 49-57, further comprising an
5 adjuvant.

59. An isolated nucleic acid molecule comprising a NA Group 3 molecule.

60. An isolated nucleic acid molecule comprising a NA Group 4 molecule.

10

61. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
----- is a Group 11 molecule or a fragment thereof. -----

62. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
15 is a Group 12 molecule or a fragment thereof.

63. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
is a Group 13 molecule or a fragment thereof.

20 64. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
is a Group 14 molecule or a fragment thereof.

65. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
is a Group 15 molecule or a fragment thereof.

25

66. The isolated nucleic acid molecule of claims 59-60, wherein the molecule
is a Group 16 molecule or a fragment thereof.

67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid
consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of
5 sufficient length to represent a sequence unique within the human genome, and identifying a
nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

10

provided that the fragment includes a sequence of contiguous nucleotides
which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1

(correct?),

15

(2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of
contiguous nucleotides is selected from the group consisting of:

20

(1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

25

at least four contiguous nucleotides nonidentical to the sequence group,

(4)

at least five contiguous nucleotides nonidentical to the sequence group,

(5)

30

at least six contiguous nucleotides nonidentical to the sequence group,

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a
5 size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides,
14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides,
26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides,
and 200 nucleotides.

10 70. The isolated nucleic acid molecule of claim 67, wherein the molecule
encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human
antibody.

71. An expression vector comprising an isolated nucleic acid molecule of
15 claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a
promoter, wherein the nucleic acid is a NA Group 2 molecule.

20 73. An expression vector comprising a NA Group 1 or Group 2 molecule and
a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims
71, 72, or 73.

25

75. A host cell transformed or transfected with an expression vector of claim
71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of
30 claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

5

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

10 80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

15

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

20 83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising
a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

25 (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

30

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

5 85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated
10 antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)

a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

15

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

(c)

20

a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes
25 of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(i)

removing an immunoreactive cell containing sample from the subject,

15

(ii)

contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

20

(iii)

introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

10

(I)

identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group-1 molecule

15

(ii)

transfecting a host cell with a nucleic acid selected from the group consisting of

20

(a) the nucleic acid molecule identified,

25

(b)

a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen,

30

(c)

deletions, substitutions or additions to (a) or (b), and

(d)

degenerates of (a), (b), or (c);

(iii)

5 culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv)

10 introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

94. The method of claim 93, further comprising:

15 (a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule,

20 wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

95. The method of claim 93, wherein the immune response comprises a B-cell
25 response or a T cell response.

96. The method of claim 95, wherein the response is a T-cell response which
comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the
expression product of the nucleic acid molecule or cells of the subject expressing the human
30 cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells
5 to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

10 administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.

15

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject
20 of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in
25 the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that
30 the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

5 (i) identifying cells from the subject which express abnormal amounts of the protein;

(ii) isolating a sample of the cells;

(iii) cultivating the cells, and

(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

10

106. The method of claim 105, wherein the cells express a protein selected from the group

consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

15

107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by

20 aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

25 109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid
30 molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising
a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

10

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

15

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

20

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

25

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

30

HY 10-12
LUCA15
DXSB237E

KEESPUPKVVNPLIGLICXGSDSYEEEEEEQTPPPQPTAQPKREEQTKKNEEDKLTVDNKLACLICRRQFPNKEVL 970
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HY 10-14
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Figure 1

YLSKRLK...
YLSKRLK...
YLSKRLK...

Figure 3b.

227bp exon:

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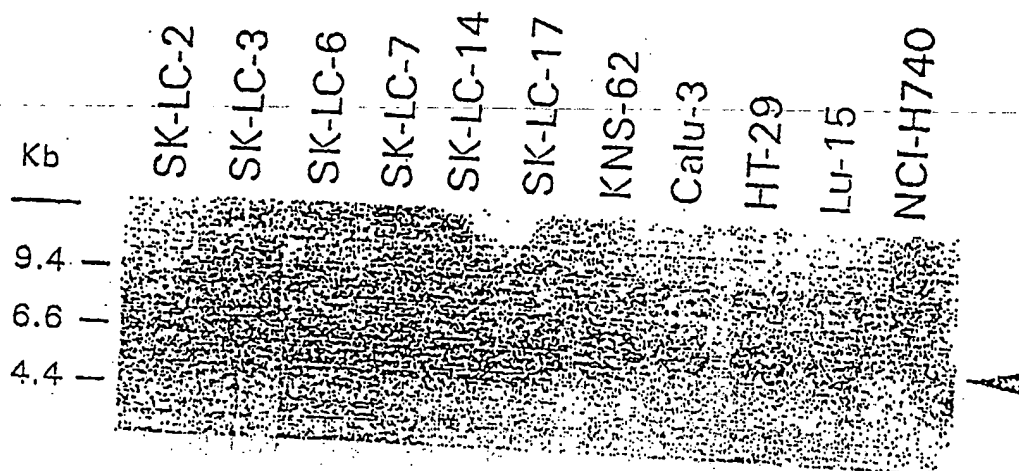


Figure 4

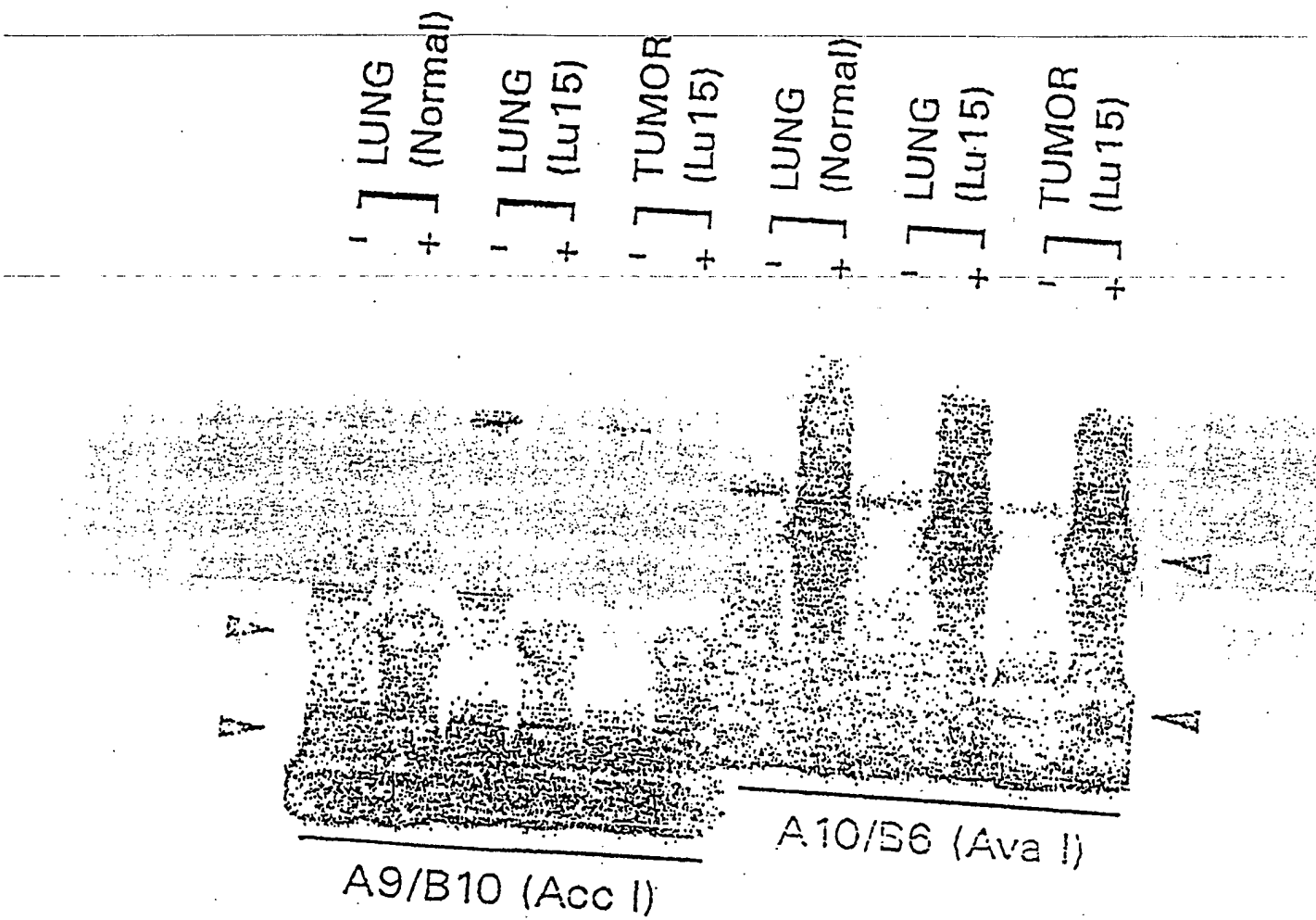


Figure 5

SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research
Old, Lloyd J.
Scanlan, Matthew J.
Stockert, Elisabeth
Gure, Ali
Chen, Yao-Tseng
Gout, Ivan
O'Hare, Michael
Obata, Yuichi
Pfreundschuh, Michael
Tureci, Ozlem
Sahin, Ugur

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 <213> Homo Sapiens

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 <211> 567
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<210> 8

<211> 730

<212> DNA

<213> Homo Sapiens

<400> 8

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<210> 9

<211> 585

<212> DNA

<213> Homo Sapiens

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<210> 10

<211> 661

<212> DNA

<213> Homo Sapiens

<400> 10

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<210> 11
 <211> 1162
 <212> DNA
 <213> Homo Sapiens

<400> 11						
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<211> 372
 <212> DNA
 <213> Homo Sapiens

<400> 13

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<210> 14

<211> 1167

<212> DNA
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<400> 14

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<211> 1148

<212> DNA
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<211> 1113

<212> DNA

<213> Homo Sapiens

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<210> 17

<211> 731

<212> DNA

<213> Homo Sapiens

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<211> 1145
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<210> 19
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<212> DNA
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<211> 484
<212> DNA
<213> Homo Sapiens

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<211> 355
<212> DNA
<213> Homo Sapiens

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<211> 1070
<212> DNA
<213> Homo Sapiens

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<210> 23

<211> 861
<212> DNA
<213> Homo Sapiens

<400> 23

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<210> 24

<211> 985

<212> DNA

<213> Homo Sapiens

<400> 24

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<210> 25

<211> 545

<212> DNA

<213> Homo Sapiens

<400> 25

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<210> 26
<211> 374
<212> DNA
<213> Homo Sapiens

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<210> 27
<211> 552
<212> DNA
<213> Homo Sapiens

<400> 27
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<210> 28
<211> 502
<212> DNA
<213> Homo Sapiens

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<210> 29

<211> 537
 <212> DNA
 <213> Homo Sapiens

<400> 29

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<210> 30
 <211> 3872
 <212> DNA
 <213> Homo Sapiens

<400> 30

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<210> 31

<211> 655

<212> DNA

<213> Homo Sapiens

<400> 31

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<210> 32

<211> 466

<212> DNA

<213> Homo Sapiens

<400> 32

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attcggaacg	agctcgtgcc	gaattcggca	cgaggggaagc	actactccca	gcgctgggcc	240
caggaggacc	tgctggagga	gcagaaggat	ggggcccg	cagcggctgt	ggctgacaag	300
aagaaaggcc	tcatggggcc	actgaccgaa	ctggacacta	aagatgtgga	tgccctgctg	360
aagaagtctg	aggcccagca	tgaacagccg	gaagatggat	gcccctttgg	tgccctgacg	420
cagcgccctc	tcgaggccct	ggtggaggaa	aatattat	tttccc		466

<210> 33

<211> 293

<212> DNA

<213> Homo Sapiens

<400> 33

gtcggcgccc	tacatgagaa	gcatgatgca	gtcgtgagc	cagaatccag	atttggtgc	60
acagatgatg	ctgaatagcc	cgctgtttac	tgcaaatcct	cagctgcagg	agcagatgcg	120
gccacagctc	ccagccttcc	tcgagcagat	gcagaatcca	gacacactat	cagccatgctc	180
aaacccaaga	gcaatgcagg	ctttaatgca	gatccagcag	gggctacaga	cattagccac	240
tgaagcacct	ggcctgattc	cgagcttcac	tccaggtgtg	ggggtggggn	tct	293

<210> 34

<211> 456

<212> DNA

<213> Homo Sapiens

<400> 34

caaagcotta	agtcagagcc	tgctagaatg	tgtccagggt	tacagctata	ctgcacagca	60
cttcccatgc	tagtctctgt	aaaacgcaaa	aagccat	caggagcagt	aggcaagtca	120
cattcaattg	aaatgcagga	tggtgcactg	ccattccaag	ttccatcttc	ctggcagatc	180
agcacagggt	tccccagaag	ttcatatcct	ggattacagg	tgtatgaaac	catggtacca	240
tacagaaagt	ttgatgaatg	tgtagcagga	gactcctttg	tattttccca	ggtttttagcc	300
actgtcccca	aatgataagg	agggtgagga	gtcacatatg	gaacttccat	catgtcgtct	360
tcttgtccta	aatatccctg	gtcatctttg	agtttagtac	agtctccaaa	atctatatga	420
ggagggaggc	cacagtctat	tggcatacca	aatttt			456

<210> 35

<211> 679

<212> DNA

<213> Homo Sapiens

<400> 35

ggcggcgctt	gtgtccgagg	tcactagttt	cccggtagtt	cagctgcaca	tgaatagaac	60
agcaatgaga	gccagtcaga	aggactttga	aaattcaata	aatcaagtga	aactcttgaa	120
aaaggatcca	ggaaacgaag	tgaagctaaa	actctacg	ctatataagc	aggccactga	180
aggaccttgt	aacatgccca	aaccaggtgt	atttgacttg	atcaacaagg	ccaaatggga	240
cgcattggaat	gcccttggca	gcctgcccaa	ggaagctgcc	aggcagaact	atgtggattt	300
ggtgtccagt	ttgagtcctt	cattggaatc	ctctagtcag	gtggagcctg	gaacagacag	360
gaaatcaact	gggtttgaaa	ctctggtggt	gacctccgaa	gatggcatca	caaagatcat	420
gttcaaccgg	cccaaaaaga	aaaatgccat	aaacactgag	atgtatcatg	aaattatgcg	480
tgcaactaaa	gctgccagca	aggatgactc	aatcatcact	gttttaacag	gaaatggtga	540
ctattacagt	agtgggaatg	atctgactaa	cttcaactgat	attccccctg	gtggagtana	600
ggagaaagct	aaaaataatg	ccgttttact	gaagggaatt	tgtgggctgt	tttatagaat	660
ttcctaagcc	tctgattgc					679

<210> 36
<211> 689
<212> DNA
<213> Homo Sapiens

<400> 36

ctaaaccagt	ggacatatca	ggccatggtc	cacgaactac	taggcataaa	caacaatcgg	60
attgatcttt	ccagagtgcc	gggaatcagt	aaagacttaa	gagaagtggg	cctatctgct	120
gaaaatgatg	aattctatgc	taataatatg	tacctgaact	ttgctgagat	tggtagcaat	180
ataaagaatc	tcattgaaga	ttttcagaag	aagaaaccaa	aagaacagca	aaaactagaa	240
tcaatagcag	acatgaaggc	gtttgttgag	aattatccac	agttcaagaa	aatgtctggg	300
actgtttcaa	agcatgtgac	agtggttgga	gaactgtctc	gattgggcag	tgaacggaat	360
ctgctggagg	tttcagaggt	tgagcaagaa	ctggcctgtc	aaaatgacca	ttctagtgtc	420
ctccagaata	taaaaaggct	tctgcagaac	cccaaagtga	cagagtttga	tgctgcccgc	480
ctgggtgatgc	tttatgcttt	acattatgag	cgacacagca	gcaatagcct	gccaggacta	540
atgatggncc	tcaggaataa	aggtgtttct	gagaagtatc	gaaagctcgt	gtctgcagtt	600
gttgaatatg	gtggtaaaac	gagtcagagg	aagtgcacct	ctcagcccca	aagatgctgt	660
tggctatcac	caaacaattc	ctcaaaggg				689

<210> 37
<211> 443
<212> DNA
<213> Homo Sapiens

<400> 37

ccacgcccgg	ccccggagca	ggcttttaag	catgccccgc	gcgccccctt	gtgtccggaa	60
tttatccctt	ccggtgggtt	cgcggtctag	ctgaccaaga	acggaactgg	ggactttcgc	120
agtgaagatt	acagctctta	aagatggcac	cgaccagggc	cgggcgcggt	ggctcaggcc	180
tgcaatcccc	gcactttggg	aggcggaggc	aggtgaatca	cgaggtcagg	aaatcgagac	240
catcctggct	aacatgggtg	aaccgcgtct	ccactaaaaa	tacaaaaaat	tagccaggca	300
tggtggctgg	cacctgtagt	cccagctact	tgggaggctg	agccaggaaa	gtggcatgaa	360
cccgcgaggc	tagagcttgca	ataagccgag	atcgtgccaa	tgcactccag	cctgggcaac	420
agaaggagac	actgtctcaa	aaa				443

<210> 38
<211> 442
<212> DNA
<213> Homo Sapiens

<400> 38

ctcgctcgg	agcagccatg	atggaaggcc	tggacgacgg	cccggacttc	ctctcagaag	60
aggaccgagg	acttaaagca	ataaatgtag	atcttcaaag	tgatgctgct	ctgcagggtg	120
acattttctg	tgctcttagt	gagcgggata	aagtaaaatt	cactgttcac	acaaagattc	180
caccagcacc	accaagacct	gattttgatg	cttcaaggga	aaaactacag	aagcttggtg	240
aaggagaagg	gtcaatgacg	aaggaagaat	tcacaaagat	gaaacaggaa	ctggaagctg	300
aatatttggc	aatattcaag	aagacagttg	cgatgcatga	agtgttcctg	tgctgtgtgg	360
cagcacatcc	tattttgaga	agagatttaa	atttccatgt	cttcttgga	tataatcaag	420
atttgagtgt	gcgaggaaaa	aa				442

<210> 39
<211> 692
<212> DNA
<213> Homo Sapiens

<400> 39

cagggacagg	ccctatctta	tatttttttc	catcttcac	atccacttct	gcttacagtt	60
tgctgcttac	aataacttaa	tgatggattg	agttatctgg	gtggtctcta	gccatctggg	120
cagtgtggtt	ctgtctaacc	aaagggcatt	ggcctcaaac	cctgcatttg	gttttagggg	180
taacagagct	cctcagataa	tcttcacaca	catgtaactg	ctggagatct	tattctatta	240
tgaataagaa	acgagaagtt	tttccaaagt	gttagtcagg	atctgaaggc	tgctattcag	300
ataaccagc	ttttcctttt	ggcttttagc	ccattcagac	tttgccagag	tcaagccaag	360
gattgctttt	ttgctacagt	tttctgcca	atggcctagt	tcctgagtag	ctggaaacca	420
gagagaaaga	ggatccagga	tgtacttgga	tgaggaggcc	tggttatctt	aggaagtcgt	480
gtctggggtg	cttattgctg	ctccatacag	ctgtacgtca	gccccttggc	cttctctgta	540
ggttcttggt	ancaatgagc	agctttcact	caagtgcac	aagtaattac	tgagtcctaa	600
tttgatagcc	accaactgta	cctgggtang	caaagtcaga	tttttgagaa	nctttttcct	660
gatttgaagt	tttaattacc	ttaatttcct	tt			692

<210> 40

<211> 619

<212> DNA

<213> Homo Sapiens

<400> 40

gaggcaccag	attctgctga	ggggaccacc	cttacagtgc	tgctgaagg	tgaggagttg	60
cccctgtgtg	tgagtgaag	caatggcctg	gagctccac	cctcagcagc	atctgatgag	120
ccacttcagg	agccactgga	ggctgacagg	acctcggaag	agctgacaga	ggccaagacc	180
ccaacctcca	gcccagagaa	gccacaggaa	ctcgttacag	ctgagggtgc	agctccatcc	240
acctcatctt	cagccacttc	ctcgcctgag	ggtccttcac	ctgcccagcc	tcctcggcgt	300
cgcaccagtg	ctgatgtgga	aattaggggt	caagggactg	gtcggccagg	acaaccacca	360
ggccccaaag	tgcttcgaaa	gctgccagga	cggctggtaa	ctgtggtaga	ggaaaaggaa	420
ctggtgcggc	ggcggcgga	gcagcgggga	gctgccaaac	accctagtgc	ctggggtctc	480
tgagactagt	gccagcccgg	gaagcccgtc	tgtccgcagc	atgtcanggc	canaatcttc	540
ccctcccatt	ggtgggccc	gtgaaaagctg	ctccttcac	cncactgcnc	actccanccc	600
agnagccctt	cattgcncg					619

<210> 41

<211> 153

<212> PRT

<213> Homo Sapiens

<400> 41

Pro	Glu	Ser	Lys	Pro	Ile	Met	Thr	Ser	Ser	Glu	Ala	Phe	Glu	Pro	Pro
1				5					10					15	
Lys	Tyr	Leu	Met	Leu	Gly	Gln	Gln	Ala	Val	Gly	Gly	Val	Pro	Ile	Gln
			20					25					30		
Pro	Ser	Val	Arg	Thr	Gln	Met	Trp	Leu	Thr	Glu	Gln	Leu	Arg	Thr	Asn
		35					40					45			
Pro	Leu	Glu	Gly	Arg	Asn	Thr	Glu	Asp	Ser	Tyr	Ser	Leu	Ala	Pro	Trp
	50					55					60				
Gln	Gln	Gln	Gln	Ile	Glu	Phe	Arg	Gln	Gly	Ser	Glu	Thr	Pro	Met	Gln
65					70				75					80	
Val	Leu	Thr	Gly	Ser	Ser	Arg	Gln	Ser	Tyr	Ser	Pro	Gly	Tyr	Gln	Asp
			85					90					95		
Phe	Ser	Lys	Trp	Glu	Ser	Met	Leu	Lys	Lys	Glu	Gly	Leu	Leu	Arg	Gln
		100					105					110			
Lys	Glu	Ile	Val	Asp	Arg	Gln	Lys	Gln	Ile	Thr	His	Leu	Ile	Arg	Asp
	115					120					125				
Asn	Glu	Leu	Pro	Ala	His	Ala	Met	Leu	Gly	His	Tyr	Val	Asn	Cys	Glu
	130					135					140				

Asp Ser Tyr Val Ala Ser Leu His His
145 150

<210> 42
<211> 95
<212> PRT
<213> Homo Sapiens

<400> 42
Ile Leu Leu Glu Phe Tyr Leu Trp Gln Ile Gly Arg Tyr Ile Phe Val
1 5 10 15
His Val Asn Asn His Ile Tyr Ile Lys Leu Tyr Asn Cys Thr Phe Leu
20 25 30
Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu
35 40 45
Ile Phe Val Ser Phe Ala Phe Arg Val Val Asn Ser Tyr Cys Pro
50 55 60
Leu Gln Phe Val Gln Phe Leu Arg Cys Leu Leu Leu Lys Arg Met
65 70 75 80
Leu Gly Glu Phe Ile Phe His Lys Glu Met Glu His Tyr Leu Lys
85 90 95

<210> 43
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 43
Ser Lys Leu Leu Leu Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr
1 5 10 15
Val Asp Pro Glu Thr Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala
20 25 30
Gly Ile Gly Lys Leu Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro
35 40 45
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu
50 55 60
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly
65 70 75 80
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala
85 90 95
Val Arg Lys Leu Leu Ile Glu Gly Arg Ser Val Phe Glu Leu Pro Glu
100 105 110
Glu Gly

<210> 44
<211> 132
<212> PRT
<213> Homo Sapiens

<400> 44
Gly Glu Lys Glu Gln Asp Lys Pro Pro Asn Leu Val Leu Lys Asp Lys
1 5 10 15
Val Lys Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln
20 25 30

Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys
 35 40 45
 Lys Thr His His Cys Ser Glu Glu Lys Glu Asp Glu Asp Tyr Met Pro
 50 55 60
 Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His
 65 70 75 80
 Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg
 85 90 95
 Asp Arg Thr Gln Asn Arg Ser Arg Ser Arg Ser Arg Glu Arg Asp Gly
 100 105 110
 His Tyr Ser Asn Ser His Lys Ser Lys Tyr Gln Thr Asp Leu Tyr Glu
 115 120 125
 Arg Glu Arg Ser
 130

<210> 45
 <211> 214
 <212> PRT
 <213> Homo Sapiens

<400> 45
 Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu
 -----1-----5-----10-----15-----
 Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile
 20 25 30
 Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys
 35 40 45
 Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg
 50 55 60
 Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser
 65 70 75 80
 Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly
 85 90 95
 Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val
 100 105 110
 Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met
 115 120 125
 Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser
 130 135 140
 Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp
 145 150 155 160
 Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser
 165 170 175
 Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala
 180 185 190
 Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser
 195 200 205
 Arg Leu Ala Thr Arg Ser
 210

<210> 46
 <211> 248
 <212> PRT
 <213> Homo Sapiens

<400> 46

Gly Ser Arg Glu Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu
 1 5 10 15
 Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser
 20 25 30
 Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser
 35 40 45
 Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu
 50 55 60
 His Leu Leu Pro Gly Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala
 65 70 75 80
 Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly
 85 90 95
 Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn
 100 105 110
 Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys
 115 120 125
 Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser
 130 135 140
 Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp
 145 150 155 160
 Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met
 165 170 175
 Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu
 180 185 190
 Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg
 195 200 205
 Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp
 210 215 220
 Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp
 225 230 235 240
 Glu Phe Ile His Lys Ile Thr Leu
 245

<210> 47

<211> 177

<212> PRT

<213> Homo Sapiens

<400> 47

Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu
 1 5 10 15
 Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile
 20 25 30
 Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val
 35 40 45
 Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr
 50 55 60
 Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys
 65 70 75 80
 Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser
 85 90 95
 Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His
 100 105 110
 Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly

115 120 125
 Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile
 130 135 140
 Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys
 145 150 155 160
 Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys
 165 170 175
 Leu

<210> 48
 <211> 102
 <212> PRT
 <213> Homo Sapiens

<400> 48
 Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala
 1 5 10 15
 Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly
 20 25 30
 Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser
 35 40 45
 Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro
 50 55 60
 Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr
 65 70 75 80
 Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu
 85 90 95
 Pro Pro Leu Lys Asn Gly
 100

<210> 49
 <211> 179
 <212> PRT
 <213> Homo Sapiens

<400> 49
 His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly
 1 5 10 15
 Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg
 20 25 30
 Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr
 35 40 45
 Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala
 50 55 60
 Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val
 65 70 75 80
 Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val
 85 90 95
 Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu
 100 105 110
 His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser
 115 120 125
 Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu
 130 135 140

Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu
 145 150 155 160
 Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile
 165 170 175
 Cys Leu Leu

<210> 50
 <211> 163
 <212> PRT
 <213> Homo Sapiens

<400> 50

Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys
 1 5 10 15
 Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu
 20 25 30
 Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile
 35 40 45
 Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly
 50 55 60
 His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly
 65 70 75 80
 Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln
 85 90 95
 Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln
 100 105 110
 Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala
 115 120 125
 Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg
 130 135 140
 Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu
 145 150 155 160
 Thr Leu Gln

<210> 51
 <211> 164
 <212> PRT
 <213> Homo Sapiens

<400> 51

Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys
 1 5 10 15
 Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu
 20 25 30
 Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe
 35 40 45
 Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala
 50 55 60
 Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu
 65 70 75 80
 Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu
 85 90 95
 Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp

	100		105		110
Glu Asp Glu Asp Phe Lys Arg Gln Asp Ala Met Lys Glu Ser Ile Pro					
	115		120		125
Phe Ala Val Val Gly Ser Cys Gln Val Val Arg Asp Gly Gly Asn Arg					
	130		135		140
Pro Val Arg Gly Arg Arg Tyr Ser Trp Gly Asn Val Glu Val Asn His					
145		150		155	160
Ile Ala Ile Ser					

<210> 52
 <211> 600
 <212> PRT
 <213> Homo Sapiens

	<400> 52	
Met Cys Pro Arg Gln Val Asp Arg Ala Lys Glu Lys Gly Ile Gly Thr		
1	5	10
Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala Glu Leu Glu Asn Ser		15
	20	25
Ser Lys Glu Asn Glu Val Ile Glu Val Lys Ser Met Gly Glu Ser Gln		30
	35	40
Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys Lys Tyr Cys Pro Tyr Ser		45
	50	55
Thr Gln Asn Leu Asn Glu Phe Thr Glu His Val Asp Met Gln His Pro		60
65	70	75
Asn Val Ile Leu Asn Pro Leu Tyr Val Cys Ala Glu Cys Asn Phe Thr		80
	85	90
Thr Lys Lys Tyr Asp Ser Leu Ser Asp His Asn Ser Lys Phe His Pro		95
	100	105
Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile Lys Arg Asn Asn Gln Thr		110
	115	120
Val Leu Glu Gln Ser Ile Glu Thr Thr Asn His Val Val Ser Ile Thr		125
	130	135
Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp Ser Gly Ile Ser Val Ser		140
145	150	155
Lys Thr Pro Ile Met Lys Pro Gly Lys Pro Lys Ala Asp Ala Lys Lys		160
	165	170
Val Pro Lys Lys Pro Glu Glu Ile Thr Pro Glu Asn His Val Glu Gly		175
	180	185
Thr Ala Arg Leu Val Thr Asp Thr Ala Glu Ile Leu Ser Arg Leu Gly		190
	195	200
Gly Val Glu Leu Leu Gln Asp Thr Leu Gly His Val Met Pro Ser Val		205
	210	215
Gln Leu Pro Pro Asn Ile Asn Leu Val Pro Lys Val Pro Val Pro Leu		220
225	230	235
Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp Thr Asn Ala Thr Met Ile		240
	245	250
Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr Gln Ala Glu Leu Ser Trp		255
	260	265
Leu Thr Ala Ala Ser Lys His Pro Glu Glu His Ile Arg Ile Trp Phe		270
	275	280
Ala Thr Gln Arg Leu Lys His Gly Ile Ser Trp Ser Pro Glu Glu Val		285
	290	295
Glu Glu Ala Arg Lys Lys Met Phe Asn Gly Thr Ile Gln Ser Val Pro		300

305 310 315 320
 Pro Thr Ile Thr Val Leu Pro Ala Gln Leu Ala Pro Thr Lys Met Thr
 325 330 335
 Gln Pro Ile Leu Gln Thr Ala Leu Pro Cys Gln Ile Leu Gly Gln Thr
 340 345 350
 Ser Leu Val Leu Thr Gln Val Thr Ser Gly Ser Thr Thr Val Ser Cys
 355 360 365
 Ser Pro Ile Thr Leu Ala Val Ala Gly Val Thr Asn His Gly Gln Lys
 370 375 380
 Arg Pro Leu Val Thr Pro Gln Ala Ala Pro Glu Pro Lys Arg Pro His
 385 390 395 400
 Ile Ala Gln Val Pro Glu Pro Pro Pro Lys Val Ala Asn Pro Pro Leu
 405 410 415
 Thr Pro Ala Ser Asp Arg Lys Lys Thr Lys Glu Gln Ile Ala His Leu
 420 425 430
 Lys Ala Ser Phe Leu Gln Ser Gln Phe Pro Asp Asp Ala Glu Val Tyr
 435 440 445
 Arg Leu Ile Glu Val Thr Gly Leu Ala Arg Ser Glu Ile Lys Lys Trp
 450 455 460
 Phe Ser Asp His Arg Tyr Arg Cys Gln Arg Gly Ile Val His Ile Thr
 465 470 475 480
 Ser Glu Ser Leu Ala Lys Asp Gln Leu Ala Ile Ala Ala Ser Arg His
 485 490 495
 Gly Arg Thr Tyr His Ala Tyr Pro Asp Phe Ala Pro Gln Lys Phe Lys
 500 505 510
 Glu Lys Thr Gln Gly Gln Val Lys Ile Leu Glu Asp Ser Phe Leu Lys
 515 520 525
 Ser Ser Phe Pro Thr Gln Ala Glu Leu Asp Arg Leu Arg Val Glu Thr
 530 535 540
 Lys Leu Ser Arg Arg Glu Ile Asp Ser Trp Phe Ser Glu Arg Arg Lys
 545 550 555 560
 Leu Arg Asp Ser Met Glu Gln Ala Val Leu Asp Ser Met Gly Ser Gly
 565 570 575
 Gln Lys Arg Pro Arg Cys Gly Lys Pro Pro Met Val Leu Cys Leu Asp
 580 585 590
 Ser Asn Ser Ser Pro Val Pro Ser
 595 600

<210> 53
 <211> 163
 <212> PRT
 <213> Homo Sapiens

<400> 53
 Arg Lys Ser Trp Glu His Lys Glu Glu Ile Ser Glu Ala Glu Pro Gly
 1 5 10 15
 Gly Gly Ser Leu Gly Asp Gly Arg Pro Pro Glu Glu Ser Ala His Glu
 20 25 30
 Met Met Glu Glu Glu Glu Glu Ile Pro Lys Pro Lys Ser Val Val Ala
 35 40 45
 Pro Pro Gly Ala Pro Lys Lys Glu His Val Asn His Val Ala Gly Lys
 50 55 60
 Ser Thr Ile Gly Gly Gln Ile Met Tyr Leu Thr Gly Met Val Asp Lys
 65 70 75 80
 Arg Thr Leu Glu Lys Tyr Glu Arg Glu Ala Lys Glu Lys Asn Arg Glu

85 90 95
 Thr Trp Tyr Leu Ser Trp Ala Leu Asp Thr Asn Gln Glu Glu Arg Asp
 100 105 110
 Lys Gly Lys Thr Val Glu Val Gly Arg Ala Tyr Phe Glu Thr Glu Lys
 115 120 125
 Lys His Phe Thr Ile Leu Asp Met Asn Pro Arg Thr Leu Ser Ser Lys
 130 135 140
 Pro Lys Ala Gln Asn Leu Lys Leu Lys Val Pro Asn Ser Lys Val Arg
 145 150 155 160
 Arg Cys Phe

<210> 54
 <211> 155
 <212> PRT
 <213> Homo Sapiens

<400> 54
 Glu Arg Trp Pro Glu Glu Gly Thr Ala Asp Leu Ala Gln Ser Gly Leu
 1 5 10 15
 Glu Gly Gly Thr Arg Ala Ser Val Ser Trp Cys Cys Leu Glu Gly
 20 25 30
 Ser Trp Leu Ser Gly Tyr Leu Thr Phe Leu Lys Thr Cys Ser His
 35 40 45
 Thr Ala Ser Leu Ala Val Ser Ser Ser Ser Cys Arg Ile Arg His Glu
 50 55 60
 Leu Val Pro Asn Ser Ala Arg Gly Lys His Tyr Ser Gln Arg Trp Ala
 65 70 75 80
 Gln Glu Asp Leu Leu Glu Glu Gln Lys Asp Gly Ala Arg Ala Ala Ala
 85 90 95
 Val Ala Asp Lys Lys Lys Gly Leu Met Gly Pro Leu Thr Glu Leu Asp
 100 105 110
 Thr Lys Asp Val Asp Ala Leu Leu Lys Lys Ser Glu Ala Gln His Glu
 115 120 125
 Gln Pro Glu Asp Gly Cys Pro Phe Gly Ala Leu Thr Gln Arg Leu Leu
 130 135 140
 Gln Ala Leu Val Glu Glu Asn Ile Ile Phe Ser
 145 150 155

<210> 55
 <211> 112
 <212> PRT
 <213> Homo Sapiens

<400> 55
 Ser Glu Arg Ala Leu Ala Pro Arg Thr Tyr Arg Met Glu Thr Ala Arg
 1 5 10 15
 Ser Ala Pro Tyr Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro
 20 25 30
 Asp Leu Ala Ala Gln Met Met Leu Asn Ser Pro Leu Phe Thr Ala Asn
 35 40 45
 Pro Gln Leu Gln Glu Gln Met Arg Pro Gln Leu Pro Ala Phe Leu Gln
 50 55 60
 Gln Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala
 65 70 75 80

Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr
85 90 95
Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly
100 105 110

<210> 56
<211> 151
<212> PRT
<213> Homo Sapiens

<400> 56
Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe
1 5 10 15
Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu
20 25 30
Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His
35 40 45
Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala
50 55 60
Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys
65 70 75 80
Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu
85 90 95
Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys
100 105 110
Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr
115 120 125
Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu
130 135 140
Ala Gly Ser Asp Leu Arg Leu
145 150

<210> 57
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 57
Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His
1 5 10 15
Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
20 25 30
Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
35 40 45
Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn
50 55 60
Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
65 70 75 80
Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
85 90 95
Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
100 105 110
Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
115 120 125
Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

130	135	140
Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg		
145	150	155
Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr		160
	165	170
Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr		175
	180	185
Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu		190
	195	200
Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser		205
210	215	220

<210> 58
 <211> 101
 <212> PRT
 <213> Homo Sapiens

<400> 58
Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser
1 5 10 15
Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn
20 25 30
Lys Phe Lys Val Ile Asn Val Asp Asp Gly Asn Glu Leu Gly Ser
35 40 45
Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys
50 55 60
Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr
65 70 75 80
Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly
85 90 95
Thr Arg Asn Leu Cys
100

<210> 59
 <211> 43
 <212> PRT
 <213> Homo Sapiens

<400> 59
Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn
1 5 10 15
Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu
20 25 30
Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu
35 40

<210> 60
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<400> 60
Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile
1 5 10 15
Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

	<400>	62															
His	Glu	Ala	Arg	Leu	Lys	Arg	Ala	Ser	Ala	Pro	Thr	Phe	Asp	Asn	Asp		
1				5					10					15			
Tyr	Ser	Leu	Ser	Glu	Leu	Leu	Ser	Gln	Leu	Asp	Ser	Gly	Val	Ser	Gln		
			20					25					30				
Ala	Val	Glu	Gly	Pro	Glu	Glu	Leu	Ser	Arg	Ser	Ser	Ser	Glu	Ser	Lys		
		35					40					45					
Leu	Pro	Ser	Ser	Gly	Ser	Gly	Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val		
	50					55					60						
Asp	Ser	Ala	Phe	Ser	Ser	Arg	Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg		
65					70					75					80		

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys
 85 90 95
 Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile
 100 105 110
 Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu
 115 120 125
 Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu
 130 135 140
 Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr
 145 150 155 160
 Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu
 165 170 175
 Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr
 180 185 190
~~Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu~~
 195 200 205
 Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln
 210 215 220
 Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu
 225 230 235

<210> 63

~~<211> 146~~

<212> PRT

<213> Homo Sapiens

<400> 63

Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe
 1 5 10 15
 Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln
 20 25 30
 Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg
 35 40 45
 Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro
 50 55 60
 Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu
 65 70 75 80
 Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu
 85 90 95
 Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
 100 105 110
 Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
 115 120 125
 Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
 130 135 140
 Gly Lys
 145

<210> 64

<211> 63

<212> PRT

<213> Homo Sapiens

<400> 64

Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe

1	5	10	15
Ser Pro Asn	Pro Arg Ile Val	Ser Val Asn Ala	Ser Tyr Ser Leu Ser
	20	25	30
Asn Glu Ser	Ser Leu Glu Gln Val	Tyr Thr Leu Lys Met	Ser Phe Ile
	35	40	45
Ala Ser Asn	Thr Tyr His Asn Gln	Leu Tyr Lys Glu Gly	Phe Leu
	50	55	60

<210> 65
 <211> 199
 <212> PRT
 <213> Homo Sapiens

<400> 65

Glu Ala Pro	Asp Ser Ala	Glu Gly Thr	Thr Leu Thr	Val Leu Pro	Glu
1	5	10	15		
Gly Glu Glu	Leu Pro Leu Cys	Val Ser Glu	Ser Asn Gly	Leu Glu Leu	
	20	25	30		
Pro Pro Ser	Ala Ala Ser Asp	Glu Pro Leu	Gln Glu Pro	Leu Glu Ala	
	35	40	45		
Asp Arg Thr	Ser Glu Glu Leu	Thr Glu Ala	Lys Thr Pro	Thr Ser Ser	
	50	55	60		
Pro Glu Lys	Pro Gln Glu	Val Thr Ala	Glu Val Ala	Ala Pro Ser	
65	70	75	80		
Thr Ser Ser	Ser Ala Thr	Ser Ser Pro	Glu Gly Pro	Ser Pro Ala	Arg
	85	90	95		
Pro Pro Arg	Arg Arg Thr	Ser Ala Asp	Val Glu Ile	Arg Gly Gln	Gly
	100	105	110		
Thr Gly Arg	Pro Gly Gln	Pro Pro Gly	Pro Lys Val	Leu Arg Lys	Leu
	115	120	125		
Pro Gly Arg	Leu Val Thr	Val Val Glu	Glu Lys Glu	Leu Val Arg	Arg
	130	135	140		
Arg Arg Gln	Gln Arg Gly	Ala Ala Ser	Thr Leu Val	Pro Gly Val	Ser
	145	150	155	160	
Glu Thr Ser	Ala Ser Pro	Gly Ser Pro	Ser Val Arg	Ser Met Ser	Gly
	165	170	175		
Pro Glu Ser	Ser Pro Pro	Ile Gly Gly	Pro Cys Glu	Ala Ala Pro	Ser
	180	185	190		
Ser Ser Leu	Pro Thr Pro	Pro			
	195				

<210> 66
 <211> 1599
 <212> DNA
 <213> Homo Sapiens

<400> 66

ttctttgaaa	cattattatt	cagaacgaag	gagaatgata	cagatacact	ggctgaggtg	60
ttttgaggtg	cattgaaatg	ttccatgctg	ttacttaggt	taacatgttc	ttgaggtacc	120
atgccatgga	ttaaaaggaa	atttggttaag	tggtctccac	ctaaacgact	tactagggaa	180
gctatgcgaa	attattttaa	agggttaagg	gatcaaatag	tacttatcct	tcatgcaaaa	240
gttgtagaga	agtcatatgg	caatcaaaaa	attttttttt	gccctcccc	ttgtgtatat	300
cttatgggca	gtggatggaa	gaaaaaaaa	gaacaaatga	aatgcgatgg	ttgttctgaa	360
cacagctctc	atccatgtgc	atttattggg	ataggaaata	gtgaccaaga	aatgcagcag	420
ctaaacttgg	aaggaaagaa	ctattgcaca	gccaaaacat	tgtacatatc	tgattcagac	480

aagcaaaagc	acttcatttt	ttctgtaaag	gtgttctatg	gcaacgggtga	tgacattggg	540
gtgttctctca	gcaagtagat	aaaagtcac	tccaaacctt	ccaaaaagaa	gcagtcattg	600
aaaaatgctg	acttatgcat	tgtctcagga	acaaagggtg	ctctgtttta	tcgactacga	660
tcccagacag	ttagtaccag	atacttgcat	gtagaaggag	gtaattttca	tgccagttca	720
cagcagtggtg	gagcatttta	cattcaattc	ttggatgatg	atggatcaga	aggagaagaa	780
ttcacagtct	gagatgccta	cattcattat	ggacaaacat	gcaaacttgt	gtgctcagtt	840
actggcatgg	cactcccaag	attgataatt	atgaaagttg	ataagcatac	cgcattattg	900
gatgcagatg	atcctgtgtc	acaactccat	aaatgtgcat	ttaccttaa	ggatacagaa	960
agaatgtatt	tgtgcctttc	tcaagaaaga	ataattcaat	ttcaggccac	tccatgtcca	1020
agagaaccaa	ataaagagat	gataaatgat	ggcgcttcct	ggacaatcat	tagcacagat	1080
aaggcagggg	atacatttta	tgagggaatg	ggcctgtcc	ttgccccagt	cactcctgtg	1140
cctgtggtag	agagccttca	gttgaatggc	ggtggggacg	tagcaatgct	tgaacttaca	1200
ggacagaatt	tactccaaa	tttacgagt	tggtttgggg	gggtagaagc	tgaactatg	1260
tacaggtgtg	gagagagtat	gctctgtgtc	gtcccagaca	tttctgcatt	ccgagaaggt	1320
tgagatggg	tccggcaacc	agtcacaggt	ccagtaactt	tggtccgaaa	tgatggaatc	1380
atttattcca	ccagccttac	ctttacctac	acaccagaac	cagggccgcg	gccacattgc	1440
agtgcagcag	gagcaatcct	tctagccaat	tcaagccagg	tgccccctaa	cgaatcaaac	1500
acaaacagcg	agggaagtta	cacaaacgcc	agcacaatt	caaccagtgt	cacatcatct	1560
acagccacag	tggtatccta	actaccgtct	ttttgctag			1599

<210> 67

<211> 729

<212> PRT

<213> Homo Sapiens

<400> 67

Met	Gly	Lys	Lys	Tyr	Lys	Asn	Ile	Val	Leu	Leu	Lys	Gly	Leu	Glu	Val
1				5				10						15	
Ile	Asn	Asp	Tyr	His	Phe	Arg	Met	Val	Lys	Ser	Leu	Leu	Ser	Asn	Asp
		20						25					30		
Leu	Lys	Leu	Asn	Leu	Lys	Met	Arg	Glu	Glu	Tyr	Asp	Lys	Ile	Gln	Ile
		35						40					45		
Ala	Asp	Leu	Met	Glu	Glu	Lys	Phe	Arg	Gly	Asp	Ala	Gly	Leu	Gly	Lys
		50					55					60			
Leu	Ile	Lys	Ile	Phe	Glu	Asp	Ile	Pro	Thr	Leu	Glu	Asp	Leu	Ala	Glu
65					70					75					80
Thr	Leu	Lys	Lys	Glu	Lys	Leu	Lys	Val	Lys	Gly	Pro	Ala	Leu	Ser	Arg
			85						90					95	
Lys	Arg	Lys	Lys	Glu	Val	His	Ala	Thr	Ser	Pro	Ala	Pro	Ser	Thr	Ser
		100						105					110		
Ser	Thr	Val	Lys	Thr	Glu	Gly	Ala	Glu	Ala	Thr	Pro	Gly	Ala	Gln	Lys
		115					120					125			
Arg	Lys	Lys	Ser	Thr	Lys	Glu	Lys	Ala	Gly	Pro	Lys	Gly	Ser	Lys	Val
		130					135					140			
Ser	Glu	Glu	Gln	Thr	Gln	Pro	Pro	Ser	Pro	Ala	Gly	Ala	Gly	Met	Ser
145					150					155					160
Thr	Ala	Met	Gly	Arg	Ser	Pro	Ser	Pro	Lys	Thr	Ser	Leu	Ser	Ala	Pro
				165					170					175	
Pro	Asn	Ser	Ser	Ser	Thr	Glu	Asn	Pro	Lys	Thr	Val	Ala	Lys	Cys	Gln
			180						185					190	
Val	Thr	Pro	Arg	Arg	Asn	Val	Leu	Gln	Lys	Arg	Pro	Val	Ile	Val	Lys
		195					200						205		
Val	Leu	Ser	Thr	Thr	Lys	Pro	Phe	Glu	Tyr	Glu	Thr	Pro	Glu	Met	Glu
		210				215						220			
Lys	Lys	Ile	Met	Phe	His	Ala	Thr	Val	Ala	Thr	Gln	Thr	Gln	Phe	Phe

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Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser
 675 680 685
 Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val
 690 695 700
 Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser
 705 710 715 720
 Met Glu Thr Ser Pro Asp Phe Phe Phe
 725

<210> 68
 <211> 754
 <212> PRT
 <213> Homo Sapiens

<400> 68
 Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro
 1 5 10 15
 Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu
 20 25 30
 Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe
 35 40 45
 Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro
 50 55 60
 Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys
 65 70 75 80
 Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln
 85 90 95
 Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr
 100 105 110
 Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln
 115 120 125
 Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile
 130 135 140
 Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly
 145 150 155 160
 Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His
 165 170 175
 Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn
 180 185 190
 Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His
 195 200 205
 Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln
 210 215 220
 Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr
 225 230 235 240
 Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro
 245 250 255
 Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu
 260 265 270
 Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln
 275 280 285
 Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys
 290 295 300
 His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala
 305 310 315 320

Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu
325 330 335
His Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val
340 345 350
Lys Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala
355 360 365
Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro
370 375 380
Asp His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu
385 390 395 400
Phe Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu
405 410 415
Pro Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu
420 425 430

Ser Ser Ser Glu Glu Ser Ser Ser Ser Ser Ser Glu Glu Glu Glu
435 440 445
Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Ser Glu Ser Ser Asp
450 455 460
Ser Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu
465 470 475 480
Arg Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser
485 490 495

Lys Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys
500 505 510
Ala Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly
515 520 525
Pro Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser
530 535 540
Gly Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro
545 550 555 560
Ser Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala
565 570 575
Pro Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser
580 585 590
Arg Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn
595 600 605
Lys Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala
610 615 620
Arg Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp
625 630 635 640
Phe Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val
645 650 655
Leu Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys
660 665 670
Pro Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu
675 680 685
Leu Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys
690 695 700
Lys Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln
705 710 715 720
Gln Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Ser Asp Ser
725 730 735
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp
740 745 750
Ser Gly

<210> 69
 <211> 210
 <212> PRT
 <213> Homo Sapiens

<400> 69
 Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr
 1 5 10 15
 Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu
 20 25 30
 Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro
 35 40 45
 Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His
 50 55 60
 Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro
 65 70 75 80
 Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu
 85 90 95
 Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro
 100 105 110
 Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu
 115 120 125
 Gln Phe Leu Gln Gln Glu Leu Ile Asn Ile Thr Glu His Glu Leu
 130 135 140
 Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu
 145 150 155 160
 Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly
 165 170 175
 Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys
 180 185 190
 Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu
 195 200 205
 Val Gln
 210

<210> 70
 <211> 621
 <212> PRT
 <213> Homo Sapiens

<400> 70
 Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr
 1 5 10 15
 His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly
 20 25 30
 Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr
 35 40 45
 Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu
 50 55 60
 Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp
 65 70 75 80
 Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly
 85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys
 100 105 110
 Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu
 115 120 125
 Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala
 130 135 140
 Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val
 145 150 155 160
 Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp
 165 170 175
 Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp
 180 185 190
 Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe
 195 200 205
 Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp
 210 215 220
 Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys
 225 230 235 240
 Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala
 245 250 255
 Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn
 260 265 270
 Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys
 275 280 285
 Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys
 290 295 300
 Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val
 305 310 315 320
 Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu
 325 330 335
 Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu
 340 345 350
 Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp
 355 360 365
 Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys
 370 375 380
 Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala
 385 390 395 400
 Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu
 405 410 415
 Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg
 420 425 430
 Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly
 435 440 445
 Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys
 450 455 460
 Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile
 465 470 475 480
 Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala
 485 490 495
 Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His
 500 505 510
 Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu
 515 520 525
 His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

530		535		540
Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys				
545		550		555
Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg				560
	565		570	
Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys				575
	580		585	
Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala				590
	595		600	
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys				605
	610		615	
				620

<210> 71

<211> 267

<212> PRT

<213> Homo Sapiens

<400> 71

Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp				
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Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn				
	20		25	30
Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro				
	35		40	45
Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu				
	50		55	60
Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp				
65	70		75	80
Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe				
	85		90	95
Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn				
	100		105	110
Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu				
	115		120	125
Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys				
	130		135	140
Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile				
145	150		155	160
Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala				
	165		170	175
Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile				
	180		185	190
Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys				
	195		200	205
Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu				
	210		215	220
Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln				
225	230		235	240
Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys				
	245		250	255
Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr				
	260		265	

<210> 72

<211> 1752

А В А / В В / В В / А В В /

<400> 72

Arg	Glu	Lys	Arg	Arg	Arg	Lys	Ser	Val	Glu	Asp	Arg	Phe	Asp	Gln	Gln
1				5					10				15		
Lys	Asn	Asp	Tyr	Asp	Gln	Leu	Gln	Lys	Ala	Arg	Gln	Cys	Glu	Lys	Glu
			20					25				30			
Asn	Leu	Gly	Trp	Gln	Lys	Leu	Glu	Ser	Glu	Lys	Ala	Ile	Lys	Glu	Lys
		35					40					45			
Glu	Tyr	Glu	Ile	Glu	Arg	Leu	Arg	Val	Leu	Leu	Gln	Glu	Glu	Gly	Thr
	50					55					60				
Arg	Lys	Arg	Glu	Tyr	Glu	Asn	Glu	Leu	Ala	Lys	Val	Arg	Asn	His	Tyr
65				70						75					80
Asn	Glu	Glu	Met	Ser	Asn	Leu	Arg	Asn	Lys	Tyr	Glu	Thr	Glu	Ile	Asn
			85						90					95	
Ile	Thr	Lys	Thr	Thr	Ile	Lys	Glu	Ile	Ser	Met	Gln	Lys	Glu	Asp	Asp
			100					105					110		
Ser	Lys	Asn	Leu	Arg	Asn	Gln	Leu	Asp	Arg	Leu	Ser	Arg	Glu	Asn	Arg
		115					120					125			
Asp	Leu	Lys	Asp	Glu	Ile	Val	Arg	Leu	Asn	Asp	Ser	Ile	Leu	Gln	Ala
	130					135					140				
Thr	Glu	Gln	Arg	Arg	Arg	Ala	Glu	Glu	Asn	Ala	Leu	Gln	Gln	Lys	Ala
145				150						155					160
Cys	Gly	Ser	Glu	Ile	Met	Gln	Lys	Lys	Gln	His	Leu	Glu	Ile	Glu	Leu
			165						170					175	
Lys	Gln	Val	Met	Gln	Gln	Arg	Ser	Glu	Asp	Asn	Ala	Arg	His	Lys	Gln
		180						185					190		
Ser	Leu	Glu	Glu	Ala	Ala	Lys	Thr	Ile	Gln	Asp	Lys	Asn	Lys	Glu	Ile
		195				200						205			
Glu	Arg	Leu	Lys	Ala	Glu	Phe	Gln	Glu	Glu	Ala	Lys	Arg	Arg	Trp	Glu
	210					215					220				
Tyr	Glu	Asn	Glu	Leu	Ser	Lys	Val	Arg	Asn	Asn	Tyr	Asp	Glu	Glu	Ile
225				230						235					240
Ile	Ser	Leu	Lys	Asn	Gln	Phe	Glu	Thr	Glu	Ile	Asn	Ile	Thr	Lys	Thr
			245						250					255	
Thr	Ile	His	Gln	Leu	Thr	Met	Gln	Lys	Glu	Glu	Asp	Thr	Ser	Gly	Tyr
		260						265					270		
Arg	Ala	Gln	Ile	Asp	Asn	Leu	Thr	Arg	Glu	Asn	Arg	Ser	Leu	Ser	Glu
		275					280					285			
Glu	Ile	Lys	Arg	Leu	Lys	Asn	Thr	Leu	Thr	Gln	Thr	Thr	Glu	Asn	Leu
	290					295					300				
Arg	Arg	Val	Glu	Glu	Asp	Ile	Gln	Gln	Gln	Lys	Ala	Thr	Gly	Ser	Glu
305					310					315					320
Val	Ser	Gln	Arg	Lys	Gln	Gln	Leu	Glu	Val	Glu	Leu	Arg	Gln	Val	Thr
			325						330					335	
Gln	Met	Arg	Thr	Glu	Glu	Ser	Val	Arg	Tyr	Lys	Gln	Ser	Leu	Asp	Asp
		340						345					350		
Ala	Ala	Lys	Thr	Ile	Gln	Asp									

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Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys
 850 855 860
 Gln Leu Ile Asp Lys Thr Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys
 865 870 875 880
 Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala
 885 890 895
 Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu
 900 905 910
 Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met
 915 920 925
 Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg
 930 935 940
 Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp
 945 950 955 960
 Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly
 965 970 975
 Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile
 980 985 990
 Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala
 995 1000 1005
 Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu
 1010 1015 1020
 Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr
 1025 1030 1035 104
 Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro
 1045 1050 1055
 Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg
 1060 1065 1070
 Ile Glu Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser
 1075 1080 1085
 Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val
 1090 1095 1100
 Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly
 1105 1110 1115 112
 Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln
 1125 1130 1135
 Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys
 1140 1145 1150
 Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr
 1155 1160 1165
 Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp
 1170 1175 1180
 Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly
 1185 1190 1195 120
 Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala
 1205 1210 1215
 Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe
 1220 1225 1230
 Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu
 1235 1240 1245
 Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser
 1250 1255 1260
 His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu
 1265 1270 1275 128
 Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

	1285		1290		1295
Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu					
	1300		1305		1310
Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys					
	1315		1320		1325
Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys					
	1330		1335		1340
Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val					
1345	1350		1355		136
Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu					
	1365		1370		1375
Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser					
	1380		1385		1390
Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln					
	1395		1400		1405
Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe					
	1410		1415		1420
Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp					
1425	1430		1435		144
Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser					
	1445		1450		1455
Gly Val Ser Asp Asp Val Phe Ser Ser Arg His Glu Ser Val Ser					
	1460		1465		1470
Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser					
	1475		1480		1485
Ser Phe Ser Asp Thr Leu Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe					
	1490		1495		1500
Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg					
1505	1510		1515		152
Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala					
	1525		1530		1535
Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu					
	1540		1545		1550
Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser					
	1555		1560		1565
Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly					
	1570		1575		1580
Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro					
1585	1590		1595		160
Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly					
	1605		1610		1615
Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile					
	1620		1625		1630
Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr					
	1635		1640		1645
Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile					
	1650		1655		1660
Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly					
1665	1670		1675		168
Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser					
	1685		1690		1695
Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser					
	1700		1705		1710
Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg					
	1715		1720		1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser
 1730 1735 1740
 Phe Ser Ser Ser Ser Ile Gly His
 1745 1750

<210> 73
 <211> 1978
 <212> PRT
 <213> Homo Sapiens

<400> 73
 Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg
 1 5 10 15
 Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met
 20 25 30
 Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala
 35 40 45
 Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met
 50 55 60
 Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro
 65 70 75 80
 Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys
 85 90 95
 Gly Lys Pro His Gly Ser Arg Trp Asp Asp Glu Pro His Ile Ser Ala
 100 105 110
 Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser
 115 120 125
 Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu
 130 135 140
 Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr
 145 150 155 160
 Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp
 165 170 175
 Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln
 180 185 190
 Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val
 195 200 205
 Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu
 210 215 220
 Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn
 225 230 235 240
 Glu Phe Gln Ser Gln Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn
 245 250 255
 Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met
 260 265 270
 Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu
 275 280 285
 Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val
 290 295 300
 Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser
 305 310 315 320
 Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro
 325 330 335
 Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro
 340 345 350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly
 355 360 365
 Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro
 370 375 380
 Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp
 385 390 395 400
 Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr
 405 410 415
 Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn
 420 425 430
 Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser
 435 440 445
 Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp
 450 455 460
 Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu
 465 470 475 480
 Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser
 485 490 495
 Arg Arg Ser Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met
 500 505 510
 His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg
 515 520 525
 Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg
 530 535 540
 Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser
 545 550 555 560
 Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys
 565 570 575
 Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn
 580 585 590
 Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln
 595 600 605
 Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser
 610 615 620
 Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys
 625 630 635 640
 Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser
 645 650 655
 Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu
 660 665 670
 His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys
 675 680 685
 Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn
 690 695 700
 Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu
 705 710 715 720
 Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro
 725 730 735
 Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys
 740 745 750
 Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys
 755 760 765
 Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val
 770 775 780
 Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

785					790					795					800
Cys	Val	Ala	Lys	Val	Asn	Lys	Ser	Thr	Gly	Lys	Ser	Ala	Ser	Ser	Val
				805					810					815	
Lys	Ser	Val	Val	Thr	Val	Ala	Val	Lys	Gly	Asn	Lys	Ala	Ser	Ile	Lys
				820					825					830	
Thr	Ala	Lys	Ser	Gly	Gly	Lys	Lys	Ser	Leu	Glu	Ala	Lys	Lys	Thr	Gly
				835				840						845	
Asn	Val	Lys	Asn	Lys	Asp	Ser	Asn	Lys	Pro	Val	Thr	Ile	Pro	Glu	Asn
				850				855						860	
Ser	Glu	Ile	Lys	Thr	Ser	Ile	Glu	Val	Lys	Ala	Thr	Glu	Asn	Cys	Ala
					870					875					880
Lys	Glu	Ala	Ile	Ser	Asp	Ala	Ala	Leu	Glu	Ala	Thr	Glu	Asn	Glu	Pro
					885					890					895
Leu	Asn	Lys	Glu	Thr	Glu	Glu	Met	Cys	Val	Met	Leu	Val	Ser	Asn	Leu
				900					905					910	
Pro	Asn	Lys	Gly	Tyr	Ser	Val	Glu	Glu	Val	Tyr	Asp	Leu	Ala	Lys	Pro
				915				920						925	
Phe	Gly	Gly	Leu	Lys	Asp	Ile	Leu	Ile	Leu	Ser	Ser	His	Lys	Lys	Ala
				930				935						940	
Tyr	Ile	Glu	Ile	Asn	Arg	Lys	Ala	Ala	Glu	Ser	Met	Val	Lys	Phe	Tyr
					950					955					960
Thr	Cys	Phe	Pro	Val	Leu	Met	Asp	Gly	Asn	Gln	Leu	Ser	Ile	Ser	Met
				965					970					975	
Ala	Pro	Glu	Asn	Met	Asn	Ile	Lys	Asp	Glu	Glu	Ala	Ile	Phe	Ile	Thr
				980					985					990	
Leu	Val	Lys	Glu	Asn	Asp	Pro	Glu	Ala	Asn	Ile	Asp	Thr	Ile	Tyr	Asp
				995				1000						1005	
Arg	Phe	Val	His	Leu	Asp	Asn	Leu	Pro	Glu	Asp	Gly	Leu	Gln	Cys	Val
				1010				1015						1020	
Leu	Cys	Val	Gly	Leu	Gln	Phe	Gly	Lys	Val	Asp	His	His	Val	Phe	Ile
				1025				1030						1035	104
Ser	Asn	Arg	Asn	Lys	Ala	Ile	Leu	Gln	Leu	Asp	Ser	Pro	Glu	Ser	Ala
					1045				1050					1055	
Gln	Ser	Met	Tyr	Ser	Phe	Leu	Lys	Gln	Asn	Pro	Gln	Asn	Ile	Gly	Asp
				1060					1065					1070	
His	Met	Leu	Thr	Cys	Ser	Leu	Ser	Pro	Lys	Ile	Asp	Leu	Pro	Glu	Val
				1075					1080					1085	
Gln	Ile	Glu	His	Asp	Pro	Glu	Leu	Glu	Lys	Glu	Ser	Pro	Gly	Leu	Lys
				1090					1095					1100	
Asn	Ser	Pro	Ile	Asp	Glu	Ser	Glu	Val	Gln	Thr	Ala	Thr	Asp	Ser	Pro
				1105					1110					1115	112
Ser	Val	Lys	Pro	Asn	Glu	Leu	Glu	Glu	Glu	Ser	Thr	Pro	Ser	Ile	Gln
					1125				1130					1135	
Thr	Glu	Thr	Leu	Val	Gln	Gln	Glu	Glu	Pro	Cys	Glu	Glu	Glu	Ala	Glu
				1140					1145					1150	
Lys	Ala	Thr	Cys	Asp	Ser	Asp	Phe	Ala	Val	Glu	Thr	Leu	Glu	Leu	Glu
				1155				1160						1165	
Thr	Gln	Gly	Glu	Glu	Val	Lys	Glu	Glu	Ile	Pro	Leu	Val	Ala	Ser	Ala
				1170				1175						1180	
Ser	Val	Ser	Ile	Glu	Gln	Phe	Thr	Glu	Asn	Ala	Glu	Glu	Cys	Ala	Leu
				1185				1190						1195	120
Asn	Gln	Gln	Met	Phe	Asn	Ser	Asp	Leu	Glu	Lys	Lys	Gly	Ala	Glu	Ile
					1205				1210					1215	
Ile	Asn	Pro	Lys	Thr	Ala	Leu	Leu	Pro	Ser	Asp	Ser	Val	Phe	Ala	Glu
				1220					1225					1230	

Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu
 1235 1240 1245
 Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu
 1250 1255 1260
 Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile
 1265 1270 1275 128
 Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp
 1285 1290 1295
 Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu
 1300 1305 1310
 Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr
 1315 1320 1325
 Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu
 1330 1335 1340

 Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys
 1345 1350 1355 136
 Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr
 1365 1370 1375
 Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro
 1380 1385 1390
 Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val
 1395 1400 1405

 Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp
 1410 1415 1420
 Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu
 1425 1430 1435 144
 Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe
 1445 1450 1455
 Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser
 1460 1465 1470
 Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys
 1475 1480 1485
 Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp
 1490 1495 1500
 Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser
 1505 1510 1515 152
 Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Glu Pro Leu Phe Pro Phe
 1525 1530 1535
 Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn
 1540 1545 1550
 Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr
 1555 1560 1565
 Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Gly
 1570 1575 1580
 Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr
 1585 1590 1595 160
 Leu Asp Glu Ile Gly Glu Glu Glu Asp Ala Ala Ala His Leu Ala Gln
 1605 1610 1615
 Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met
 1620 1625 1630
 Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu
 1635 1640 1645
 Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr
 1650 1655 1660
 Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu

1665	1670	1675	168
Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu			
1685	1690	1695	
Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly			
1700	1705	1710	
Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu			
1715	1720	1725	
Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser			
1730	1735	1740	
Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp			
1745	1750	1755	176
Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr			
1765	1770	1775	
Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val			
1780	1785	1790	
Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn			
1795	1800	1805	
Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu			
1810	1815	1820	
Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys			
1825	1830	1835	184
Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val			
1845	1850	1855	
Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro			
1860	1865	1870	
Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser			
1875	1880	1885	
Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp			
1890	1895	1900	
Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp			
1905	1910	1915	192
Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe			
1925	1930	1935	
Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His			
1940	1945	1950	
Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu			
1955	1960	1965	
Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg			
1970	1975		

<210> 74

<211> 366

<212> PRT

<213> Homo Sapiens

<400> 74

Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala	
1	5
Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe	10
20	25
Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala	30
35	40
Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala	45
50	55
Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly	60

65		70		75		80									
Pro	Glu	Tyr	Trp	Asp	Arg	Glu	Thr	Gln	Lys	Tyr	Lys	Arg	Gln	Ala	Gln
				85					90					95	
Thr	Asp	Arg	Val	Ser	Leu	Arg	Asn	Leu	Arg	Gly	Tyr	Tyr	Asn	Gln	Ser
			100					105					110		
Glu	Ala	Gly	Ser	His	Ile	Ile	Gln	Arg	Met	Tyr	Gly	Cys	Asp	Val	Gly
		115					120					125			
Pro	Asp	Gly	Arg	Leu	Leu	Arg	Gly	Tyr	Asp	Gln	Tyr	Ala	Tyr	Asp	Gly
	130					135					140				
Lys	Asp	Tyr	Ile	Ala	Leu	Asn	Glu	Asp	Leu	Arg	Ser	Trp	Thr	Ala	Ala
145					150					155				160	
Asp	Thr	Ala	Ala	Gln	Ile	Thr	Gln	Arg	Lys	Trp	Glu	Ala	Ala	Arg	Glu
			165					170					175		
Ala	Glu	Gln	Leu	Arg	Ala	Tyr	Leu	Glu	Gly	Leu	Cys	Val	Glu	Trp	Leu
		180						185					190		
Arg	Arg	Tyr	Leu	Lys	Asn	Gly	Lys	Glu	Thr	Leu	Gln	Arg	Ala	Glu	His
		195					200					205			
Pro	Lys	Thr	His	Val	Thr	His	His	Pro	Val	Ser	Asp	His	Glu	Ala	Thr
	210					215					220				
Leu	Arg	Cys	Trp	Ala	Leu	Gly	Phe	Tyr	Pro	Ala	Glu	Ile	Thr	Leu	Thr
225					230					235				240	
Trp	Gln	Trp	Asp	Gly	Glu	Asp	Gln	Thr	Gln	Asp	Thr	Glu	Leu	Val	Glu
			245					250					255		
Thr	Arg	Pro	Ala	Gly	Asp	Gly	Thr	Phe	Gln	Lys	Trp	Ala	Ala	Val	Val
			260					265					270		
Val	Pro	Ser	Gly	Glu	Glu	Gln	Arg	Tyr	Thr	Cys	His	Val	Gln	His	Glu
		275					280					285			
Gly	Leu	Pro	Glu	Pro	Leu	Thr	Leu	Arg	Trp	Glu	Pro	Ser	Ser	Gln	Pro
	290					295					300				
Thr	Ile	Pro	Ile	Val	Gly	Ile	Val	Ala	Gly	Leu	Ala	Val	Leu	Ala	Val
305					310					315				320	
Leu	Ala	Val	Leu	Gly	Ala	Val	Val	Ala	Val	Val	Met	Cys	Arg	Arg	Lys
			325					330					335		
Ser	Ser	Gly	Gly	Lys	Gly	Gly	Ser	Cys	Ser	Gln	Ala	Ala	Ser	Ser	Asn
		340						345					350		
Ser	Ala	Gln	Gly	Ser	Asp	Glu	Ser	Leu	Ile	Ala	Cys	Lys	Ala		
		355					360					365			

<210> 75
 <211> 240
 <212> PRT
 <213> Homo Sapiens

<400> 75

Met	Gly	Leu	Glu	Leu	Tyr	Leu	Asp	Leu	Leu	Ser	Gln	Pro	Cys	Arg	Ala
1				5					10					15	
Val	Tyr	Ile	Phe	Ala	Lys	Lys	Asn	Asp	Ile	Pro	Phe	Glu	Leu	Arg	Ile
		20						25					30		
Val	Asp	Leu	Ile	Lys	Gly	Gln	His	Leu	Ser	Asp	Ala	Phe	Ala	Gln	Val
		35					40					45			
Asn	Pro	Leu	Lys	Lys	Val	Pro	Ala	Leu	Lys	Asp	Gly	Asp	Phe	Thr	Leu
	50					55					60				
Thr	Glu	Ser	Val	Ala	Ile	Leu	Leu	Tyr	Leu	Thr	Arg	Lys	Tyr	Lys	Val
65				70					75					80	
Pro	Asp	Tyr	Trp	Tyr	Pro	Gln	Asp	Leu	Gln	Ala	Arg	Ala	Arg	Val	Asp

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<210> 76
<211> 953
<212> PRT-----
<213> Homo Sapiens
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225		230		235		240
Asn Leu Leu Met	Ala Tyr Gln Ile Cys Phe Asp Leu Tyr Glu Ser Ala					
	245		250		255	
Ser Gln Gln Phe Leu Ser Ser Val Ile Gln Asn Leu Arg Thr Val Gly						
	260		265		270	
Thr Pro Ile Ala Ser Val Pro Gly Ser Thr Asn Thr Gly Thr Val Pro						
	275		280		285	
Gly Ser Glu Lys Asp Ser Asp Ser Met Glu Thr Glu Glu Lys Thr Ser						
	290		295		300	
Ser Ala Phe Val Gly Lys Thr Pro Glu Ala Ser Pro Glu Pro Lys Asp						
305		310		315		320
Gln Thr Leu Lys Met Ile Lys Ile Leu Ser Gly Glu Met Ala Ile Glu						
	325		330		335	
Leu His Leu Gln Phe Leu Ile Arg Asn Asn Thr Asp Leu Met Ile						
	340		345		350	
Leu Lys Asn Thr Lys Asp Ala Val Arg Asn Ser Val Cys His Thr Ala						
	355		360		365	
Thr Val Ile Ala Asn Ser Phe Met His Cys Gly Thr Thr Ser Asp Gln						
	370		375		380	
Phe Leu Arg Asp Asn Leu Glu Trp Leu Ala Arg Ala Thr Asn Trp Ala						
385		390		395		400
Lys Phe Thr Ala Thr Ala Ser Leu Gly Val Ile His Lys Gly His Glu						
	405		410		415	
Lys Glu Ala Leu Gln Leu Met Ala Thr Tyr Leu Pro Lys Asp Thr Ser						
	420		425		430	
Pro Gly Ser Ala Tyr Gln Glu Gly Gly Gly Leu Tyr Ala Leu Gly Leu						
	435		440		445	
Ile His Ala Asn His Gly Gly Asp Ile Ile Asp Tyr Leu Leu Asn Gln						
	450		455		460	
Leu Lys Asn Ala Ser Asn Asp Ile Val Arg His Gly Gly Ser Leu Gly						
465		470		475		480
Leu Gly Leu Ala Ala Met Gly Thr Ala Arg Gln Asp Val Tyr Asp Leu						
	485		490		495	
Leu Lys Thr Asn Leu Tyr Gln Asp Asp Ala Val Thr Gly Glu Ala Ala						
	500		505		510	
Gly Leu Ala Leu Gly Leu Val Met Leu Gly Ser Lys Asn Ala Gln Ala						
	515		520		525	
Ile Glu Asp Met Val Gly Tyr Ala Gln Glu Thr Gln His Glu Lys Ile						
	530		535		540	
Leu Arg Gly Leu Ala Val Gly Ile Ala Leu Val Met Tyr Gly Arg Met						
545		550		555		560
Glu Glu Ala Asp Ala Leu Ile Glu Ser Leu Cys Arg Asp Lys Asp Pro						
	565		570		575	
Ile Leu Arg Arg Ser Gly Met Tyr Thr Val Ala Met Ala Tyr Cys Gly						
	580		585		590	
Ser Gly Asn Asn Lys Ala Ile Arg Arg Leu Leu His Val Ala Val Ser						
	595		600		605	
Asp Val Asn Asp Asp Val Arg Ser Ala Ala Val Glu Ser Leu Gly Phe						
	610		615		620	
Ile Leu Phe Arg Thr Pro Glu Gln Cys Pro Ser Val Val Ser Leu Leu						
625		630		635		640
Ser Glu Ser Tyr Asn Pro His Val Arg Tyr Gly Ala Ala Met Ala Leu						
	645		650		655	
Gly Ile Cys Cys Ala Gly Thr Gly Asn Lys Glu Ala Ile Asn Leu Leu						
	660		665		670	

Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu
 675 680 685
 Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro
 690 695 700
 Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys
 705 710 715 720
 His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile
 725 730 735
 Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr
 740 745 750
 Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln
 755 760 765
 Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr
 770 775 780
 Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val
 785 790 795 800
 Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro
 805 810 815
 Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val
 820 825 830
 Leu Ser Ile Thr Ala Lys Ala Lys Lys Lys Glu Lys Glu Lys Glu Lys
 835 840 845
 Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu
 850 855 860
 Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn
 865 870 875 880
 Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu
 885 890 895
 Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile
 900 905 910
 Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val
 915 920 925
 Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro
 930 935 940
 Pro Glu Pro Phe Glu Tyr Ile Asp Asp
 945 950

<210> 77
 <211> 335
 <212> PRT
 <213> Homo Sapiens

<400> 77
 Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
 1 5 10 15
 Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
 20 25 30
 Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
 35 40 45
 Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn
 50 55 60
 Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
 65 70 75 80
 Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val
 85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu
 100 105 110
 Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala
 115 120 125
 Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu
 130 135 140
 Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
 145 150 155 160
 Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
 165 170 175
 Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
 180 185 190
 Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro
 195 200 205
 Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
 210 215 220
 Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val
 225 230 235 240
 Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
 245 250 255
 Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly
 260 265 270
 Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser
 275 280 285
 Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
 290 295 300
 Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr
 305 310 315 320
 Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu
 325 330 335

<210> 78
 <211> 117
 <212> PRT
 <213> Homo Sapiens

<400> 78
 Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala
 1 5 10 15
 Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr
 20 25 30
 Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val
 35 40 45
 Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu
 50 55 60
 Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly
 65 70 75 80
 Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu
 85 90 95
 Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln
 100 105 110
 Ser Gln Lys Ala Lys
 115

<210> 79

<211> 614
<212> PRT
<213> Homo Sapiens

<400> 79

Arg	Ser	Gly	Gln	Pro	Arg	Ala	Glu	Gly	Leu	Gly	Ala	Gly	Ala	Ala	Gly
1				5					10					15	
Pro	Leu	Arg	Ala	Met	Ala	Ala	Pro	Val	Lys	Gly	Asn	Arg	Lys	Gln	Ser
			20					25					30		
Thr	Glu	Gly	Asp	Ala	Leu	Asp	Pro	Pro	Ala	Ser	Pro	Lys	Pro	Ala	Gly
		35					40					45			
Lys	Gln	Asn	Gly	Ile	Gln	Asn	Pro	Ile	Ser	Leu	Glu	Asp	Ser	Pro	Glu
	50					55					60				
Ala	Gly	Gly	Glu	Arg	Glu	Glu	Glu	Gln	Glu	Arg	Glu	Glu	Glu	Gln	Ala
65					70					75					80
Phe	Leu	Val	Ser	Leu	Tyr	Lys	Phe	Met	Lys	Glu	Arg	His	Thr	Pro	Ile
			85						90					95	
Glu	Arg	Val	Pro	His	Leu	Gly	Phe	Lys	Gln	Ile	Asn	Leu	Trp	Lys	Ile
		100						105					110		
Tyr	Lys	Ala	Val	Glu	Lys	Leu	Gly	Ala	Tyr	Glu	Leu	Val	Thr	Gly	Arg
	115						120					125			
Arg	Leu	Trp	Lys	Asn	Val	Tyr	Asp	Glu	Leu	Gly	Gly	Ser	Pro	Gly	Ser
130						135					140				
Thr	Ser	Ala	Ala	Thr	Cys	Thr	Arg	Arg	His	Tyr	Glu	Arg	Leu	Val	Leu
145					150					155					160
Pro	Tyr	Val	Arg	His	Leu	Lys	Gly	Glu	Asp	Asp	Lys	Pro	Leu	Pro	Thr
			165						170					175	
Ser	Lys	Pro	Arg	Lys	Gln	Tyr	Lys	Met	Ala	Lys	Glu	Asn	Arg	Gly	Asp
		180						185					190		
Asp	Gly	Ala	Thr	Glu	Arg	Pro	Lys	Lys	Ala	Lys	Glu	Glu	Arg	Arg	Met
	195						200					205			
Asp	Gln	Met	Met	Pro	Gly	Lys	Thr	Lys	Ala	Asp	Ala	Ala	Asp	Pro	Ala
	210					215					220				
Pro	Leu	Pro	Ser	Gln	Glu	Pro	Pro	Arg	Asn	Ser	Thr	Glu	Gln	Gln	Gly
225				230						235					240
Leu	Ala	Ser	Gly	Ser	Ser	Val	Ser	Phe	Val	Gly	Ala	Ser	Gly	Cys	Pro
			245						250					255	
Glu	Ala	Tyr	Lys	Arg	Leu	Leu	Ser	Ser	Phe	Tyr	Cys	Lys	Gly	Thr	His
		260						265					270		
Gly	Ile	Met	Ser	Pro	Leu	Ala	Lys	Lys	Lys	Leu	Leu	Ala	Gln	Val	Ser
	275						280					285			
Lys	Val	Glu	Ala	Leu	Gln	Cys	Gln	Glu	Glu	Gly	Cys	Arg	His	Gly	Ala
	290					295					300				
Glu	Pro	Gln	Ala	Ser	Pro	Ala	Val	His	Leu	Pro	Glu	Ser	Pro	Gln	Ser
305				310						315					320
Pro	Lys	Gly	Leu	Thr	Glu	Asn	Ser	Arg	His	Arg	Leu	Thr	Pro	Gln	Glu
			325						330					335	
Gly	Leu	Gln	Ala	Pro	Gly	Gly	Ser	Leu	Arg	Glu	Glu	Ala	Gln	Ala	Gly
		340						345					350		
Pro	Cys	Pro	Ala	Ala	Pro	Ile	Phe	Lys	Gly	Cys	Phe	Tyr	Thr	His	Pro
	355					360						365			
Thr	Glu	Val	Leu	Lys	Pro	Val	Ser	Gln	His	Pro	Arg	Asp	Phe	Phe	Ser
	370					375					380				
Arg	Leu	Lys	Asp	Gly	Val	Leu	Leu	Gly	Pro	Pro	Gly	Lys	Glu	Gly	Leu
385					390					395					400

Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro
 405 410 415
 Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys
 420 425 430
 Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser
 435 440 445
 Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys
 450 455 460
 Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg
 465 470 475 480
 Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala
 485 490 495
 Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu
 500 505 510
 Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro
 515 520 525
 Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu
 530 535 540
 Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala
 545 550 555 560
 Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro
 565 570 575
 Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser
 580 585 590
 Ala Trp His Ala Pro Pro Val Thr Tyr Ala Ala Pro His Phe Phe
 595 600 605
 His Leu Asn Thr Lys Leu
 610

<210> 80.

<211> 114

<212> PRT

<213> Homo Sapiens

<400> 80

Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu
 1 5 10 15
 His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile
 20 25 30
 Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala
 35 40 45
 Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly
 50 55 60
 Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro
 65 70 75 80
 Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala
 85 90 95
 Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu
 100 105 110
 Phe Asp

<210> 81

<211> 596

<212> PRT

<400> 81

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Asp	Arg	Pro	Ala	Asp	Glu	Tyr	Asp	Gln	Pro	Trp	Glu	Trp	Asn	Arg	Val			
			420					425					430					
Thr	Ser	Pro	Ala	Leu	Ala	Ala	Gln	Phe	Asn	Gly	Asn	Glu	Lys	Arg	Gln			
		435					440					445						
Ser	Ser	Pro	Ser	Pro	Ser	Arg	Asp	Arg	Arg	Arg	Gln	Leu	Arg	Ala	Pro			
		450				455					460							
Gly	Gly	Gly	Phe	Lys	Pro	Ile	Lys	His	Gly	Ser	Pro	Glu	Phe	Cys	Gly			
465					470					475					480			
Ile	Leu	Gly	Glu	Arg	Val	Asp	Pro	Ala	Val	Pro	Leu	Glu	Lys	Gln	Ile			
			485					490						495				
Trp	Tyr	His	Gly	Ala	Ile	Ser	Arg	Gly	Asp	Ala	Glu	Asn	Leu	Leu	Arg			
			500					505					510					
Leu	Cys	Lys	Glu	Cys	Ser	Tyr	Leu	Val	Arg	Asn	Ser	Gln	Thr	Ser	Lys			
		515					520					525						
His	Asp	Tyr	Pro	Leu	Ser	Leu	Arg	Ser	Asn	Gln	Gly	Phe	Met	His	Met			
		530				535					540							
Lys	Leu	Ala	Lys	Thr	Lys	Glu	Lys	Tyr	Val	Leu	Gly	Gln	Asn	Ser	Pro			
545					550					555					560			
Pro	Phe	Asp	Ser	Val	Pro	Glu	Val	Ile	His	Tyr	Tyr	Thr	Thr	Arg	Lys			
			565					570						575				
Leu	Pro	Ile	Lys	Gly	Ala	Glu	His	Leu	Ser	Leu	Leu	Tyr	Pro	Val	Ala			
			580					585						590				
Val	Arg	Thr	Leu															
			595															

<210> 82
 <211> 207
 <212> PRT
 <213> Homo Sapiens

<400> 82

Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	Leu			
1			5					10					15					
Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln			
		20						25					30					
Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln			
		35					40					45						
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val			
		50				55				60								
Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly			
65					70					75					80			
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln			
			85					90						95				
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly			
			100					105					110					
Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys			
		115					120					125						
Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Arg	Ala	Ala	Thr	Pro	His	His	Arg			
		130				135					140							
Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	Pro			
145					150					155					160			
Ser	Pro	Ala	Asp	Ile	Thr	His	Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	Ala			
			165					170					175					
His	Ala	Ala	Pro	Ser	Thr	Thr	Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Ala			
			180					185					190					

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205

<210> 83
 <211> 429
 <212> PRT
 <213> Homo Sapiens

<400> 83

Glu	Cys	Asp	Val	Met	Thr	Tyr	Val	Arg	Glu	Thr	Cys	Gly	Cys	Cys	Asp
1				5					10					15	
Cys	Glu	Lys	Arg	Cys	Gly	Ala	Leu	Asp	Val	Val	Phe	Val	Ile	Asp	Ser
			20					25					30		
Ser	Glu	Ser	Ile	Gly	Tyr	Thr	Asn	Phe	Thr	Leu	Glu	Lys	Asn	Phe	Val
			35				40					45			
Ile	Asn	Val	Val	Asn	Arg	Leu	Gly	Ala	Ile	Ala	Lys	Asp	Pro	Lys	Ser
50					55						60				
Glu	Thr	Gly	Thr	Arg	Val	Gly	Val	Val	Gln	Tyr	Ser	His	Glu	Gly	Thr
65				70					75					80	
Phe	Glu	Ala	Ile	Gln	Leu	Asp	Asp	Glu	His	Ile	Asp	Ser	Leu	Ser	Ser
			85					90					95		
Phe	Lys	Glu	Ala	Val	Lys	Asn	Leu	Glu	Trp	Ile	Ala	Gly	Gly	Thr	Trp
			100				105						110		
Thr	Pro	Ser	Ala	Leu	Lys	Phe	Ala	Tyr	Asp	Arg	Leu	Ile	Lys	Glu	Ser
		115				120						125			
Arg	Arg	Gln	Lys	Thr	Arg	Val	Phe	Ala	Val	Val	Ile	Thr	Asp	Gly	Arg
130					135						140				
His	Asp	Pro	Arg	Asp	Asp	Asp	Leu	Asn	Leu	Arg	Ala	Leu	Cys	Asp	Arg
145				150					155					160	
Asp	Val	Thr	Val	Thr	Ala	Ile	Gly	Ile	Gly	Asp	Met	Phe	His	Glu	Lys
			165				170						175		
His	Glu	Ser	Glu	Asn	Leu	Tyr	Ser	Ile	Ala	Cys	Asp	Lys	Pro	Gln	Gln
			180				185					190			
Val	Arg	Asn	Met	Thr	Leu	Phe	Ser	Asp	Leu	Val	Ala	Glu	Lys	Phe	Ile
		195				200						205			
Asp	Asp	Met	Glu	Asp	Val	Leu	Cys	Pro	Asp	Pro	Gln	Ile	Val	Cys	Pro
210					215						220				
Asp	Leu	Pro	Cys	Gln	Thr	Glu	Leu	Ser	Val	Ala	Gln	Cys	Thr	Gln	Arg
225				230					235					240	
Pro	Val	Asp	Ile	Val	Phe	Leu	Leu	Asp	Gly	Ser	Glu	Arg	Leu	Gly	Glu
			245					250					255		
Gln	Asn	Phe	His	Lys	Ala	Arg	Arg	Phe	Val	Glu	Gln	Val	Ala	Arg	Arg
		260				265						270			
Leu	Thr	Leu	Ala	Arg	Arg	Asp	Asp	Asp	Pro	Leu	Asn	Ala	Arg	Val	Ala
	275					280						285			
Leu	Leu	Gln	Phe	Gly	Gly	Pro	Gly	Glu	Gln	Gln	Val	Ala	Phe	Pro	Leu
290					295						300				
Ser	His	Asn	Leu	Thr	Ala	Ile	His	Glu	Ala	Leu	Glu	Thr	Thr	Gln	Tyr
305				310					315					320	
Leu	Asn	Ser	Phe	Ser	His	Val	Gly	Ala	Gly	Val	Val	His	Ala	Ile	Asn
			325					330					335		
Ala	Ile	Val	Arg	Ser	Pro	Arg	Gly	Gly	Ala	Arg	Arg	His	Ala	Glu	Leu
		340					345					350			
Ser	Phe	Val	Phe	Leu	Thr	Asp	Gly	Val	Thr	Gly	Asn	Asp	Ser	Leu	His
	355					360						365			

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu
 370 375 380
 Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu
 385 390 395 400
 Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala
 405 410 415
 Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys
 420 425

<210> 84
 <211> 113
 <212> PRT
 <213> Homo Sapiens

<400> 84
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 1 5 10 15
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 20 25 30
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 35 40 45
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 50 55 60
 Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln
 65 70 75 80
 Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp
 85 90 95
 Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val
 100 105 110
 Gly

<210> 85
 <211> 258
 <212> PRT
 <213> Homo Sapiens

<400> 85
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 1 5 10 15
 Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu
 20 25 30
 Ala His Ser Gln Ile Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe
 35 40 45
 Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg
 50 55 60
 Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys
 65 70 75 80
 Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro
 85 90 95
 Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala
 100 105 110
 Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe
 115 120 125
 Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130 135 140
 Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys
 145 150 155 160
 Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu
 165 170 175
 Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly
 180 185 190
 Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met
 195 200 205
 Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser
 210 215 220
 Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His
 225 230 235 240
 Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile
 245 250 255
 Val Leu

<210> 86
 <211> 569
 <212> PRT
 <213> Homo Sapiens

<400> 86
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 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
 20 25 30
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
 35 40 45
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
 50 55 60
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
 65 70 75 80
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
 85 90 95
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
 100 105 110
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
 115 120 125
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
 130 135 140
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
 145 150 155 160
 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
 165 170 175
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
 180 185 190
 Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
 195 200 205
 Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
 210 215 220
 Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
 225 230 235 240
 Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile

50 55 60
 Leu Gln Leu Val His Val Thr Gln Glu Asp Lys Arg Lys Thr Thr Gly
 65 70 75 80
 Glu Glu Asn Gly Val Glu Ala Glu Glu Trp Gly Lys Phe Leu His Thr
 85 90 95
 Lys Asn Lys Leu Tyr Thr Asp Phe Asp Glu Ile Arg Gln Glu Ile Glu
 100 105 110
 Asn Glu Thr Glu Arg Ile Ser Gly Asn Asn Lys Gly Val Ser Pro Glu
 115 120 125
 Pro Ile His Leu Lys Ile Phe Ser Pro Asn Val Val Asn Leu Thr Leu
 130 135 140
 Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly Asp Gln Pro Lys
 145 150 155 160
 Asp Ile Glu Leu Gln Ile Arg Glu Leu Ile Leu Arg Phe Ile Ser Asn
 165 170 175
 Pro Asn Ser Ile Ile Leu Ala Val Thr Ala Ala Asn Thr Asp Met Ala
 180 185 190
 Thr Ser Glu Ala Leu Lys Ile Ser Arg Glu Val Asp Pro Asp Gly Arg
 195 200 205
 Arg Thr Leu Ala Val Ile Thr Lys Leu Asp Leu Met Asp Ala Gly Thr
 210 215 220
 Asp Ala Met Asp Val Leu Met Gly Arg Val Ile Pro Val Lys Leu Gly
 225 230 235 240
 Ile Ile Gly Val Val Asn Arg Ser Gln Leu Asp Ile Asn Asn Lys Lys
 245 250 255
 Ser Val Thr Asp Ser Ile Arg Asp Glu Tyr Ala Phe Leu Gln Lys Lys
 260 265 270
 Tyr Pro Ser Leu Ala Asn Arg Asn Gly Thr Lys Tyr Leu Ala Arg Thr
 275 280 285
 Leu Asn Arg Leu Leu Met His His Ile Arg Asp Cys Leu Pro Glu Leu
 290 295 300
 Lys Thr Arg Ile Asn Val Leu Ala Ala Gln Tyr Gln Ser Leu Leu Asn
 305 310 315 320
 Ser Tyr Gly Glu Pro Val Asp Asp Lys Ser Ala Thr Leu Leu Gln Leu
 325 330 335
 Ile Thr Lys Phe Ala Thr Glu Tyr Cys Asn Thr Ile Glu Gly Thr Ala
 340 345 350
 Lys Tyr Ile Glu Thr Ser Glu Leu Cys Gly Gly Ala Arg Ile Cys Tyr
 355 360 365
 Ile Phe His Glu Thr Phe Gly Arg Thr Leu Glu Ser Val Asp Pro Leu
 370 375 380
 Gly Gly Leu Asn Thr Ile Asp Ile Leu Thr Ala Ile Arg Asn Ala Thr
 385 390 395 400
 Gly Pro Arg Pro Ala Leu Phe Val Pro Glu Val Ser Phe Glu Leu Leu
 405 410 415
 Val Lys Arg Gln Ile Lys Arg Leu Glu Glu Pro Ser Leu Arg Cys Val
 420 425 430
 Glu Leu Val His Glu Glu Met Gln Arg Ile Ile Gln His Cys Ser Asn
 435 440 445
 Tyr Ser Thr Gln Glu Leu Leu Arg Phe Pro Lys Leu His Asp Ala Ile
 450 455 460
 Val Glu Val Val Thr Cys Leu Leu Arg Lys Arg Leu Pro Val Thr Asn
 465 470 475 480
 Glu Met Val His Asn Leu Val Ala Ile Glu Leu Ala Tyr Ile Asn Thr
 485 490 495

Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile
 500 505 510
 Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val
 515 520 525
 Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser
 530 535 540
 Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile
 545 550 555 560
 Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly
 565 570 575
 Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met
 580 585 590
 Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys
 595 600 605
 Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn
 610 615 620
 Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu
 625 630 635 640
 Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu
 645 650 655
 Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His
 660 665 670
 Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly
 675 680 685
 Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu
 690 695 700
 Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu
 705 710 715 720
 Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp
 725 730 735

<210> 88
 <211> 37
 <212> PRT
 <213> Homo Sapiens

<400> 88
 Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly
 1 5 10 15
 Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
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 Lys Leu Leu Leu Gln
 35

<210> 89
 <211> 1381
 <212> DNA
 <213> Homo Sapiens

<400> 89
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 tanaacagca atgagagccn ctcncaaaga ctttgaaaat tcaactgaatc nagtgaaact 180
 ctngaaaaag gatccangaa acgaaatgaa nctnaaactc tncgcgctat atnancangc 240
 cncatgaanga cttgtntcat gccnaacca nggtgtntttg acttgatcna caagggggcca 300

atggggacaca tggaatgccc ttggcancct gccnaagaa ctgccaggca naactatgtg 360
 gatttggtgt ccantttgan tcntccttg gaatcctcna atcnngtgga ncctggaaca 420
 nacaggaaat ccaactgggtt tgaaactctg gtggtgacct ccgaagatgg catcacaaaag 480
 atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt 540
 atgcgtgcac ttaaagctgc cagcaaggat gactcaatca tcaactgtttt aacaggaaat 600
 ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc cctggtgga 660
 gtagaggaga aagctaaaaa taatgccgtt ttaactgaggg aatttgtggg ctgttttata 720
 gattttccta agcctctgat tgcagtggtc aatgggtccag ctgtgggcct ctcggtcacc 780
 ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt 840
 agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc 900
 ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt 960
 gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc 1020
 aggctgaagg catttgcaaa gcttccccca aatgccttga gaatttcaaa agaggtaatc 1080
 aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtccttcag 1140
 ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttate cagaaaatca 1200
 aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct 1260
 ctgatttcca gtactggaac taaataagct tcattgtgcc tttttagtg ctagaatatc 1320
 aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa 1380
 a 1381

<210> 90

<211> 298

<212> PRT

<213> Homo Sapiens

<400> 90

Thr Cys Met Pro Val Phe Asp Leu Ile Lys Gly Pro Met Gly His
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 Met Glu Cys Pro Trp Pro Ala Arg Thr Ala Arg Asn Tyr Val Asp Leu
 20 25 30
 Val Ser Leu Pro Ser Leu Glu Ser Ser Asn Val Pro Gly Thr Arg Lys
 35 40 45
 Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
 50 55 60
 Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
 65 70 75 80
 Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
 85 90 95
 Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
 100 105 110
 Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
 115 120 125
 Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
 130 135 140
 Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
 145 150 155 160
 Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
 165 170 175
 Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
 180 185 190
 Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
 195 200 205
 Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
 210 215 220
 Cys Ala Gln Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys

Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile
 50 55 60
 Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp
 65 70 75 80
 Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu
 85 90 95
 Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly
 100 105 110
 Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly
 115 120 125
 Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr
 130 135 140
 Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu
 145 150 155 160
~~Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu~~
 165 170 175
 Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu
 180 185 190
 Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly
 195 200 205
 Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn
 210 215 220
~~Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala~~
 225 230 235 240
 Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys
 245 250 255
 Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Ile Lys His Asn
 260 265 270
 Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro
 275 280 285
 Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro
 290 295 300
 Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala
 305 310 315 320
 Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Pro Gln Pro
 325 330 335
 Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val
 340 345 350
 Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly
 355 360 365
 Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu
 370 375 380
 Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro
 385 390 395 400
 Lys Asp Phe Asp Trp Glu Ile
 405

<210> 93
 <211> 2236
 <212> DNA
 <213> Homo Sapiens

<400> 93
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 gggtcgtgca acgacgcagc tggacctggc ccagccatgg accgaaaagt ggcccagaaa 120

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ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tctgaggaga cctgaagctg 240
gtcatcaatg aaccagccg tctgcctctg tttgatgcca ttccggccgt gatccactg 300
aagcaccagg tggaatatga tcagctgacc ccccgccgt ccaggaagct gaaggagggtg 360
cgtctggacc gtctgcaccc cgaaggcctc ggcctgagtg tgcgtggtgg cctggagttt 420
ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg taccatgag 540
gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagttag acacatcggc 600
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gagaagaagg tcttcatcag cctggtaggc tcccagggcc ttggctgcag catttccagc 780
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cagcgtgagc tgcagcggca ggagcttctc atgcagaagc ggctggcgat ggagtccaac 1080
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gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag 1200
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gaacctgagc tcgagcccg agatgacctg gatggaggca cggaggagca gggagagcag 1380
gatttccgga aatatgagga aggctttgac ccctactcta tgttcacccc agagcagatc 1440
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gaaggcgggtg tggactcccc cattgggaag gtggtcgttt ctgctgtgta tgagcgggga 1560
gctgctgagc ggcattggtg cattgtgaaa ggggacgaga tcatggcaat caacggcaag 1620
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ggcggggact ggatcgacct tgtggttgcc gtctgcccc caaaggagta tgacgatgag 1740
ctgaccttct tgcgtgaagtc caaaagggga aaccaaattc acgcgttagg aaacagttag 1800
ctccggcccc acctcgtgaa cacaagcct cggaccagcc ttgagagagg ccacatgaca 1860
cacaccagat ggcactcctg ggacctgaat ctatcaccca ggaatctcaa actcccttg 1920
gccctgaacc agggccagat aaggaacagc tcgggcact tttttgaagg ccaatgtgga 1980
ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcattccttt 2040
cctctggccc agtgaatttg gtctctccca gctttggggg actccttctc tgaaccctaa 2100
taagacccca ctggagtctc tctctctcca tccctctcct ctgccctctg ctctaattgc 2160
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ttccagctta aaaaaa 2236

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<210> 94
 <211> 652
 <212> PRT
 <213> Homo Sapiens

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<400> 94
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Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85          90          95

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Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100 105 110
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
~~Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys~~
~~210 215 220~~
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
~~Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile~~
~~275 280 285~~
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
 420 425 430
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
 435 440 445
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
 450 455 460
 Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
 465 470 475 480
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
 485 490 495
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
 500 505 510
 Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
 515 520 525
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

530 535 540
 Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
 545 550 555 560
 Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
 565 570 575
 Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
 580 585 590
 His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
 595 600 605
 Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
 610 615 620
 Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
 625 630 635 640
 Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
 645 650

<210> 95
 <211> 831
 <212> DNA
 <213> Homo Sapiens

<400> 95
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 agaaaccaca atgccagat ctcaagtaga tgaagagttt ttgaagcaaa gtttaaagga 120
 aaaacnattg cagaaaacat ttagattnta tgaaatatat aananancc aaaanccatt 180
 tgaanttaat nganccttac ctgtcntcac taaatcaggg ttntctgcgc caccnaaggg 240
 cngcccanog cctgctgtgt tggttanta ggctnagca tangggcagn tgcaatcctt 300
 tcctcctnng gcggcanatg ggcttctgga anaacccttn ccttatcccc ancgaaggc 360
 ggccccctccc ctgccctnaa aggaaacctc ntggacncag ggaatatang gccaccttga 420
 aggggtggact ggctatcntg gaagatcaga taccaccaag caatttggag acagttcctg 480
 ttgagaataa ccacggtttc catgaaaaga cagcagcgt gaagcttgag gccgagggcg 540
 aggccatgga agatgcagcc gcgccaggga acgaccgagg cggcacacag gagccagccc 600
 cagtgcctgc tgagccgttt gacaacacta cctacaagaa cctgcagcat catgactaca 660
 gcacgtacac cttcttagac ctcaacctcg aactctcaaa attcaggatg cctcagccct 720
 cctcaggccg ggagtcacct cgacactgag ggccctcggg gtgaagatga accttccacc 780
 gtcttcaactg catcctggag tgcaaaaata aaatccactc aagagtcaaa a 831

<210> 96
 <211> 184
 <212> PRT
 <213> Homo Sapiens

<400> 96
 Arg Lys Asn Cys Arg Lys His Leu Asp Met Lys Tyr Ile Lys His Leu
 1 5 10 15
 Leu Pro Tyr Leu Ser Ser Leu Asn Gln Gly Leu Arg His Arg Ala Ala
 20 25 30
 Arg Leu Leu Cys Trp Leu Arg Pro His Gly Cys Asn Pro Phe Leu Leu
 35 40 45
 Arg Met Gly Phe Trp Asn Pro Leu Ile Pro Ala Arg Arg Pro Leu Pro
 50 55 60
 Cys Pro Arg Lys Pro Gly Arg Glu Tyr Ala Thr Leu Lys Gly Gly Leu
 65 70 75 80
 Ala Ile Glu Asp Gln Ile Pro Pro Ser Asn Leu Glu Thr Val Pro Val
 85 90 95

Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu
 100 105 110
 Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg
 115 120 125
 Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn
 130 135 140
 Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe
 145 150 155 160
 Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser
 165 170 175
 Ser Gly Arg Glu Ser Pro Arg His
 180

<210> 97

<211> 1008

<212> DNA

<213> Homo Sapiens

<400> 97

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ttcctcatga	cccagttgcc	cttgaagagc	acttcaggga	tgatgatgag	gggccagtgt	120
ccaaccaggg	ctacatgcct	tatttaaaca	ggttcatttt	ggaaaagggtc	caagacaact	180
ttgacaagat	tgaattcaat	aggatgtgtt	ggaccctctg	tgtcaaaaaa	aacctcacia	240
agaatcccct	gctcattaca	gaagaanatg	catttaaaat	atgggttatt	ttcaactttt	300
tatctgagga	caagtatcca	ttaattattg	tgtcagaana	gattgaatac	ctgcttaaga	360
agcttacaga	agctatggga	ggaggttggc	agcaagaaca	atttgaacat	tataaaatca	420
actttgatga	cagtaaaaaat	ggcctttctg	catgggaact	tattgagctt	attggaaatg	480
gacagtttag	caaaggcatg	gaccggcaga	ctgtgtctat	ggcaattaat	gaagtcttta	540
atgaacttat	attagatgtg	ttaaagcagg	gttacatgat	gaaaaagggc	cacagacgga	600
aaaactggac	tgaacgatgg	tttgtactaa	aacccaacat	aatttcttac	tatgtgagtg	660
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tgcttgacaa	agatggaaag	aaatgccttt	ttctcgtaaa	atgttttgat	aagacttttg	780
aatcagtg	ttcagataag	aanaanaaac	aggagtggat	tcaagccatt	cattctacta	840
ttcatctgtt	gaagctgncc	agccctccac	canacaaaga	agccnncag	cttctnaaan	900
aactccgna	gaatcatctg	gctgaacaag	angaactgga	gcgacaaatg	aangaactcc	960
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<210> 98

<211> 312

<212> PRT

<213> Homo Sapiens

<400> 98

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 20 25 30
 Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu
 35 40 45
 Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu
 50 55 60
 Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys
 65 70 75 80
 Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe
 85 90 95

Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile
 100 105 110
 Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln
 115 120 125
 Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn
 130 135 140
 Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe
 145 150 155 160
 Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val
 165 170 175
 Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys
 180 185 190
 Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys
 195 200 205
~~Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys~~
 210 215 220
 Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp
 225 230 235 240
 Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr
 245 250 255
 Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile
 260 265 270
~~His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala~~
 275 280 285
 Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg
 290 295 300
 Gln Met Glu Leu Gln Ala Arg Gln
 305 310

<210> 99
 <211> 1009
 <212> DNA
 <213> Homo Sapiens

<400> 99
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 aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taattttgctt 120
 tgaagaacac attcgggctt tagaaaagga ggaagaagaa gaaaaacaga agagtttgc 180
 gagagaaagg agacgacagc gaaaaaatag ggaatctttc cagatatttt tagatgaatt 240
 acatgaacat ggacaactgc attctatgtc atcttggatg gaattgtatc caactattag 300
 ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt 360
 caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaaga 420
 cattctaaag gataaaggat ttgtagttga agtaaacact acttttgaag attttgtggc 480
 gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcctt 540
 caatagttta ctagaaaagg cagaagcccg tgaacgtgaa agagaaaaag aagaggctcg 600
 gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctccctccgat 660
 agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga 720
 ggacataact ctagaatctg aaagaaaacg aatattttaa gattttatgc atgtgcttga 780
 gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca 840
 tcataggaaa cgttcccgcg ctcgatcggg gtcagattca ngatgatgat gatagccatt 900
 caaagaaaaa aagacagcga tgagaagtct cgggtctgntt canaacattc ttccantngc 960
 agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagt 1009

<210> 100
 <211> 292

<212> PRT
<213> Homo Sapiens

<400> 100
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1 5 10 15
Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp
20 25 30
Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu
35 40 45
Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg
50 55 60
Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu
65 70 75 80
His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr
85 90 95
Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro
100 105 110
Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys
115 120 125
Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp
130 135 140
Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala
145 150 155 160
Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile
165 170 175
Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg
180 185 190
Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala
195 200 205
Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala
210 215 220
Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu
225 230 235 240
Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met
245 250 255
His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys
260 265 270
His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg
275 280 285
Ser Gly Ser Asp
290

<210> 101
<211> 983
<212> DNA
<213> Homo Sapiens

<400> 101
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ttttatttca gtattaaaat agcaatttta tttattactt ttttatatat agaatttgac 180
accaaatttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240
acctggtgca ggaagcttca tctgaagatg tcctgggcgt tcatatggtg gacaaagaca 300
cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc 420
 gtgacgaagg ctccttgggc aagccattgt gtccaccga gatactctcg gagacgttgc 480
 caggctctgt gaagaaaagg gtatgctttc catcagaaga tcactctagag gagtttatag 540
 cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag 600
 gcacccaaac caacggtgac ctggaagacc tggaggagca tgggccaggg cagacagtct 660
 ctgaggaagc cacagaagtt cacatgatgg agggggacc agacacactg gccgaacttc 720
 tgatcaggga tgtacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg 780
 aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg 840
 tgncagggca gnnnttctct gaggaagcca caggggttca catgatgcag gtggaccag 900
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<210> 102

<211> 230

<212> PRT

<213> Homo Sapiens

<400> 102

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 20 25 30
 Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
 35 40 45
 Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
 50 55 60
 Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
 65 70 75 80
 Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
 85 90 95
 Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
 100 105 110
 Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
 115 120 125
 Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
 130 135 140
 Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
 145 150 155 160
 Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
 165 170 175
 Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
 180 185 190
 Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
 195 200 205
 Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
 210 215 220
 Glu Ala Thr Gly Val His
 225 230

<210> 103

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 103

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cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga      180
aaagtgcaga aggaagggaa gatcagctat gccgactttg tctggttttt gatctctgag      240
gaagacaaaa aaacaccgac cagcatcgag tactgggttc gctgcatgga cctggacggg      300
gacggcgccc tgtccatgtt cgagctcgag tacttctacg aggagcagtg ccgaaggctg      360
gacagcatgg ccacgcaggc cctgcccttc caggactgcc tctgccagat gctggacctg      420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc      480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcagaaagag      540
cagatctccc tgctcagggg cggtgacagc ggcggggccc agctctcgga ctgggagaag      600
tnccggccga agagtnccgac atcctgggtg ccgangaac cgtggggana nccctgggga      660
agacgggttc naaggcgaac tcacccccnt ggancanaaa ctgantgcgc tgcgtccccc      720
gctggggccan aggccttctt ccaagcgctt cccgctgggg cgccgtggaa ctgttncaaa      780
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gnt

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843

<210> 104
 <211> 197
 <212> PRT
 <213> Homo Sapiens

<400> 104

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Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp Asp
20     25     30
Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp Arg
35     40     45
Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu Gly
50     55     60
Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu Asp
65     70     75     80
Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp Leu
85     90     95
Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr Glu
100    105    110
Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro Phe
115    120    125
Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr Glu
130    135    140
Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn Val
145    150    155    160
Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Leu Asp His Glu Gln Lys
165    170    175
Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro Glu Leu
180    185    190
Ser Asp Trp Glu Lys
195

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<210> 105
 <211> 2264
 <212> DNA
 <213> Homo Sapiens

<400> 105

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cgacaacagg	gctctattat	gaccccaact	cgcaatacta	ctataattcc	ttgaccagc	180
agtaccttta	ctgggatggg	gaaaaagaga	cctacgtgcc	agctgcagag	tctagctccc	240
accagcagtc	gggcctgcct	cctgcaaaag	aggggaaaga	gaagaaggag	aaaccaaga	300
gcaaaacagc	ccagcagatt	gccaaagaca	tggaaagctg	ggctaagagt	ttgaataagc	360
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gagaatctgc	tgcagcagac	gctggctttg	ctctctttga	gaagaaggga	gccttagctg	480
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ggggtctggt	tgctgcttac	agtgggtgaca	gtgacaatga	ggaggagctg	gtggagagac	600
ttgagagtga	ggaagagaag	ctagctgact	ggaagaagat	ggcctgtctg	ctctgccggc	660
gccagttccc	gaacaaagat	gccctagtca	ggcaccagca	actctcagac	cttcacaagc	720
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ttccagaacc	tccagagccc	aagcgcaaga	agcagtttga	tgccggcact	gtgaattacg	900
agcaaccac	caaagatggc	attgaccaca	gtaacattgg	caacaagatg	ctgcaggcca	960
tgggctggcg	ggaaggctct	ggcttgggac	gaaagtgtca	aggcattacg	gctcccattg	1020
aggctcaagt	tgggctaaag	ggagctggcc	taggagccaa	aggcagcgca	tatggtttgt	1080
cgggcgcga	ttcctacaaa	gatgctgtcc	ggaaagccat	gtttgcccgg	ttcactgaga	1140
tggagtgaga	gagagagaga	gagagagatg	acaaggagca	caagaagtgg	tccatctccc	1200
gaattcgctg	ttaccgctg	tctctttaag	ggcatgcctt	gtgctgttaa	tagatcttag	1260
ggtgaaccac	ttcattctgc	agggttctcc	ctcccacctt	aaagaagttc	cccttatgtg	1320
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nttcnga	gggnaaaccc	tnggggttt	ccaaatattaa	cccctttgaa	aaaaaandcc	1860
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gggtttaa	nnacgggntt	ccaaanttgn	ttgggggaat	ttttaaattc	ccaannnccc	2040
aaggggnca	atthagnggn	ccccnaatcc	cccaaaaant	ggttcnnggn	tnaaancngc	2100
cnnnccnaa	tttntanggg	tttacttngn	tttaaaaaac	ccnccccaaa	actcccccn	2160
gaaccnaaaa	anaaaaagga	ngccattttt	ngnngnaaac	ttttttaann	nncnnttaa	2220
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<210> 106

<211> 381

<212> PRT

<213> Homo Sapiens

<400> 106

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Gly	Thr	Lys	Tyr	Ala	Val	Pro	Asp	Thr	Ser	Thr	Tyr	Gln	Tyr	Asp	Glu
			20					25					30		
Ser	Ser	Gly	Tyr	Tyr	Tyr	Asp	Pro	Thr	Thr	Gly	Leu	Tyr	Tyr	Asp	Pro
		35					40					45			
Asn	Ser	Gln	Tyr	Tyr	Tyr	Asn	Ser	Leu	Thr	Gln	Gln	Tyr	Leu	Tyr	Trp
		50				55					60				
Asp	Gly	Glu	Lys	Glu	Thr	Tyr	Val	Pro	Ala	Ala	Glu	Ser	Ser	Ser	His
65					70					75					80

Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu
 85 90 95
 Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg
 100 105 110
 Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe
 115 120 125
 Gln Pro Val Asn Ser Leu Arg Glu Glu Glu Arg Arg Glu Ser Ala Ala
 130 135 140
 Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu
 145 150 155 160
 Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn
 165 170 175
 Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn
 180 185 190
 Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala
 195 200 205
 Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn
 210 215 220
 Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln
 225 230 235 240
 Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu
 245 250 255
 Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala
 260 265 270
 Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg
 275 280 285
 Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys
 290 295 300
 Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met
 305 310 315 320
 Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr
 325 330 335
 Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala
 340 345 350
 Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala
 355 360 365
 Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu
 370 375 380

<210> 107

<211> 1367

<212> DNA

<213> Homo Sapiens

<400> 107

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 tcgaatgcat attcttcagc gagttccacc ccacgctggg acccaagatc acctatcagg 180
 tccctgaaga cttcatctcc cgagagctgt ttgacacagt ccaagtgtac atcatcacca 240
 agccagagct gcagaacaag cttatcactg tcacagctat ggaaaagaag ctgatcggtc 300
 gtctgtgtg catcgaaac aagaagtaca gccgcaatgc tctcctcttc aacctgggct 360
 tcgtgtgtga tgcccaggcc aagacctgcg cctcgagcc cattgttaaa aagctggctg 420
 gctatctgac cacactagag ctagagagca gcttcgtgtc catggaggag agcaagcaga 480
 agttggtgcc catcatgacc atcttgctgg aggagctaaa tgcctcaggc cgggtgcactc 540
 tgccattga tgagtccaac accatccact tgaaggtgat tgagcagcgg ccagaccctc 600

cggtggccca ggagtatgat gtacctgtct ttaccaaaga caaggaggat ttcttcaact 660
 cacagtggga cctcactaca caacaaatcc tgcctacat tgatgggttc cgccacatcc 720
 agaagatttc agcagaggca gatgtggagc tcaacctggt gcgcattgct atccagaacc 780
 tgctgtacta cggcggtgtg acactggtgt ccactctcca gtactccaat gtatactgcc 840
 caacgccc aa ggtccaggac ctggtagatg acaagtcctt gcaagaggca tgtctatcct 900
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 agaagtatcc tgtgcgggtg actcggaag agcagagcca ccctgcccgg ctttatacag 1140
 gctgccacag ctatgacgag atctgctgca agacaggcat gagctaccat gagctggatg 1200
 agcggcttga aaatgacccc aacatcatca tctgctggaa gtgaggctgg tagtgactgg 1260
 atggacacat tgctgtgggt agtccctcct actaggaggc ttgtcatact gtctagaggt 1320
 tgactcttag ttctgtaa at aaagacatcc atttcaaaca gccaaaa 1367

<210> 108

<211> 413

<212> PRT

<213> Homo Sapiens

<400> 108

Asp Thr Gly Leu Glu Ala Val Ser Asp Lys Cys Ser Gln Glu Val Gly
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 20 25 30
 Ala Met Gly Ser Gly Cys Arg Ile Glu Cys Ile Phe Phe Ser Glu Phe
 35 40 45
 His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
 50 55 60
 Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
 65 70 75 80
 Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
 85 90 95
 Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
 100 105 110
 Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
 115 120 125
 Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
 130 135 140
 Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
 145 150 155 160
 Leu Val Pro Ile Met Thr Ile Leu Leu Glu Leu Asn Ala Ser Gly
 165 170 175
 Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
 180 185 190
 Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
 195 200 205
 Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
 210 215 220
 Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
 225 230 235 240
 Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
 245 250 255
 Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
 260 265 270
 Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val

275	280	285
Asp Asp Lys Ser Leu Gln Glu Ala Cys Leu Ser Tyr Val Thr Lys Gln		
290	295	300
Gly His Lys Arg Ala Ser Leu Arg Asp Val Phe Gln Leu Tyr Cys Ser		
305	310	315
Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln		
325	330	335
Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met		
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Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr		
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<400> 109

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<400> 110

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<211> 2765

<212> DNA

<213> Homo Sapiens

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<212> PRT

<213> Homo. Sapiens.

<400> 112

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 Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
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 Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
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 115 120 125
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 Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
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 Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
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Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile
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Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala
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Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp
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Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg
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Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
275 280 285
Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
290 295 300

Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
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gagcaaaaag egaagattgc ggaacagggt gccagcttcc aggaagaaaa gagcaagctg 2160
gatgctgaag tgtccaaatg ggacgacagt ggcaatgaca tcattgtgct ggccaagcag 2220
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acatcggatg tcatcagtgc tgccaagaaa attgctgagg caggatccag gatggacaag 2340
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gaggtgcaga atctcggcgg ggagcttggt gtctctgggg tggacagcgc catgtccctg 2520
atccaggcag ccaagaactt gatgaatgct gtggtgcaga cagtgaaggc atcctacgtc 2580
geetctacca aataccaaaa gtcacagggt atggcttccc tcaaccttcc tgctgtgtca 2640
tggaagatga aggcaccaga gaaaaagcca ttggtgaaga gagagaaaca ggatgagaca 2700
cagaccaaga ttaaaccggc atctcagaag aagcacgtga acccggtgca ggccctcagc 2760
gagttcaaag ctatggacag catctaagtc tgcccagcc ggccgcccc acccctcggg 2820
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ttgtatgctt aaataaaaaa aaaaattcat aaccaaagag aatcccacat tagcttggtta 3060
gtaatgctct gaccaagccg agatgcccatt tctcttagtg atggcgccgt taggggttga 3120
gagaaggga tttggctcaa cttcagttga gaggtgagc tccagacagc ttgactgctt 3180
ttaaatgacc aaagatgacc tgtggtgaagc aacctgggca tcttagaagc agtccctgga 3240
gaaggcatgt tcccagaaaag gtctctggag ggacaaactc actcagtaaa acataatgta 3300
tcatcatgaa gaaaactgat totctatgac atgaaatgaa aatttttaag cattgttata 3360
attactaatg tacgtgtgtg caggacatta ataaagttgc ttttttaggc tacagtgtct 3420
cgtgccat 3429

<210> 114
<211> 906
<212> PRT
<213> Homo Sapiens

<400> 114
Met Thr Ala Val His Ala Gly Asn Ile Asn Phe Lys Trp Asp Pro Lys
1 5 10 15
Ser Leu Glu Ile Arg Thr Leu Ala Val Glu Arg Leu Leu Glu Pro Leu
20 25 30
Val Thr Gln Val Thr Thr Leu Val Asn Thr Asn Ser Lys Gly Pro Ser
35 40 45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
50 55 60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65 70 75 80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp

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Ala	Leu	Gln	Glu	Lys	Asp	Val	Asp	Gly	Leu	Asp	Arg	Thr	Ala	Gly	Ala	530	535	540
Ile	Arg	Gly	Arg	Ala	Ala	Arg	Val	Ile	His	Val	Val	Thr	Ser	Glu	Met	545	550	555
Asp	Asn	Tyr	Glu	Pro	Gly	Val	Tyr	Thr	Glu	Lys	Val	Leu	Glu	Ala	Thr	565	570	575
Lys	Leu	Leu	Ser	Asn	Thr	Val	Met	Pro	Arg	Phe	Thr	Glu	Gln	Val	Glu	580	585	590
Ala	Ala	Val	Glu	Ala	Leu	Ser	Ser	Asp	Pro	Ala	Gln	Pro	Met	Asp	Glu	595	600	605
Asn	Glu	Phe	Ile	Asp	Ala	Ser	Arg	Leu	Val	Tyr	Asp	Gly	Ile	Arg	Asp	610	615	620
Ile	Arg	Lys	Ala	Val	Leu	Met	Ile	Arg	Thr	Pro	Glu	Glu	Leu	Asp	Asp	625	630	635
Ser	Asp	Phe	Glu	Thr	Glu	Asp	Phe	Asp	Val	Arg	Ser	Arg	Thr	Ser	Val	645	650	655
Gln	Thr	Glu	Asp	Gln	Leu	Ile	Ala	Gly	Gln	Ser	Ala	Arg	Ala	Ile		660	665	670
Met	Ala	Gln	Leu	Pro	Gln	Glu	Gln	Lys	Ala	Lys	Ile	Ala	Glu	Gln	Val	675	680	685
Ala	Ser	Phe	Gln	Glu	Glu	Lys	Ser	Lys	Leu	Asp	Ala	Glu	Val	Ser	Lys	690	695	700
Trp	Asp	Asp	Ser	Gly	Asn	Asp	Ile	Ile	Val	Leu	Ala	Lys	Gln	Met	Cys	705	710	715
Met	Ile	Met	Met	Glu	Met	Thr	Asp	Phe	Thr	Arg	Gly	Lys	Gly	Pro	Leu	725	730	735
Lys	Asn	Thr	Ser	Asp	Val	Ile	Ser	Ala	Ala	Lys	Lys	Ile	Ala	Glu	Ala	740	745	750
Gly	Ser	Arg	Met	Asp	Lys	Leu	Gly	Arg	Thr	Ile	Ala	Asp	His	Cys	Pro	755	760	765
Asp	Ser	Ala	Cys	Lys	Gln	Asp	Leu	Leu	Ala	Tyr	Leu	Gln	Arg	Ile	Ala	770	775	780
Leu	Tyr	Cys	His	Gln	Leu	Asn	Ile	Cys	Ser	Lys	Val	Lys	Ala	Glu	Val	785	790	795
Gln	Asn	Leu	Gly	Gly	Glu	Leu	Val	Val	Ser	Gly	Val	Asp	Ser	Ala	Met	805	810	815
Ser	Leu	Ile	Gln	Ala	Ala	Lys	Asn	Leu	Met	Asn	Ala	Val	Val	Gln	Thr	820	825	830
Val	Lys	Ala	Ser	Tyr	Val	Ala	Ser	Thr	Lys	Tyr	Gln	Lys	Ser	Gln	Gly	835	840	845
Met	Ala	Ser	Leu	Asn	Leu	Pro	Ala	Val	Ser	Trp	Lys	Met	Lys	Ala	Pro	850	855	860
Glu	Lys	Lys	Pro	Leu	Val	Lys	Arg	Glu	Lys	Gln	Asp	Glu	Thr	Gln	Thr	865	870	875
Lys	Ile	Lys	Arg	Ala	Ser	Gln	Lys	Lys	His	Val	Asn	Pro	Val	Gln	Ala	885	890	895
Leu	Ser	Glu	Phe	Lys	Ala	Met	Asp	Ser	Ile							900	905	

<210> 115

<211> 1701

<212> DNA

<213> Homo Sapiens

<400> 115

eggccggccg ccatggctaa cgtggctgac acgaagctgt acgacatcct gggcgttccc 60
 gcgggcgcca gcgagaacga gctgaagaag gcatacagaa agttagccaa ggaatatcat 120
 cctgataaga atcccccatt gcaggagaca aacttttaag aaataagttt tgcatatgaa 180
 gtactatcaa atcctgagaa gcgtgagtta tatgacagat acggagagca aggtcttcgg 240
 gaaggcagcg gcggaggtgg gtggcatgga ttgatatttt ctctcac'cgt tttttgtggg 300
 ggattgttcg gcttcatggg caatcagagt agaagtcgaa atggcagaag aagaggagag 360
 gacatgatgc atccactcaa agtatcttta gaagatctgt ataatggcaa gacaacccaa 420
 ctacaactta gcaagaatgt gctctgtagt gcatgcagtg gccaggcg aaagtctgga 480
 gctgtccaaa agtgtagtgc ttgtcgaggt cgaggtgtgc gcatcatgat cagacagctg 540
 gctccaggga tggtaacaac gatgcagtct gtgtgctctg attgtaatgg tgaaggagag 600
 gtaattaatg aaaaagaccg ctgtaaaaaa tgtgaaggga agaaggtgat taaagaagtc 660
 aagattcttg aagtcacagt agacaaaggc atgaaacatg gacagagaat tacattcact 720
 ggggaagcag accaggcccc agagtggaaac ccggagacat tgttcttttt gctaccagga 780
 gaaaagaaca tggaggtatt tcagagagat gggaatgatt tgcacatgac atataaaata 840
 -----ggacttgttg-aagctctatg-tggatttcag-ttcacattaa-gccacettga-tggacgtcag----- 900
 attgtggtga aataccccc tggcaaagta attgaaccag ggtgtgttcg tgtagtctga 960
 ggtgaaggga tgccgcagta tcgtaatccc tttgaaaaag gtgggcttta cataaagttt 1020
 gatgtgcagt ttctgaaaa caactggatc aaccagaca agctttctga actagaagat 1080
 cttctgccat ctagaccgga agttcctaac ataattggag aaacagagga ggtagagctt 1140
 caggaatttg atagcactcg aggtcagga ggtggtcaga ggcgtgaagc ctataatgat 1200
 agctctgatg aagaaagcag cagccatcat ggacctggag tgcagtgtgc ccatcagtaa 1260
 actctgcaaa caaattgcac aggtggattt tctttccaca tttgcctgat ttgttctcag 1320
 -----caatccagct-ggagtgtctt-atcaatccag-atgaactgag-ggacatctgt-tgggtctatgt----- 1380
 ataactttta aaattggat agtatctaca gagtgtataa tttaaactaa ccacaaagct 1440
 ttacatcttc attttgactg ttccatagca gaataaagca cttgaaagga aacaagactc 1500
 cttttcacac atggattatt ataagtttca atcctggat ctgtgcttga tttttatcag 1560
 ttttgtgtag atttttatgt ttcatatattt aaattttaa cccacattgt aaagtttgta 1620
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 agaatttcat agcctgtaaa a 1701

<210> 116
 <211> 415
 <212> PRT
 <213> Homo Sapiens

<400> 116
 Met Ala Asn Val Ala Asp Thr Lys Leu Tyr Asp Ile Leu Gly Val Pro
 1 5 10 15
 Ala Gly Ala Ser Glu Asn Glu Leu Lys Lys Ala Tyr Arg Lys Leu Ala
 20 25 30
 Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
 35 40 45
 Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
 50 55 60
 Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
 65 70 75 80
 Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
 85 90 95
 Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
 100 105 110
 Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
 115 120 125
 Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
 130 135 140
 Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Ser Gly Ala Val Gln Lys

145		150		155		160
Cys Ser Ala Cys Arg	Gly Arg Gly Val Arg	Ile Met Ile Arg	Gln Leu			
	165		170		175	
Ala Pro Gly Met Val	Gln Gln Met Gln Ser	Val Cys Ser Asp	Cys Asn			
	180		185		190	
Gly Glu Gly Glu Val	Ile Asn Glu Lys Asp	Arg Cys Lys Lys	Cys Glu			
	195		200		205	
Gly Lys Lys Val Ile	Lys Glu Val Lys Ile	Leu Glu Val His	Val Asp			
	210		215		220	
Lys Gly Met Lys His	Gly Gln Arg Ile Thr	Phe Thr Gly Glu	Ala Asp			
	225		230		235	
Gln Ala Pro Glu Trp	Asn Pro Glu Thr Leu	Phe Phe Leu Leu	Pro Gly			
	245		250		255	
Glu Lys Asn Met Glu	Val Phe Gln Arg Asp	Gly Asn Asp Leu	His Met			
	260		265		270	
Thr Tyr Lys Ile Gly	Leu Val Glu Ala Leu	Cys Gly Phe Gln	Phe Thr			
	275		280		285	
Leu Ser His Leu Asp	Gly Arg Gln Ile Val	Val Lys Tyr Pro	Pro Gly			
	290		295		300	
Lys Val Ile Glu Pro	Gly Cys Val Arg Val	Val Arg Gly Glu	Gly Met			
	305		310		315	
Pro Gln Tyr Arg Asn	Pro Phe Glu Lys Gly	Gly Leu Tyr Ile	Lys Phe			
	325		330		335	
Asp Val Gln Phe Pro	Glu Asn Asn Trp Ile	Asn Pro Asp Lys	Leu Ser			
	340		345		350	
Glu Leu Glu Asp Leu	Leu Pro Ser Arg Pro	Glu Val Pro Asn	Ile Ile			
	355		360		365	
Gly Glu Thr Glu Glu	Val Glu Leu Gln Glu	Phe Asp Ser Thr	Arg Gly			
	370		375		380	
Ser Gly Gly Gly Gln	Arg Arg Glu Ala Tyr	Asn Asp Ser Ser	Asp Glu			
	385		390		395	
Glu Ser Ser Ser His	His Gly Pro Gly Val	Gln Cys Ala His	Gln			
	405		410		415	

<210> 117
 <211> 1821
 <212> DNA
 <213> Homo Sapiens

<400> 117

cgcgtgaact gcttcctgca ggctggccat ggcgcttcac gttcccaagg ctccgggctt	60
tgcccagatg ctcaaggagg gagcgaaaca cttttcagga ttagaagagg ctgtgtatag	120
aaacatacaa gcttgcaagg agcttgccca aaccactcgt acagcatatg gacccaaaagg	180
aatgaacaaa atgggttatca accacttgga gaagttgttt gtgacaaaacg atgcagcaac	240
tattttaaga gaactagaag tacagcatcc tgctgcaaaa atgattgtaa tggcttctca	300
tatgcaagag caagaagttg gagatggcac aaactttgtt ctggtatttg ctggagctct	360
cctggaatta gctgaagaac ttctgaggat tggcctgtca gtttcagagg tcatagaagg	420
ttatgaaata gcctgcagaa aagctcatga gattcttctt aatttggtat gttgttctgc	480
aaaaaacctt cgagatattg atgaagtctc atctctactt cgtacctcca taatgagtaa	540
acaatatggt aatgaagtat ttctggccaa gcttattgct caggcatgcg tatctatttt	600
tcttgattcc ggccatttca atgttgataa catcagagtt tgtaaaattc tgggctctgg	660
tatcagttcc tcttcagtat tgcattggcat ggtttttaag aaggaaaccg aagggtgatgt	720
aacatctgtc aaagatgcaa aaatagcagt gtactcttgt ccttttgatg gcatgataac	780
agaaactaag ggaacagtgt tgataaagac tgctgaagaa ttgatgaatt ttagtaaggg	840
agaagaaaac ctcattggatg cacaagtcaa agctattgct gatactggtg caaatgtcgt	900

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agtaacaggt ggcaaagtgg cagacatggc tcttcattat gcaaataaat ataatatcat      960
gttagtgagg ctaaactcaa aatgggatct ccgaagactt tgtaaaactg ttggtgctac      1020
agctcttcct agattgacac ctctgtcct tgaagaaatg ggacactgtg acagtgttta      1080
cctctcagaa gttggagata ctgaggtggg ggtttttaag catgaaaagg aagatggcgc      1140
catttctacc atagtacttc gaggtctctac agacaatctg atggatgaca tagaaagggg      1200
agtagacgat ggtgttaata ctttcaaagt tcttacaagg gataaacgtc ttgtaccggg      1260
aggtggagca acagaaattg aattagccaa acagatcaca tcatatggag agacatgtcc      1320
tggaacttgaa cagtatgcta ttaagaagtt tgctgaggca tttgaagcta tccccgcgc      1380
actggcagaa aactctggag ttaaggccaa tgaagtaatc tctaaacttt atgcagtaca      1440
tcaagaagga aataaaaacg ttggattaga tattgaggct gaagtccctg ctgtaaagga      1500
catgctggaa gctggtattc tagatactta cctgggaaaa tattgggcta tcaaactcgc      1560
tactaatgct gcagtcactg tacttagagt ggatcagatc atcatggcaa aaccagctgg      1620
tgggcccaag cctccaagtg ggaagaaaga ctgggatgat gaccaaagt attgaaattg      1680
gcttaatttt tactgtaggg gaaggctgta tttgtagtag tactcaagaa tcacctgatg      1740
ttttcttatt ctctttaat taagagttat tttgtgttg tattcttggc tggatgttat      1800
aataaacata ttgttactgt c                                     1821

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<210> 118
 <211> 548
 <212> PRT
 <213> Homo Sapiens

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<400> 118
Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
1          5          10          15
Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
20         25         30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
35         40         45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
50         55         60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
65         70         75         80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
85         90         95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
100        105        110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
115        120        125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
130        135        140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
145        150        155        160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
165        170        175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
180        185        190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
195        200        205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
210        215        220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
225        230        235        240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
245        250        255

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Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu
 260 265 270
 Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala
 275 280 285
 Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr
 290 295 300
 Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp
 305 310 315 320
 Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu
 325 330 335
 Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu
 340 345 350
 Ser Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu
 355 360 365
 ----- Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu -----
 370 375 380
 Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys
 385 390 395 400
 Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu
 405 410 415
 Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly
 420 425 430
 ----- Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile -----
 435 440 445
 Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile
 450 455 460
 Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu
 465 470 475 480
 Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly
 485 490 495
 Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr
 500 505 510
 Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys
 515 520 525
 Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp
 530 535 540
 Asp Gln Asn Asp
 545

<210> 119
 <211> 1321
 <212> DNA
 <213> Homo Sapiens

<400> 119
 cccccaagat ggctgctgag gacgagttac agctgccgcg gctccccgag ctgttcgaaa 60
 ctggttagaca gttactggac gaagtagaag tggcgactga acccgccggt tcccgatag 120
 tccaggagaa ggtgttcaag ggcttggacc tccttgagaa ggctgccgaa atgttatcgc 180
 agctcgactt gttcagccga aatgaagatt tggaagagat tgcttccacc gacctgaagt 240
 accttttgggt gccagcgttt caaggagccc tcacatgaa acaagtcaac cccagcaagc 300
 gtctagatca tttgcagcgg gctcgagaac actttataaa ctacttaact cagtgccatt 360
 gctatcatgt ggcagagttt gagctgcccc aaacatgaa caactctgct gaaaatcaca 420
 ctgccaatte ctccatggct taccatagtc tcgttgctat ggcattctca agacaggcta 480
 aaatacagag atacaagcag aagaaggagt tggagcatag gttgtctgca atgaaatctg 540
 ctgtggaaag tgggtcaagca gatgatgagc gtgttcgtga atattatctt cttcaccttc 600

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agaggtggat tgatattcagc ttagaagaga ttgagagcat tgaccaggaa ataaagatcc      660
tgagagaaag agactcttca agagaggcat caacttctaa ctcatctcgc caggagaggc      720
ctccagtga acccttcatt ctactcggga acatggctca agccaaagta tttggagctg      780
gttatccaag tctgccaact atgacggtga gtgactggta tgagcaacat cggaaatatg      840
gagcattacc ggatcaggga atagccaagg cagcaccaga ggaattcaga aaagcagctc      900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaaca ctccacagag      960
cccgaggagt ggatgactgg aaggacacccc atcctagggg ctatgggaac cgacagaaca    1020
tgggctgata ttcccacaac accacaggac tgcagggtgc acaactccct gccaaggaaa    1080
accatgcagt cctcccctcc ctggctctct gcttcagctc tgtacaacga gggcaaagat    1140
gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta    1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc    1260
ttaagtggaa ggaaaagagt gctgagaaat ggctctgtat aatctatggc tatccgaatt    1320
c

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<210> 120
<211> 339
<212> PRT
<213> Homo Sapiens

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<400> 120
Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
 1          5          10          15
Glu Thr Gly Arg Gln Leu Leu Asp Glu Val Glu Val Ala Thr Glu Pro
 20          25          30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
 35          40          45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
 50          55          60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
 65          70          75          80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
 85          90          95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
 100         105         110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
 115         120         125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
 130         135         140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
 145         150         155         160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
 165         170         175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
 180         185         190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
 195         200         205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
 210         215         220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
 225         230         235         240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
 245         250         255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
 260         265         270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala

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275 280 285
Ala Pro Glu Glu Phe Arg Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu
290 295 300
Glu Lys Glu Glu Glu Asp Asp Glu Gln Thr Leu His Arg Ala Arg Glu
305 310 315 320
Trp Asp Asp Trp Lys Asp Thr His Pro Arg Gly Tyr Gly Asn Arg Gln
325 330 335
Asn Met Gly

<210> 121
<211> 2965
<212> DNA
<213> Homo Sapiens

<400> 121

gcggagggtcg	gcggtcgggt	ccgtctctgc	ccgcggctgt	ggcggcgccg	gcggatccag	60
ccttagcggt	cctctctggg	cggcggcggc	ggcggctcgg	ttgacgcctc	ctccgccagc	120
tgagcccgcg	ggagcccagg	acgccgcttc	cccgcccctc	cccgtcctcc	gaggccggcc	180
gcctgggtcat	ggcgccagccg	ggcccggctt	cccagcctga	cgtttctctt	cagcaacggg	240
tagcagaatt	ggaaaaaatt	aatgcagaat	ttttacgtgc	acaacagcag	cttgaacaag	300
aatttaataca	aaagagagca	aaatttaagg	agttatattt	ggctaaagag	gaggatctga	360
agaggcaaaa	tgcagtattt	caagctgcac	aagatgattt	gggacacctt	cgaacccagc	420
tgtgggaagc	tcaagcagag	atggagaata	ttaaggcgat	tgccacagtc	tctgagaaca	480
ccaagcaaga	agctatagat	gaagtgaata	gacagtggag	agaagaagtt	gcttcacttc	540
aggctgttat	gaaagaaaca	gttcgtgact	atgagcacca	gttcacactt	aggctggagc	600
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gaagaaggct	gtctgaagg	caagaggagg	aaaatttaga	aaatgaaatg	aaaaaggccc	720
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tcattcttag agcaacagta attattattt aactcttaac tgaagaaaga gaagtcacaa 2880
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cagcaaacag tggggtgatc tgcag 2965

<210> 122

<211> 862

<212> PRT

<213> Homo Sapiens

<400> 122

Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
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20 25 30
----- Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu -----
35 40 45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
50 55 60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
65 70 75 80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
85 90 95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
100 105 110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
115 120 125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
130 135 140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
145 150 155 160
Leu Ser Glu Gly Gln Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
165 170 175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
180 185 190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
195 200 205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
210 215 220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
225 230 235 240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
245 250 255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
260 265 270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
275 280 285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val

290	295	300
Leu Thr Ser Glu Gln	Leu Arg Gln Val Glu Glu	Leu Lys Lys Lys Asp
305	310	315
Gln Glu Asp Asp Glu	Gln Gln Arg Leu Asn Lys	Arg Lys Asp His Lys
325	330	335
Lys Ala Asp Val Glu	Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu	
340	345	350
Thr Gln Glu Glu Ser Ser	Ala Gln Leu Ser Asn Glu Glu Glu His Leu	
355	360	365
Asp Ser Thr Arg Gly Ser	Val His Ser Leu Asp Ala Gly Leu Leu Leu	
370	375	380
Pro Ser Gly Asp Pro	Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp	
385	390	395
Gly Leu Arg Arg Ala	Gln Ser Thr Asp Ser Leu Gly Thr Ser Gly Ser	
405	410	415
Leu Gln Ser Lys Ala	Leu Gly Tyr Asn Tyr Lys Ala Lys Ser Ala Gly	
420	425	430
Asn Leu Asp Glu Ser	Asp Phe Gly Pro Leu Val Gly Ala Asp Ser Val	
435	440	445
Ser Glu Asn Phe Asp	Thr Ala Ser Leu Gly Ser Leu Gln Met Pro Ser	
450	455	460
Gly Phe Met Leu Thr	Lys Asp Gln Glu Arg Ala Ile Lys Ala Met Thr	
465	470	475
Pro Glu Gln Glu Glu	Thr Ala Ser Leu Leu Ser Ser Val Thr Gln Gly	
485	490	495
Met Glu Ser Ala Tyr	Val Ser Pro Ser Gly Tyr Arg Leu Val Ser Glu	
500	505	510
Thr Glu Trp Asn Leu	Leu Gln Lys Glu Val His Asn Ala Gly Asn Lys	
515	520	525
Leu Gly Arg Arg Cys	Asp Met Cys Ser Asn Tyr Glu Lys Gln Leu Gln	
530	535	540
Gly Ile Gln Ile Gln	Glu Ala Glu Thr Arg Asp Gln Val Lys Lys Leu	
545	550	555
Gln Leu Met Leu Arg	Gln Ala Asn Asp Gln Leu Glu Lys Thr Met Lys	
565	570	575
Asp Lys Gln Glu Leu	Glu Asp Phe Ile Lys Gln Ser Ser Glu Asp Ser	
580	585	590
Ser His Gln Ile Ser	Ala Leu Val Leu Arg Ala Gln Ala Ser Glu Ile	
595	600	605
Leu Leu Glu Glu Leu	Gln Gln Gly Leu Ser Gln Ala Lys Arg Asp Val	
610	615	620
Gln Glu Gln Met Ala	Val Leu Met Gln Ser Arg Glu Gln Val Ser Glu	
625	630	635
Glu Leu Val Arg Leu	Gln Lys Asp Asn Asp Ser Leu Gln Gly Lys His	
645	650	655
Ser Leu His Val Ser	Leu Gln Gln Ala Glu Asp Phe Ile Leu Pro Asp	
660	665	670
Thr Thr Glu Ala Leu	Arg Glu Leu Val Leu Lys Tyr Arg Glu Asp Ile	
675	680	685
Ile Asn Val Arg Thr	Ala Ala Asp His Val Glu Glu Lys Leu Lys Ala	
690	695	700
Glu Ile Leu Phe Leu	Lys Glu Gln Ile Gln Ala Glu Gln Cys Leu Lys	
705	710	715
Glu Asn Leu Glu Glu	Thr Leu Gln Leu Glu Ile Glu Asn Cys Lys Glu	
725	730	735

Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys
 740 745 750
 Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln
 755 760 765
 Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys
 770 775 780
 Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu
 785 790 795 800
 Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln
 805 810 815
 Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu
 820 825 830
 Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu
 835 840 845
 Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr
 850 855 860

<210> 123
 <211> 544
 <212> DNA
 <213> Homo Sapiens

<400> 123

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 ttggtttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa 180
 atgaagtaga aaaggttaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa 240
 atgacaatta tagaacaacg ggaattgcta caatcgaggt gtttttacca ccaagactaa 300
 aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt 360
 ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga 420
 agcaactacn actagggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga 480
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<210> 124
 <211> 178
 <212> PRT
 <213> Homo Sapiens

<400> 124

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 35 40 45
 Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys
 50 55 60
 Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn
 65 70 75 80
 Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro
 85 90 95
 Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His
 100 105 110
 Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu

115 120 125
 Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys
 130 135 140
 Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu
 145 150 155 160
 Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu
 165 170 175
 Glu Glu

<210> 125
 <211> 1302
 <212> DNA
 <213> Homo Sapiens

<400> 125
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 ggtatggaca cgttcatcca ccgcatcgac tccaccgagg tcatctacca gccgcgccgc 120
 aagcgggcca agctcatcgg caagtacctg atggggggacc tgctggggga aggtctttac 180
 ggcaaggtga aggaggtgct ggactcggag acgctgtgca ggagggccgt caagatcctc 240
 aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa 300
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 gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg 420
 gacagcgtgc cggagaagcg ttccccagtg tgccaggccc acgggtactt ctgtcagctg 480
 attgacggcc tggagtacct gcatagccag ggcattgtgc acaaggacat caagccgggg 540
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 ccgcccgaaga ttgccaacgg cctggacacc ttctccggt tcaaggtgga catctggctg 720
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 atctacactc aggacttcac ggtgcccgga caggctccag aagaggaggc cagtcacaat 1140
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 agcaccaaat ccagggcgga gggccgggccc cccaacctg cccgcaaggc ctgctccgcc 1260
 agcagcaaga tccgccggct gtcggcctgc aagcagcagt ga 1302

<210> 126
 <211> 433
 <212> PRT
 <213> Homo Sapiens

<400> 126
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 20 25 30
 Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys
 35 40 45
 Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys
 50 55 60
 Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu
 65 70 75 80

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys
 85 90 95
 Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln
 100 105 110
 Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val
 115 120 125
 Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro
 130 135 140
 Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu
 145 150 155 160
 Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp
 165 170 175
 Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile
 180 185 190
 Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp
 195 200 205
 Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile
 210 215 220
 Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
 225 230 235 240
 Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
 245 250 255
 Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr
 260 265 270
 Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly
 275 280 285
 Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
 290 295 300
 Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val
 305 310 315 320
 Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
 325 330 335
 Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp
 340 345 350
 Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val
 355 360 365
 Pro Gly Gln Val Pro Glu Glu Glu Ala Ser His Asn Gly Gln Arg Arg
 370 375 380
 Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu
 385 390 395 400
 Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys
 405 410 415
 Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln
 420 425 430
 Gln

<210> 127
 <211> 1488
 <212> DNA
 <213> Homo Sapiens

<400> 127
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 ccaagccaca aaaagtacag ggccgccctg aagaaggaga aacgaaagaa acgtcggcag 120

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gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt 180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat 240
gaggagtggg tgctaagaga gcagaaggca caagaagaat tcagaataaa gaaggaaaag 300
gaagaggcgg ctaaaaaacg gcaagaagaa caagagagaa agttaagga acaatgggaa 360
gaacagcaga ggaaagagag agaagaggag gagcagaaac gacaggagaa gaaagaaaaa 420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tgggtaccaca 480
tggcaaaacc cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt 540
cccttctaca gtaaaacagg agcttgcaga tttggagata gatgttcacg taaacataat 600
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cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc 720
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aagagtcggg agaggcacia ttcacgaagc agagggaaga atagggaccg cagcagggac 1320
cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccgc 1380
agccggagcc aaagtctctc taggtcccga agtcgtggca ggaggaggtc gggtaataga 1440
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gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt -----1488

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<210> 128

<211> 482

<212> PRT

<213> Homo Sapiens

<400> 128

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20          25          30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
35          40          45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Lys Leu Leu
50          55          60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
65          70          75          80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
85          90          95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
100         105         110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Gln Lys Arg Gln Glu
115         120         125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
130         135         140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
145         150         155         160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
165         170         175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
180         185         190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr

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195	200	205
Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser		
210	215	220
Leu Glu Tyr Ser Glu Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr		
225	230	235
Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe		
245	250	255
Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val		
260	265	270
Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn		
275	280	285
Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val		
290	295	300
Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys		
305	310	315
Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn		
325	330	335
Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg		
340	345	350
Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly		
355	360	365
His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser		
370	375	380
Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser		
385	390	395
Arg His Arg Gly Lys Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu		
405	410	415
Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp		
420	425	430
Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg		
435	440	445
Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg		
450	455	460
Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys		
465	470	475
Ser Lys		480

<210> 129
 <211> 1663
 <212> DNA
 <213> Homo Sapiens

<400> 129

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tccaggcctg ggtgcaggag cattgcccg agagcgctga agaggctgtc actctcctcg	180
aagatctgga gcggaactg gatgagccag gacaccaggt ctcaactcct ccaaacgaac	240
agaaaccggt gtgggagaag atatcctcct caggaaactgc aaaggaatcc ccgagcagca	300
tgcagccaca gcccttgagg accagtcaca aatacagatc ttggggggccc ctgtacatcc	360
aagagtctgg tgaggagcag gagttcgctc aagatccaag aaaggtccga gattgcagat	420
tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gaggggctca	480
aaggggatat aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt	540
gcgtaaacct tgaaaatgaa aaaggaacaa aacccccctc tcaagaggca ggctccaaga	600
aaggtagaga atcagttcct actaaaccta cccaggaga gagacgttat atatgtgctg	660

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aatgtggcaa agccttttagt aatagctcaa atctcaccaa acacaggaga acacacactg      720
gggagaaacc ttacgtgtgc accaagtgtg ggaaagcttt cagccacagc tcaaacctca      780
ccctccacta cagaacacac ttggtggacc ggccctatga ctgtaagtgt ggaaaagctt      840
ttgggcagag ctacagacctt cttaaaccatc agagaatgca cacagaagag gcgccatata      900
agtgtcaaaga ttgtggcaag gcttttcagcg ggaaaggcag cctcattcgt cactatcgga      960
tccacactgg ggagaagcct tatcagtgtg acgaatgtgg gaagagcttc agtcagcatg     1020
cgggcctcag ctcccaccag agactccaca ccggagagaa gccatataag tgtaaggagt     1080
gtgggaaagc cttcaaccac agctccaact tcaataaaca ccacagaate cacaccgggg     1140
aaaagcccta ctggtgtcat cactgtggaa agaccttctg tagcaagtcc aatctttcca     1200
aacatcagcg agtcacact ggagagggag aagcaccgta actttcaagc gctcctgttg     1260
ttgtcgttgt tttaaacttt agaattctgaa aaccagaaag aagtottgtc attgcagcag     1320
catcgattcc ggtgatagag tttgtatcac tcaacatcag gggatgcctg aggagtgcga     1380
gctccacagc aacatggcag gcaggaggtc ctcaagaagg gtcaggaggt tccacactcg     1440
ccagttcact ggagcagagt cccttcgcca cacttagggg cccagtaagc catgccagca     1500
ttaccttttg cgtagttaaa cagacgtgta tccagtctag ttaaggaaga aacattaaga     1560
ttgtttaatt tttacatat attcaagaat ttttaattgt aaagaattga gccacattga     1620
acacaattga atgagattca gaataaactt ataacatctt aaa                        1663

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<210> 130
<211> 412
<212> PRT
<213> Homo Sapiens

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<400> 130
Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp Leu Arg Pro Glu
 1              5              10              15
Ile His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe
      20              25              30
Leu Thr Ile Leu Pro Gln Glu Leu Gln Ala Trp Val Gln Glu His Cys
      35              40              45
Pro Glu Ser Ala Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu Arg
      50              55              60
Glu Leu Asp Glu Pro Gly His Gln Val Ser Thr Pro Pro Asn Glu Gln
      65              70              75              80
Lys Pro Val Trp Glu Lys Ile Ser Ser Ser Gly Thr Ala Lys Glu Ser
      85              90              95
Pro Ser Ser Met Gln Pro Gln Pro Leu Glu Thr Ser His Lys Tyr Glu
      100             105             110
Ser Trp Gly Pro Leu Tyr Ile Gln Glu Ser Gly Glu Glu Gln Glu Phe
      115             120             125
Ala Gln Asp Pro Arg Lys Val Arg Asp Cys Arg Leu Ser Thr Gln His
      130             135             140
Glu Glu Ser Ala Asp Glu Gln Lys Gly Ser Glu Ala Glu Gly Leu Lys
      145             150             155             160
Gly Asp Ile Ile Ser Val Ile Ile Ala Asn Lys Pro Glu Ala Ser Leu
      165             170             175
Glu Arg Gln Cys Val Asn Leu Glu Asn Glu Lys Gly Thr Lys Pro Pro
      180             185             190
Leu Gln Glu Ala Gly Ser Lys Lys Gly Arg Glu Ser Val Pro Thr Lys
      195             200             205
Pro Thr Pro Gly Glu Arg Arg Tyr Ile Cys Ala Glu Cys Gly Lys Ala
      210             215             220
Phe Ser Asn Ser Ser Asn Leu Thr Lys His Arg Arg Thr His Thr Gly
      225             230             235             240
Glu Lys Pro Tyr Val Cys Thr Lys Cys Gly Lys Ala Phe Ser His Ser

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	245		250		255
Ser Asn Leu Thr	Leu His Tyr Arg	Thr His Leu Val	Asp Arg Pro Tyr		
	260		265		270
Asp Cys Lys Cys	Gly Lys Ala Phe	Gly Gln Ser Ser	Asp Leu Leu Lys		
	275		280		285
His Gln Arg Met	His Thr Glu Glu	Ala Pro Tyr Gln	Cys Lys Asp Cys		
	290		295		300
Gly Lys Ala Phe	Ser Gly Lys Gly	Ser Leu Ile Arg	His Tyr Arg Ile		
305		310		315	320
His Thr Gly Glu	Lys Pro Tyr Gln	Cys Asn Glu Cys	Gly Lys Ser Phe		
	325		330		335
Ser Gln His Ala	Gly Leu Ser Ser	His Gln Arg Leu	His Thr Gly Glu		
	340		345		350
Lys Pro Tyr Lys	Cys Lys Glu Cys	Gly Lys Ala Phe	Asn His Ser Ser		
	355		360		365
Asn Phe Asn Lys	His His Arg Ile	His Thr Gly Glu	Lys Pro Tyr Trp		
	370		375		380
Cys His His Cys	Gly Lys Thr Phe	Cys Ser Lys Ser	Asn Leu Ser Lys		
385		390		395	400
His Gln Arg Val	His Thr Gly Glu	Gly Glu Ala Pro			
	405		410		

<210> 131
 <211> 724
 <212> DNA
 <213> Homo Sapiens

<400> 131
 ggagaatgaa aagcagaaag tggcagagct gtattctatc cataactctg gagacaaatc 60
 tgatattcag gacctcctgg agagtgtcag gctggacaaa gaaaaagcag agactttggc 120
 tagtagcttg caggaagatc tggctcatac ccgaaatgat gccaatcgat tacaggatgc 180
 cattgctaag gtagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga 240
 agatttgaat atgacgttag aaaaatttag atcagacctg gatgaaaaag aaacagaaag 300
 gagtgacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt 360
 gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga 420
 ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc 480
 tgcggaatgg cggcagtttc aggctgatct ccagactgca gtagtcattg caaatgacat 540
 taaatctgaa gcccaagagg agattggtga tctaaagcgc cgggtacatg aggctcaaga 600
 aaaaaatgag aaactcacia aagaattgga ggaaataagt ccgccaagcc agaagangac 660
 gangccggtg ttccantaca tgnatgcccg tgagagagaa tttggcaggc cttaaggcag 720
 ggaa 724

<210> 132
 <211> 218
 <212> PRT
 <213> Homo Sapiens

<400> 132
 Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser
 1 5 10 15
 Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp
 20 25 30
 Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala
 35 40 45
 His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val

50 55 60
 Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu
 65 70 75 80
 Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys
 85 90 95
 Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp
 100 105 110
 Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile
 115 120 125
 Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp
 130 135 140
 Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser
 145 150 155 160
 Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile
 165 170 175
 Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys
 180 185 190
 Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu
 195 200 205
 Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys
 210 215

<210> 133
 <211> 719
 <212> DNA
 <213> Homo Sapiens

<400> 133

gagaactaca gagctgggtg cggggccaac ggccagaaag tggcgaggag gcagtgcgc
 1 5 10 15
 ttggtggagg tttgcagaaa caaccagga gaccaaggcg gtgactgtcc atgttcacgg
 20 25 30
 ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaata
 35 40 45
 gctgcaggat cctgtgcaaa gctcgacccc cgagcagtc cctgaggaaa ccacacagag
 50 55 60
 cccagatctg ggggcaccgg cagagcagcg tccacaccag gaagaggagc tccagaccct
 65 70 75
 gcaggagagc gaggtccag tgcccagga cccagacctt cctgcagaga ggagctctgg
 80 85 90
 agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga
 95 100 105
 tgtggccgta tgcttttccc aggaccagtg gactgatctg gaccaaacac agaaagagtt
 110 115 120
 ctatggagaa tatgtcttgg aagaagactg tggaattgtt gtctctctgt catttccaat
 125 130 135
 cccagacct gatgatct cccaggtag agaggaagag cccttgggtc ccagatatcc
 140 145 150
 aagagcctna ggagactcaa gagccagaaa tcttgagttt tacctacaca ggagatagga
 155 160 165
 gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca
 170 175 180 185 190 195 200 205 210 215

<210> 134
 <211> 217
 <212> PRT
 <213> Homo Sapiens

<400> 134

Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly
 1 5 10 15
 Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys
 20 25 30
 Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr
 35 40 45
 Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro
 50 55 60

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser
 65 70 75 80
 Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu
 85 90 95
 Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp
 100 105 110
 Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu
 115 120 125
 Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys
 130 135 140
 Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe
 145 150 155 160
 Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu
 165 170 175

 Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu
 180 185 190
 Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg
 195 200 205
 Asn Pro Glu Phe Tyr Leu His Arg Arg
 210 215

<210> 135

<211> 1027

<212> DNA

<213> Homo Sapiens

<400> 135

gcgagggcgga gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60
 actacgacgc cggcaggtac agcccgcggc tgctcacggc gcacgagctg ccaactggacg 120
 cgacagtgt ggaaccggat gaggacctgc agcgctgca gctctcgcg cagcagctcc 180
 aggtcacggg agacgccagc gagagcgccg aggacatctt ctcccgcgcg gccaaaggagg 240
 gcatggggcca ggaagaggcg cagttcagcg tggagatgcc actcaccggc aaggcctacc 300
 tgtggggcca caagtaccgg ccacgcaagc cgcgcttctt caaccgcgtg cacacggggt 360
 tcgagtggaa caagtacaac cagacgcact acgactttga caaccaccg cccaagatcg 420
 tgcagggata caagttcaac atcttctacc cggacctcat cgacaagcgc tccacgcccg 480
 agtacttctt ggaggcctgc gccgacaaca aggatttcgc catcttgcgc ttcacgcggg 540
 gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtgggaata ctngcaccgc 600
 cacggcttcc gctgccagtt tgccaacggc attttccanc tgngctttca cttcaagcgc 660
 tnccgctatc ggcggtgacg gccttgggga acggcaggcc aggagggccg agggccacac 720
 ggggtgccaca gcccaggtcg gagtggccca gccggcaggc ttgtttttca gcatccgacg 780
 ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccaccca 840
 acctcaccag tcaccagccc cagaccacc acagcccctc ccagacaccc cgcctcatct 900
 ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaa atcttttgggt 960
 ctcattggaat tggcctattg gcaagatcgc atgttttttt aataaacgtt gtatttttaga 1020
 ataaaaa 1027

<210> 136

<211> 299

<212> PRT

<213> Homo Sapiens

<400> 136

Glu Gly Glu Gly Glu Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln
 1 5 10 15
 Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr

20	25	30
Ala His Glu Leu Pro Leu Asp	Ala His Val Leu Glu Pro	Asp Glu Asp
35	40	45
Leu Gln Arg Leu Gln Leu Ser	Arg Gln Gln Leu Gln Val	Thr Gly Asp
50	55	60
Ala Ser Glu Ser Ala Glu Asp	Ile Phe Phe Arg Arg Ala	Lys Glu Gly
65	70	75
Met Gly Gln Asp Glu Ala Gln	Phe Ser Val Glu Met Pro	Leu Thr Gly
85	90	95
Lys Ala Tyr Leu Trp Ala Asp	Lys Tyr Arg Pro Arg Lys	Pro Arg Phe
100	105	110
Phe Asn Arg Val His Thr Gly	Phe Glu Trp Asn Lys Tyr	Asn Gln Thr
115	120	125
His Tyr Asp Phe Asp Asn Pro	Pro Pro Lys Ile Val Gln	Gly Tyr Lys
130	135	140
Phe Asn Ile Phe Tyr Pro Asp	Leu Ile Asp Lys Arg Ser	Thr Pro Glu
145	150	155
Tyr Phe Leu Glu Ala Cys Ala	Asp Asn Lys Asp Phe Ala	Ile Leu Arg
165	170	175
Phe Thr Arg Gly Arg Leu Arg	Gly His Arg Phe Gln Asp	Arg Gln Pro
180	185	190
Arg Val Gly Ile Leu Ala Pro	Pro Arg Leu Pro Leu Pro	Val Cys Gln
195	200	205
Arg His Phe Pro Leu Ser Leu	Gln Ala Leu Pro Leu Ser	Ala Val Thr
210	215	220
Ala Leu Gly Asn Gly Arg Pro	Gly Gly Pro Arg Ala Thr	Arg Val Pro
225	230	235
Gln Pro Arg Ser Glu Trp Pro	Ser Arg Gln Ala Cys Phe	Ser Ala Ser
245	250	255
Asp Gly Asn Ile Ser Asn Arg	Ser Lys Thr Glu Ser Ala	Ser Arg Thr
260	265	270
Pro Arg Gly Pro Pro Asn Leu	Thr Ser His Gln Pro Gln	Thr Thr His
275	280	285
Ser Pro Ser Gln Thr Pro Arg	Leu Ile Trp Lys	
290	295	

<210> 137
 <211> 766
 <212> DNA
 <213> Homo Sapiens

<400> 137

caaagggttta	cacagtaa	aatgtgaatg	tgatcaccaa	aatacgcaca	gaacatctga	60
ccgaggagga	aaaaaagaga	tataaagaca	ggaacccgct	ggaatctttg	ctgggaactg	120
tggaacacca	atttggtgca	caaggggacc	tcaccacgga	atgtgctact	gcaaacaacc	180
ccacagccat	cacgcctgat	gagtacttca	atgaagagtt	tgatctgaaa	gacagggaca	240
ttggaaggcc	gaaagagctg	acgattagaa	cacagaagtt	taaagcaatg	ttgtggatgt	300
gtgaagagtt	tccctctctt	ctggtggagc	aggtcattcc	catcattgac	ctaattggctc	360
gaacgagtgc	tcattttgca	agactgagag	atttcatcaa	attggaattc	ccacctggat	420
ttcctgtcaa	aatagcttcc	cacatcacaa	actttgaggt	tgatcaatct	gtgtttgaaa	480
ttcccgaatc	ttactatggt	caagacaatg	gcagaaatgt	gcatttgcaa	gatgaagatt	540
acgagataat	gcagtttgcc	atccagcaaa	gtctgctgga	gtccagcagg	agccaggaac	600
tttcaggacc	agcttcgaat	ggagggatca	gccagacaaa	cacctatgac	gcccagtatg	660
agagggccat	ncaggagagc	cttctaccag	cacagaaagc	ctgtgcccc	agcgccccctg	720
agcgagacna	gccgttttga	taatggactt	gcagctaagc	catgga		766

<210> 138
 <211> 243
 <212> PRT
 <213> Homo Sapiens

<400> 138
 Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr
 1 5 10 15
 Glu His Leu Thr Glu Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro
 20 25 30
 Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly
 35 40 45
 Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr
 50 55 60
 Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile
 65 70 75 80
 Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met
 85 90 95
 Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile
 100 105 110
 Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu
 115 120 125
 Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile
 130 135 140
 Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile
 145 150 155 160
 Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln
 165 170 175
 Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu
 180 185 190
 Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly
 195 200 205
 Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu
 210 215 220
 Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg
 225 230 235 240
 Asp Pro Phe

<210> 139
 <211> 3060
 <212> DNA
 <213> Homo Sapiens

<400> 139
 ccgggcgagg gtgaggcgag agccggctgg ctgagcttag cgtccgagga ggcggcgggc 60
 gcggcgggcg cagcgggcggc ggcggggctg tggggcggtg cggaagcgag aggcgaggag 120
 cgcgcgggcc gtggccagag tctggcgggc gcctggcgga gcggagagca gcgcccgcg 180
 ctgcgcgtgc ggaggagccc cgcacacaat agcggcgcgc gcagcccgcg cccttcccc 240
 cggcgcgccc cgcgccgcgc gccgagcgcc ccgctccgcc tcacctgcca ccagggagtg 300
 ggcgggcatt gttgcgcgc gccgcgcgc cgcggggcca tgggggcgc ccggcgccc 360
 gggccgggccc tggcgaggcc gccgcgcgc cgctgagacg ggcgccgcgc gcagcccggc 420
 ggcgcaggta aggcgggcgc gccatggtg gaccgggtg gcttcgcgga ggcgtggaag 480
 gcgcagttcc cggactcaga gccccgcgc atggagctgc gctcagtggg cgacatcgag 540
 caggagctgg agcgcctgcaa ggcctccatt cggcgccctg agcaggaggt gaaccaggag 600

cgcttccgca tgatctacct gcagacgttg ctggccaagg aaaagaagag ctatgaccgg 660
cagcgatggg gcttccggcg cgcggcgcag gccccgcag cgcgctccga gccccgagcg 720
tcccgctcgc gccccgagcc agcggccgcc gacggagccg acccgccgcc cgccgaggag 780
cccaggcccc ggccccgacg cgagggttct cggggaagg ccaggccccg gaccgccccg 840
aggccccggg cagccgcgtc gggggaacgg gacgaccggg gacccccgc cagcgtggcg 900
gcgctcaggt ccaacttcga gcggatccgc aagggccatg gccagccccg ggcgagacc 960
gagaagccct tctacgtgaa cgtcagagtt caccacgagc gcggcctggt gaaggtcaac 1020
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ccccgcttcc tgaaggacaa cctgatcgac gccaatggcg gtagcaggcc cccttggccg 1260
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cgaggtcct actcccccg gagttttgag gattgcggag gcggctatac cccgactgc 1440
----- agtccaatg agaacctcac ctccagcgag gaggaettct cctetggcca gtccagccgc 1500
gtgtcccaa gccccaccac ctaccgcatg ttccgggaca aaagccgctc tccctcgag 1560
aactcgcaac agtccttcga cagcagcagt cccccacgc cgcagtgcc taagcggcac 1620
cggcactgcc cggttgtcgt gtccgaggcc accatcgtgg gcgtccgcaa gaccgggag 1680
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agccgggatg cgtcgtgctc gggagccctg gaggccacta aagcgagtga gctggacttg 1920
----- gaaaagggct tggagatgag aaaatgggtc ctgtcgggaa tcctggctag cgaggagact 1980
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gccttcgtgg acaactacgg agttgccatg gaaatggctg agaagtgtg tcaggccaat 2280
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acacccccgac ggcagtcocat gacggtgaag aaggagagc accggcagct gctgaaggac 2580
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tgcaaatggt acattccgct cacggatctc agcttcaga tgggtgatga actggaggca 2760
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cagatcaaga gtgacatcca gagagagaag agggcgaaca agggcagcaa ggctacggag 2880
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gccttcaggg tgcacagccg caacggcaag agttacacgt tcctgatctc ctctgactat 3000
gagcgtgcag agtggaggga gaacatccgg gagcagcaga agaagtgttt cagaagcttc 3060

<210> 140
<211> 872
<212> PRT
<213> Homo Sapiens

<400> 140
Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15
Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45
Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala

50	55	60
Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala		
65	70	75
Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg		80
	85	90
Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu		95
	100	105
Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro		110
	115	120
Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp		125
	130	135
Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg		140
145	150	155
Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe		160
	165	170
Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn		175
	180	185
Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met		190
	195	200
Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly		205
	210	215
Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys		220
225	230	235
Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu		240
	245	250
Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro		255
	260	265
Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met		270
	275	280
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu		285
	290	295
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser		300
305	310	315
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu		320
	325	330
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg		335
	340	345
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg		350
	355	360
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro		365
	370	375
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser		380
385	390	395
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn		400
	405	410
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr		415
	420	425
Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg		430
	435	440
His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro		445
	450	455
His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly		460
465	470	475
Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu		480
	485	490
		495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
 500 505 510
 Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
 515 520 525
 Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
 530 535 540
 Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe
 545 550 555 560
 Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
 565 570 575
 Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
 580 585 590
 Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
 595 600 605
 Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
 610 615 620
 Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
 625 630 635 640
 Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
 645 650 655
 Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
 660 665 670
 Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
 675 680 685
 Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly
 690 695 700
 Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
 705 710 715 720
 Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu
 725 730 735
 Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
 740 745 750
 Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
 755 760 765
 Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
 770 775 780
 Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
 785 790 795 800
 Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
 805 810 815
 Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met
 820 825 830
 Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
 835 840 845
 Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
 850 855 860
 Gln Lys Lys Cys Phe Arg Ser Phe
 865 870

<210> 141
 <211> 691
 <212> DNA
 <213> Homo Sapiens

<400> 141

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gttggagttc gatcttttcc cgacgtctac ttccctgagt cccttctacc ttccggccacc      180
ctccttctcg cgggcaccca gctgggtttga cactggactc tcagagatgc gcctggagaa      240
ggacaggttc tctgtcaacc tggatgtgaa gcacttctcc ccagaggaac tcaaagttaa      300
ggtgttgagg gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg      360
tttcatctcc agggagttcc acaggaaata ccggatccca gctgatgtag accctctcac      420
cattacttca tccctgtcat ctgatgggtt cctcactgtg aatggacca ggaacaggt      480
ctctggccct gagcgacca ttcccatcac ccgtgaagag aagcctgctg tcaccgcgc      540
ccccaagaaa tagatgcctt ttcttgaatt gcatttttta aaacaagaaa gtttccccac      600
cagtgaatga aagtcttctg actagtgtg aagcttatta atgctaaggg caggcccaaa      660
ttatcaagct aataaaatat cattcagcaa c                                     691

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<210> 142

<211> 175

<212> PRT

<213> Homo Sapiens

<400> 142

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Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
1          5          10          15
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
20          25          30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
35          40          45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
50          55          60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65          70          75          80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
85          90          95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
100         105         110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
115         120         125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
130         135         140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145         150         155         160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
165         170         175

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<210> 143

<211> 1300

<212> DNA

<213> Homo Sapiens

<400> 143

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tggtcaaaat gcagaggcta acattagaac acttgaatca gatgggttga atcgagtaca      180
tccttttgca tgctcaagag cccattcttt tcatcattcg gaagcaacag cggcagtcct      240
ctgcccaggt tatccacta gctgattact atatcattgc tggagtgatc tatcaggcac      300
cagacttggg atcagttata aactctagag tgcttactgc agtgcattgt attcagtcag      360
cttttgatga agctatgtca tactgtcgat atcatccttc caaagggtat tgggtggcact      420

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tcaaagatca	tgaagagcaa	gataaagtca	gaacctaaagc	caaaaggaaa	gaagaaccaa	480
gctctatttt	tcagagacaa	cgtgtgggatg	ctttactttt	agacctcaga	caaaaatttc	540
cacccaaaatt	tgtgcagcta	aagcctggag	aaaagcctgt	tcaagtggat	caaacaaaga	600
aagaggcaga	acctatacca	gaaactgtaa	aacctgagga	gaaggagacc	cccnagaat	660
gtacaaccag	accgggagtg	ctaaaggccc	ccctgaaaaa	cggatgagac	ttcagtgagt	720
actggacaaa	agagaagcct	ggaagactcc	tcattgctagt	tatcatacct	cagtactgtg	780
gctcttgagc	tttgaagtac	tttattgtaa	ccttcttatt	tgtatggaat	gcgcttattt	840
tttgaaagga	tattaggccg	gatgtggtgg	ctcacgcctg	taatcccagc	actttggggag	900
gccatggcgg	gtggatcact	tgaggtcaga	agttcaagac	cagcctgacc	aatatggtga	960
aaccccgctct	ctactaaaaa	tacaaaaatt	agccgggcgt	ggtggcgggc	gcccgtagtc	1020
ccagctactc	gggaggctga	gacaggagac	ttgcttgaac	ccgggaggtg	gaggttgccc	1080
tgagctgatt	atcatgctgt	tgcactccag	cttgggcgac	agagcgagac	tttgtctcaa	1140
aaaagaagaa	aagatattac	tcccatcatg	atttcttgtg	aatatttgtt	atatgtcttc	1200
tgtaaccttt	cctctcccgg	acttgagcaa	cctacacact	cacatgttta	ctggtagata	1260
tgtttaaaag	caaaataaag	gtatttgtat	atattgaaaa			1300

<210> 144
 <211> 233
 <212> PRT
 <213> Homo Sapiens

<400> 144

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1				5					10					15	
Ser	Gly	Ser	Val	Leu	Asp	Tyr	Phe	Ser	Glu	Arg	Ser	Asn	Pro	Phe	Tyr
			20					25					30		
Asp	Arg	Thr	Cys	Asn	Asn	Glu	Val	Val	Lys	Met	Gln	Arg	Leu	Thr	Leu
		35				40					45				
Glu	His	Leu	Asn	Gln	Met	Val	Gly	Ile	Glu	Tyr	Ile	Leu	Leu	His	Ala
	50					55					60				
Gln	Glu	Pro	Ile	Leu	Phe	Ile	Ile	Arg	Lys	Gln	Gln	Arg	Gln	Ser	Pro
65					70					75				80	
Ala	Gln	Val	Ile	Pro	Leu	Ala	Asp	Tyr	Tyr	Ile	Ile	Ala	Gly	Val	Ile
			85						90					95	
Tyr	Gln	Ala	Pro	Asp	Leu	Gly	Ser	Val	Ile	Asn	Ser	Arg	Val	Leu	Thr
			100					105					110		
Ala	Val	His	Gly	Ile	Gln	Ser	Ala	Phe	Asp	Glu	Ala	Met	Ser	Tyr	Cys
		115					120					125			
Arg	Tyr	His	Pro	Ser	Lys	Gly	Tyr	Trp	Trp	His	Phe	Lys	Asp	His	Glu
	130					135					140				
Glu	Gln	Asp	Lys	Val	Arg	Pro	Lys	Ala	Lys	Arg	Lys	Glu	Glu	Pro	Ser
145					150					155				160	
Ser	Ile	Phe	Gln	Arg	Gln	Arg	Val	Asp	Ala	Leu	Leu	Leu	Asp	Leu	Arg
			165						170					175	
Gln	Lys	Phe	Pro	Pro	Lys	Phe	Val	Gln	Leu	Lys	Pro	Gly	Glu	Lys	Pro
			180					185					190		
Val	Gln	Val	Asp	Gln	Thr	Lys	Lys	Glu	Ala	Glu	Pro	Ile	Pro	Glu	Thr
		195					200					205			
Val	Lys	Pro	Glu	Glu	Lys	Glu	Thr	Pro	Glu	Cys	Thr	Thr	Arg	Pro	Gly
	210					215					220				
Val	Leu	Lys	Ala	Pro	Leu	Lys	Asn	Gly							
225					230										

<210> 145
 <211> 1528

<212> DNA
<213> Homo Sapiens

<400> 145

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gcggccaaact ccaatggggc tttccagccc gtggtccttc tccatattcg agatgttccct    180
cctgctgacg aagagaagct ttttatccag aagttacgtc agtgttgctg cctctttgac    240
tttgtttctg atccactaag tgacctaaag tggaaggaag taaaacgagc tgctttaagt    300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttaccagaa    360
gtagtccata tgtttgcagt taacatgttt cgaacattac caccttcctc caatcctacg    420
ggagcggaat ttgaccgga ggaagatgaa ccaacgttag aagcagcctg gcctcatcta    480
cagcttgttt atgaattttt cttaagattt ttagagtctc cagatttcca acctaatata    540
gcgaagaaat atattgatca gaagtttgta ttgcagcttt tagagctctt tgacagtgaa    600
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gatectcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta    660
ggcttgagag cttacatcag aaaacagata aataatatat tttatagggt tatttatgaa    720
acagagcatc ataatggcat agcagagtta ctggaaatat tgggaagtat aattaatgga    780
tttgccttac cactaaaaga agagcacaag attttcttat tgaaggtgtt actaccttg    840
cacaaagtga aatctctgag tgtctacat cccagctgg catactgtgt agtgcagttt    900
ttagaaaagg acagcacct caggaacca gtggtgatgg cacttctcaa atactggcca    960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat tttagatgtc   1020
attgaaccat cagaatttgt gaagatcatg gaacccctct tccggcagtt ggccaaatgt   1080
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gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac   1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tcttctcttg   1200
taccgcaact caaagacca ttggaacaag acaatacatg gcttgatata caacgccctg   1260
aagctcttca tggagatgaa ccaaaagcta tttgatgact gtacacaaca gttcaaagca   1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa   1380
aatctagcca aagccaatcc ccaggtacta aaaaagagaa taacatgaaa aggccagggg   1440
tacttgaat gtttttataa gataggaata tatgtcttca ccatggggggg ggtctcgatt   1500
tcactaacgt tgtatatgaa aatgtctg                                     1528

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<210> 146
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 146

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Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
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Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
 20              25              30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
 35              40              45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
 50              55              60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
 65              70              75              80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
 85              90              95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
100              105              110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
115              120              125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Phe Leu Arg Phe
130              135              140

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Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp
 145 150 155 160
 Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro
 165 170 175
 Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys
 180 185 190
 Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe
 195 200 205
 Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu
 210 215 220
 Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys
 225 230 235 240
 Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys
 245 250 255
 Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val
 260 265 270
 Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala
 275 280 285
 Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe
 290 295 300
 Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe
 305 310 315 320
 Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser
 325 330 335
 Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn
 340 345 350
 Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro
 355 360 365
 Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys
 370 375 380
 Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met
 385 390 395 400
 Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys
 405 410 415
 Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys
 420 425 430
 Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile
 435 440 445
 Thr

<210> 147
 <211> 1580
 <212> DNA
 <213> Homo Sapiens

<400> 147
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 catgctccat cgcctgggaa atttggtgag cggcctccac ctaaaccgact tactagggaa 180
 gctatgcgaa attattttaa agagcgaggg gatcaaacag tacttattct tcatgcaaaa 240
 gttgcacaga agtcatatgg aaatgaaaaa aggttttttt gccacactcc ttgtgtatat 300
 cttatgggca gcggatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa 360
 caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420
 ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac 480

aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattggt 540
gtgttcctca gcaagcggat aaaagtcac tcacaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgcctcagga acaaagggtg ctctgtttta tgcactacga 660
tcccagacag ttagtaccag ataacttgc atgagaaggag gtaattttca tgccagttca 720
cagcagtggt gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa 780
ttcacagtcc gagatgtcta catccattat ggacaaacat gcaaacttgt gtgctcagtt 840
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gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttacacctta ggatacagaa 960
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agtgtagcag gagcaatcct tccagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
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<210> 148

<211> 500

<212> PRT

<213> Homo Sapiens

<400> 148

Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
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Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr
20 25 30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
35 40 45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
50 55 60
Arg Phe Phe Cys Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
65 70 75 80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
85 90 95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
100 105 110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
115 120 125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
130 135 140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
145 150 155 160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
165 170 175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
180 185 190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
195 200 205
Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu
210 215 220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

aatcggattg agaagaacat cctgagctca gccgactacg tggaacgtgg gcaggagcac 840
gtcaagacgg ccctggagaa ccagaagaag gtgaggaaga agaaagtctt gattgccatc 900
tgtgtgtcca tcaccgtcgt cctcctagca gtcattcatt gcgtcacagt ggttggataa 960
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aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt 1248

<210> 150
<211> 297
<212> PRT
<213> Homo Sapiens

<400> 150

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Glu	Glu	Asp	Lys	Glu	Arg	Val	Ala	Leu	Val	Val	His	Pro	Gly	Thr	Ala
			20					25					30		
Arg	Leu	Gly	Ser	Pro	Asp	Glu	Glu	Phe	Phe	His	Lys	Val	Arg	Thr	Ile
	35					40					45				
Arg	Gln	Thr	Ile	Val	Lys	Leu	Gly	Asn	Lys	Val	Gln	Glu	Leu	Glu	Lys
50						55					60				
Gln	Gln	Val	Thr	Ile	Leu	Ala	Thr	Pro	Leu	Pro	Glu	Glu	Ser	Met	Lys
65				70					75					80	
Gln	Glu	Leu	Gln	Asn	Leu	Arg	Asp	Glu	Ile	Lys	Gln	Leu	Gly	Arg	Glu
			85					90					95		
Ile	Arg	Leu	Gln	Leu	Lys	Ala	Ile	Glu	Pro	Gln	Lys	Glu	Glu	Ala	Asp
			100					105				110			
Glu	Asn	Tyr	Asn	Ser	Val	Asn	Thr	Arg	Met	Arg	Lys	Thr	Gln	His	Gly
	115					120					125				
Val	Leu	Ser	Gln	Gln	Phe	Val	Glu	Leu	Ile	Asn	Lys	Cys	Asn	Ser	Met
	130					135					140				
Gln	Ser	Glu	Tyr	Arg	Glu	Lys	Asn	Val	Glu	Arg	Ile	Arg	Arg	Gln	Leu
145				150					155					160	
Lys	Ile	Thr	Asn	Ala	Gly	Met	Val	Ser	Asp	Glu	Glu	Leu	Asp	Gln	Met
			165					170					175		
Leu	Asp	Ser	Gly	Gln	Ser	Glu	Val	Phe	Val	Ser	Asn	Ile	Leu	Lys	Asp
			180					185					190		
Thr	Gln	Val	Thr	Arg	Gln	Ala	Leu	Asn	Glu	Ile	Ser	Ala	Arg	His	Ser
	195					200						205			
Glu	Ile	Gln	Gln	Leu	Glu	Arg	Ser	Ile	Arg	Glu	Leu	His	Asp	Ile	Phe
210				215						220					
Thr	Phe	Leu	Ala	Thr	Glu	Val	Glu	Met	Gln	Gly	Glu	Met	Ile	Asn	Arg
225				230						235				240	
Ile	Glu	Lys	Asn	Ile	Leu	Ser	Ser	Ala	Asp	Tyr	Val	Glu	Arg	Gly	Gln
			245					250					255		
Glu	His	Val	Lys	Thr	Ala	Leu	Glu	Asn	Gln	Lys	Lys	Val	Arg	Lys	Lys
			260					265					270		
Lys	Val	Leu	Ile	Ala	Ile	Cys	Val	Ser	Ile	Thr	Val	Val	Leu	Leu	Ala
	275					280							285		
Val	Ile	Ile	Gly	Val	Thr	Val	Val	Gly							
290						295									

<210> 151

<211> 1953
 <212> DNA
 <213> Homo Sapiens

<400> 151

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ccaacctgcc	ggccatggag	accccgctcc	agcggcgcg	cacccgcagc	ggggcgagc	180
ccagctccac	tccgctgtcg	cccacccgca	tcacccggct	gcaggagaag	gaggacctgc	240
aggagctcaa	tgatcgcttg	gcggtctaca	tcgaccgtgt	gcgctcgctg	gaaacggaga	300
acgcagggct	gcgccttcgc	atcacccagt	ctgaagaggt	ggtcagccgc	gaggtgtccg	360
gcacgaagcc	cgccctacgag	gccgagctcg	gggatgccc	caagaccctt	gactcagtag	420
ccaaggagcg	cgcccgccctg	cagctggagc	tgagcaaagt	gcgtgaggag	tttaaggagc	480
tgaaagcgcg	caataccaag	aaggagggtg	acctgatagc	tgctcaggct	cggctgaagg	540
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gcacgctgga	gggcgagctg	catgatctgc	ggggccaggt	ggccaagctt	gaggcagccc	660
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<210> 152
 <211> 572
 <212> PRT
 <213> Homo Sapiens

<400> 152

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			20					25					30		
Glu	Asp	Leu	Gln	Glu	Leu	Asn	Asp	Arg	Leu	Ala	Val	Tyr	Ile	Asp	Arg
		35					40					45			
Val	Arg	Ser	Leu	Glu	Thr	Glu	Asn	Ala	Gly	Leu	Arg	Leu	Arg	Ile	Thr
		50				55					60				
Glu	Ser	Glu	Glu	Val	Val	Ser	Arg	Glu	Val	Ser	Gly	Ile	Lys	Ala	Ala
65					70					75					80

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
 85 90 95
 Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
 100 105 110
 Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
 115 120 125
 Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
 130 135 140
 Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
 145 150 155 160
 Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
 165 170 175
 Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
 180 185 190

Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
 195 200 205
 Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
 210 215 220
 Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
 225 230 235 240
 Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
 245 250 255

Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
 260 265 270
 Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
 275 280 285
 His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
 290 295 300
 Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
 305 310 315 320
 Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
 325 330 335
 Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
 340 345 350
 Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
 355 360 365
 Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
 370 375 380
 Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
 385 390 395 400
 Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
 405 410 415
 Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
 420 425 430
 His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
 435 440 445
 Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
 450 455 460
 Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
 465 470 475 480
 Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
 485 490 495
 Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
 500 505 510
 Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr

515 520 525
 Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
 530 535 540
 Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
 545 550 555 560
 Leu Leu His His His His Val Ser Gly Ser Arg Arg
 565 570

<210> 153
 <211> 1610
 <212> DNA
 <213> Homo Sapiens

<400> 153

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cgggcctttg	tgaaaatgtg	taagcaggat	ccgagcgttc	tgtacaccga	ggaaatgcgc	180
ttcctgaggg	agtgggtgga	gagcataggt	ggtaaagtac	cacctgctac	tcagaaagct	240
atatcagaag	aaaataccaa	ggaagaaaaa	cctgatagta	agaaggtgga	ggaagactta	300
aaggcagacg	aacctatcaag	tgaggaaagt	gatctagaaa	ttgataaaga	aggtgtgatt	360
gaaccagaca	ctgatgctcc	tcaagaaatg	ggagatgaaa	atgcggagat	aacggaggag	420
atgatggatc	aggcaaatga	taaaaaagtg	gctgctattg	aagccctaaa	tgatggtgaa	480
ctccagaaag	ccattgactt	attcacagat	gccatcaagc	tgaatcctcg	cttggccatt	540
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gactgtgaca	gagccattga	aataaatcct	gattcagctc	agccttacia	gtggcggggg	660
aaagcacaca	gacttctagg	ccactgggaa	gaagcagccc	atgatcttgc	ccttgccctgt	720
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aaaattgcag	aacatcggag	aaagtatgag	cgaaaacgtg	aagagcgaga	gatcaaagaa	840
agaatagaac	gagttaagaa	ggctcgagaa	gagcatgaga	gagcccagag	ggaggaagaa	900
gccagacgac	agtcaggagc	tcagtatggc	tcttttccag	gtggccttcc	tgggggaatg	960
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<210> 154
 <211> 369
 <212> PRT
 <213> Homo Sapiens

<400> 154

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 Lys Gln Asp Pro Ser Val Leu Tyr Thr Glu Glu Met Arg Phe Leu Arg
 20 25 30
 Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys
 35 40 45
 Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys

50	55	60
Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp		
65	70	75
Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro		80
	85	90
Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp		95
	100	105
Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly		110
	115	120
Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn		125
	130	135
Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys		140
145	150	155
Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu		160
	165	170
Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His		175
	180	185
Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala		190
	195	200
Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val		205
	210	215
Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg		220
225	230	235
Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys		240
	245	250
Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg		255
	260	265
Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly		270
	275	280
Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met		285
	290	295
Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro		300
305	310	315
Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln		320
	325	330
Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro		335
	340	345
Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln		350
	355	360
Ala		

<210> 155
 <211> 1323
 <212> DNA
 <213> Homo Sapiens

<400> 155

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cagaaaagat ggaaaaaagg acatgtgcac tctgccccaa agatgtcgaa tataatgtcc	180
tgtacttttg acaatcagag aatatagctg ctcatgagaa ttgtttgctg tattcttcag	240
gacttgtgga atgtgaggat caggatccac ttaatcctga tagaagtttt gatgtggaat	300
cagtaaagaa agaaatccag agaggaagga agttgaaatg caaattttgt cataaaagag	360
gagccaccgt gggatgtgat ttaaaaaact gtaacaagaa ttaccacttt ttctgtgcca	420


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agaaggacga cgcagttcca cagtctgatg gagttcgagg aatttataaa ctgctttgcc 480
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gtaatacatt cataagacaa gtgaaagaag agcatggcag acacacagat gcaactgtga 660
aagttccttt tcttaagaaa tgcaagggaa gcaggacttc ttaattactt acttgaagaa 720
atattagnca aagttcattc aattccagaa aaactcatgg atgagactta cttcagaatc 780
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<210> 156
 <211> 191
 <212> PRT
 <213> Homo Sapiens

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-----<400> 156-----
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Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
             20             25             30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
             35             40             45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
             50             55             60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
             65             70             75             80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
             85             90             95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
             100            105            110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
             115            120            125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
             130            135            140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
             145            150            155            160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
             165            170            175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
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<210> 157
 <211> 4065
 <212> DNA
 <213> Homo Sapiens

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-----<400> 157-----
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tatgcattcc	aagatgatcg	ttatctctac	atggtgatgg	aatacatgcc	tggtggagat	480
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gaagtagttc	ttgcatttga	tgcaatccat	tccatgggtt	ttattcacag	agatgtgaag	600
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gccagcaaag	agagtgtat	tgagcaattg	cgtgtataac	ttttggacct	ctcggattct	3300
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<210> 158

<211> 1354

<212> PRT

<213> Homo Sapiens

<400> 158

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Leu	Leu	Arg	Asp	Pro	Lys	Ser	Glu	Val	Asn	Ser	Asp	Cys	Leu	Leu	Asp
				20				25					30		
Gly	Leu	Asp	Ala	Leu	Val	Tyr	Asp	Leu	Asp	Phe	Pro	Ala	Leu	Arg	Lys
			35				40					45			
Asn	Lys	Asn	Ile	Asp	Asn	Phe	Leu	Ser	Arg	Tyr	Lys	Asp	Thr	Ile	Asn
	50					55					60				
Lys	Ile	Arg	Asp	Leu	Arg	Met	Lys	Ala	Glu	Asp	Tyr	Glu	Val	Val	Lys
65					70					75				80	
Val	Ile	Gly	Arg	Gly	Ala	Phe	Gly	Glu	Val	Gln	Leu	Val	Arg	His	Lys
			85					90						95	
Ser	Thr	Arg	Lys	Val	Tyr	Ala	Met	Lys	Leu	Leu	Ser	Lys	Phe	Glu	Met
			100					105						110	
Ile	Lys	Arg	Ser	Asp	Ser	Ala	Phe	Trp	Glu	Glu	Arg	Asp	Ile	Met	
			115					120				125			
Ala	Phe	Ala	Asn	Ser	Pro	Trp	Val	Val	Gln	Leu	Phe	Tyr	Ala	Phe	Gln
			130				135					140			
Asp	Asp	Arg	Tyr	Leu	Tyr	Met	Val	Met	Glu	Tyr	Met	Pro	Gly	Gly	Asp
145						150					155				160
Leu	Val	Asn	Leu	Met	Ser	Asn	Tyr	Asp	Val	Pro	Glu	Lys	Trp	Ala	Arg
				165					170					175	
Phe	Tyr	Thr	Ala	Glu	Val	Val	Leu	Ala	Leu	Asp	Ala	Ile	His	Ser	Met
			180						185					190	
Gly	Phe	Ile	His	Arg	Asp	Val	Lys	Pro	Asp	Asn	Met	Leu	Leu	Asp	Lys
			195				200					205			
Ser	Gly	His	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Thr	Cys	Met	Lys	Met	Asn
			210				215					220			
Lys	Glu	Gly	Met	Val	Arg	Cys	Asp	Thr	Ala	Val	Gly	Thr	Pro	Asp	Tyr
225						230					235				240
Ile	Ser	Pro	Glu	Val	Leu	Lys	Ser	Gln	Gly	Gly	Asp	Gly	Tyr	Tyr	Gly
				245						250				255	
Arg	Glu	Cys	Asp	Trp	Trp	Ser	Val	Gly	Val	Phe	Leu	Tyr	Glu	Met	Leu
			260						265					270	
Val	Gly	Asp	Thr	Pro	Phe	Tyr	Ala	Asp	Ser	Leu	Val	Gly	Thr	Tyr	Ser
			275					280						285	

Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp
 290 295 300
 Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg
 305 310 315 320
 Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu
 325 330 335
 Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val
 340 345 350
 Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe
 355 360 365
 Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Glu Thr Phe Pro Ile Pro
 370 375 380
 Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr
 385 390 395 400
 Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr
 405 410 415
 Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile
 420 425 430
 Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu
 435 440 445
 Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met
 450 455 460
 Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr
 465 470 475 480
 Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn
 485 490 495
 Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val
 500 505 510
 Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys
 515 520 525
 Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln
 530 535 540
 Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr
 545 550 555 560
 Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser
 565 570 575
 Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu
 580 585 590
 Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala
 595 600 605
 Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile
 610 615 620
 Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His
 625 630 635 640
 Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln
 645 650 655
 Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp
 660 665 670
 Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val
 675 680 685
 Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser
 690 695 700
 Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu
 705 710 715 720
 Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln

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Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val
 1170 1175 1180
 Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr
 1185 1190 1195 1200
 Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln
 1205 1210 1215
 Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile
 1220 1225 1230
 Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro
 1235 1240 1245
 Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys
 1250 1255 1260
 His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile
 1265 1270 1275 1280
~~Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu~~
~~1285 1290 1295~~
 Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu
 1300 1305 1310
 Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser
 1315 1320 1325
 Pro Arg Thr Leu Ser Thr Arg Ser Thr Ala Asn Gln Ser Phe Arg Lys
 1330 1335 1340
~~Val Val Lys Asn Thr Ser Gly Lys Thr Ser~~
~~1345 1350~~

<210> 159
 <211> 683
 <212> DNA
 <213> Homo Sapiens

<400> 159

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aggcaccggc	atccccctgt	gctggaaacc	cacctgggac	cccaaagggg	aagagagagc	180
tgatgagcaa	tggcccaggt	tccattattg	gtgctaaagc	tgggaagaat	tctggcaaaa	240
agaagggcct	taacaatgaa	ctgaacaacc	ttccagtaat	ctccaacatg	acggctgcgt	300
tagacagttg	ctcggcagca	gacggcagtt	tggctgctga	gatgcctaaa	ctggaagcag	360
aaggattaat	tgacaagaaa	aatttaggag	ataaagaaaa	gggcaaaaaa	gctaacaact	420
gcaaaacgga	caaaaacctc	tctaaactga	aaagtgcccg	gcccattgcc	cctgccccag	480
ccccactcc	cccgagcta	atcgctatac	ccactgcaac	ctttacaacg	accaccactg	540
ggacaatacc	cggactgcc	tccctcacia	caactgttgt	tcaggctaca	ccaaagagtc	600
ctccgttaaa	acccattcaa	ccaaagccca	caattatggg	agagcccatc	accgtgaacc	660
cagctctggt	gtcactcaaa	gac				683

<210> 160
 <211> 227
 <212> PRT
 <213> Homo Sapiens

<400> 160

Lys Leu Glu Phe Glu Pro Asp Ser Glu Asp Lys Ile Ser Asp Cys Glu
 1 5 10 15
 Glu Gly Leu Ser Asn Val Ala Leu Glu Cys Ser Glu Pro Ser Thr Ser
 20 25 30
 Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly Ala Gly

35	40	45
Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser Asn Gly		
50	55	60
Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly Lys Lys		
65	70	75
Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser Asn Met		
85	90	95
Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu Ala Ala		
100	105	110
Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys Asn Leu		
115	120	125
Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr Asp Lys		
130	135	140
Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala Pro Ala		
145	150	155
Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe Thr Thr		
165	170	175
Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr Thr Val		
180	185	190
Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln Pro Lys		
195	200	205
Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu Val Ser		
210	215	220
Leu Lys Asp		
225		

<210> 161
 <211> 662
 <212> DNA
 <213> Homo Sapiens

<400> 161

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agtactggcc tgcttgtaaa aatggggatg agtgtgccta ccatcacccc atctcaccct	180
gcaaagcctt ccccaattgt aaatttgctg aaaaatgttt gtttgttcac ccaaattgta	240
aatatgatgc aaagtgtact aaaccagatt gtcccttcac tcatgtgagt agaagaattc	300
cagtactgtc tccaaaacca gttgcaccac cagcaccacc ttccagtagt cagctctgcc	360
gttacttccc tgcttgtaag aagatggaat gtcccttcta tcatccaaaa cattgtaggt	420
ttaacactca atgtacaaga ccggaactgca cattctacca tcccaccatt aatgtcccac	480
cacgacatgc cttgaaatgg attcgacctc aaaccagcga atagcaccca gtcctgacctg	540
gcagaagatc atgcagtttg gaagttttca tgtctgatga aagatctcta cagaacttgt	600
caaatctttg aaacttggaat tatattgctt tcataatatg aaggtttatt ggctatctaa	660
aa	662

<210> 162
 <211> 173
 <212> PRT
 <213> Homo Sapiens

<400> 162

Pro Gln Gln Leu His Leu Leu Ser Arg Gln Leu Glu Asp Pro Asn Gly	
1	5
Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro	
20	25
	30

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly
 35 40 45
 Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro
 50 55 60
 Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys
 65 70 75 80
 Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser
 85 90 95
 Arg Arg Ile Pro Val Leu Ser Pro Lys Pro Val Ala Pro Pro Ala Pro
 100 105 110
 Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met
 115 120 125
 Glu Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys
 130 135 140
~~Thr Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro~~
 145 150 155 160
 Arg His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu
 165 170

<210> 163

<211> 2912

<212> DNA

<213> Homo Sapiens

<400> 163

cagttgcttc	agcgtcccg	tgtggctgtg	ccgttggtcc	tgtgcggtca	cttagccaag	60
atgcctgagg	aaaccagac	ccaagaccaa	ccgatggagg	aggaggaggt	tgagacgttc	120
gcctttcagg	cagaaattgc	ccagttgatg	tcattgatca	tcaatacttt	ctactcgaac	180
aaagagatct	ttctgagaga	gtcattttca	aattcatcag	atgcattgga	caaaatccgg	240
tatgaaactt	tgacagatcc	cagtaaatta	gactctggga	aagagctgca	tattaacctt	300
atacgaaca	aacaagatcg	aactctcact	attgtggata	ctggaattgg	aatgaccaag	360
gctgacttga	tcaataacct	tggtactatc	gccaaagtctg	ggaccaaagc	gttcattggaa	420
gctttgcagg	ctggtgcaga	tatctctatg	attggccagt	tcggtgttgg	tttttattct	480
gcttatttgg	ttgctgagaa	agtaactgtg	atcaccaaac	ataacgatga	tgagcagtac	540
gcttgggagt	cctcagcagg	gggatcattc	acagtggagg	cagacacagg	tgaacctatg	600
ggtcgtggaa	caaaagttat	cctacacctg	aaagaagacc	aaactgagta	cttggaggaa	660
cgaagaataa	aggagattgt	gaagaaacat	tctcagttta	ttggatatcc	cattactctt	720
tttgtggaga	aggaacgtga	taaagaagta	agcgatgatg	aggctgaaga	aaaggaagac	780
aaagaagaag	aaaaagaaaa	agaagagaaa	gagtcggaag	acaaacctga	aattgaagat	840
gttggttctg	atgaggaaga	agaaaagaag	gatggtgaca	agaagaagaa	gaagaagatt	900
aaggaaaaag	acatcgatca	agaagagctc	aacaaaacaa	agcccatctg	gaccagaaat	960
cccgcagata	ttactaatga	ggagtacgga	gaattctata	agagcttgac	caatgactgg	1020
gaagatcact	tggcagtga	gcatttttca	gttgaaggac	agttggaatt	cagagccctt	1080
ctatttgtcc	cacgacgtgc	tccttttcat	ctgtttgaaa	acagaaaaga	aaagaacaat	1140
atcaaattgt	atgtacgcag	agttttcatt	atggataact	gtgaggagct	aatccctgaa	1200
tatctgaact	tcattagagg	ggtggtagac	tcggaggatc	tcctctaaa	catatcccg	1260
gagatgttgc	aacaaagcaa	aattttgaaa	gttatcagga	agaatttgg	caaaaaatgc	1320
ttagaactct	ttactgaact	ggcggaagat	aaagagaact	acaagaaatt	ctatgagcag	1380
ttctctaaaa	acataaagct	tggaaatacac	gaagactctc	aaaatcgga	gaagctttca	1440
gagctgttaa	ggtactacac	atctgcctct	ggtgatgaga	tggtttctct	caaggactac	1500
tgcaccagaa	tgaaggagaa	ccagaaacat	atctattata	tcacagggtga	gaccaaggac	1560
caggtagcta	actcagcctt	tgtggaacgt	cttcggaaac	atggcttaga	agtgatctat	1620
atgattgagc	ccattgatga	gtactgtgtc	caacagctga	aggaatttga	ggggaagact	1680
ttagtgtcag	tcaccaaaga	aggcctggaa	cttcagagg	atgaagaaga	gaaaaagaag	1740
caggaagaga	aaaaaacaaa	gtttgagaac	ctctgcaaaa	tcatagaaga	catattggag	1800


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aaaaaagttg aaaaggtggt tgtgtcaaac cgattggtga catctccatg ctgtattgtc 1860
acaagcacat atggctggac agcaaacatg gagagaatca tgaaagctca agccctaaga 1920
gacaactcaa caatgggtta catggcagca aagaaacacc tggagataaa ccctgaccat 1980
tccattattg agaccttaag gcaaaaggca gaggtgata agaācgaāā gtctgtgaag 2040
gatctggtca tcttgcttta tgaaactgog ctctgtctt ctggcttcag tctggaagat 2100
ccccagacac atgctaacag gatctacagg atgatcaaac ttggtctggg tattgatgaa 2160
gatgacccta ctgctgatga taccagtgt gctgtaactg aagaaatgcc accccttgaa 2220
ggagatgacg acacatcacg catggaagaa gtagactaat ctctggctga gggatgactt 2280
acctgttcag tactctacaa ttctctgat aatatatttt caaggatgtt tttctttatt 2340
tttgtaata ttaaaaagtc tgtatggcat gacaactact ttaaggggaa gataagattt 2400
ctgtctacta agtgatgctg tgatacctta ggcactaaag cagagctagt aatgcttttt 2460
gagtttcag ttggttcttt cacagatggg gtaacgtgca ctgtaagacg tatgtaacat 2520
gatgttaact ttgtgtggtc taaagtgttt agctgtcaag ccggatgcct aagtagacca 2580
aatcttgta ttgaagtgtt ctgagctgta tcttgatgtt tagaaaagta ttcgttacat 2640
cttgtaggat ctactttttg aacttttcat tccctgtagt tgacaattct gcattgacta 2700
gtcctctaga aataggttaa actgaagcaa cttgatggaa ggatctctcc acagggcttg 2760
ttttccaaag aaaagtattg tttggaggag caaagttaaa agcctaccta agcatatcgt 2820
aaagctgttc aaatactcga gccagtcct gtggatggaa atgtagtgct cgagtcacat 2880
tctgcttaaa gttgtaacaa atacagatga gt 2912

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<210> 164

<211> 732

<212> PRT

<213> Homo Sapiens

<400> 164

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Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
1          5          10          15
Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
20          25          30
Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
35          40          45
Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu
50          55          60
Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
65          70          75          80
Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
85          90          95
Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
100         105         110
Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
115         120         125
Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val
130         135         140
Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
145         150         155         160
Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
165         170         175
Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
180         185         190
Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
195         200         205
Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
210         215         220
Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp

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225		230		235		240
Lys Glu Glu Glu	Lys Glu Lys Glu Glu	Lys Glu Ser Glu Asp Lys Pro				
	245	250		255		
Glu Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Lys Lys Asp Gly						
	260	265		270		
Asp Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln Glu						
	275	280		285		
Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp Ile						
	290	295		300		
Thr Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp Trp						
305	310	315		320		
Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu						
	325	330		335		
Phe Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu Phe						
	340	345		350		
Glu Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg Val						
	355	360		365		
Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn Phe						
370	375	380				
Ile Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg						
385	390	395		400		
Glu Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Leu						
	405	410		415		
Val Lys Lys Cys Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys Glu						
	420	425		430		
Asn Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu Gly						
	435	440		445		
Ile His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu Arg						
450	455	460				
Tyr Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp Tyr						
465	470	475		480		
Cys Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr Gly						
	485	490		495		
Glu Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu Arg						
	500	505		510		
Lys His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu Tyr						
	515	520		525		
Cys Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser Val						
530	535	540				
Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Lys Lys Lys						
545	550	555		560		
Gln Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met Lys						
	565	570		575		
Asp Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg Leu						
	580	585		590		
Val Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala						
	595	600		605		
Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr						
	610	615		620		
Met Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp His						
625	630	635		640		
Ser Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp						
	645	650		655		
Lys Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu Leu						
	660	665		670		

Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile
675 680 685
Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr
690 695 700
Ala Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu Glu
705 710 715 720
Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp
725 730

<210> 165
<211> 790
<212> DNA
<213> Homo Sapiens

<400> 165
ccgactcaga aatggcggcc tccatgttct acggcaggct agtggccgtg gccacccttc 60
ggaaccaccg gcctcggacg gcccagcggg ctgctgctca ggttctggga agttctggat 120
tgtttaataa ccatggactc caagtacagc agcaacagca aaggaatctc tcactacatg 180
aatacatgag tatggaatta ttgcaagaag ctggtgtctc cgttcccaaa ggatatgtgg 240
caaagtcacc agatgaagct tatgcaattg ccaaaaaatt aggttcaaaa gatgtcgtga 300
taaaggcaca ggttttagct ggtggtagag gaaaaggaac atttgaaagt ggcctcaaag 360
gaggagtga gtagtatttc tctccagaag aagcaaaagc tgtttcttca caaatgattg 420
ggaaaaaatt gtttaccaag caaacgggag aaaagggcag aatatgcaat caagtattgg 480
tctgtgagcg aaaatatccc aggagagaat actactttgc aataacaatg gaaagggtcat 540
ttcaagggtcc tgtattaata ggaagttcac atggtggtgt caacattgaa gatgttgctg 600
ctgagtctcc tgaagcaata attaaagaac ctattgatat tgaagaaggc atcaaaaagg 660
aacaagctct tcagcttgca cagaagaatg ggatttcccc taatattgng ggaatcagca 720
gcaggaaaac atggtcaagc tttacagnn ttttcttgaa atacgatgca acccttgata 780
ggaaattaaa 790

<210> 166
<211> 259
<212> PRT
<213> Homo Sapiens

<400> 166
Asp Ser Glu Met Ala Ala Ser Met Phe Tyr Gly Arg Leu Val Ala Val
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Ala Thr Leu Arg Asn His Arg Pro Arg Thr Ala Gln Arg Ala Ala Ala
20 25 30
Gln Val Leu Gly Ser Ser Gly Leu Phe Asn Asn His Gly Leu Gln Val
35 40 45
Gln Gln Gln Gln Gln Arg Asn Leu Ser Leu His Glu Tyr Met Ser Met
50 55 60
Glu Leu Leu Gln Glu Ala Gly Val Ser Val Pro Lys Gly Tyr Val Ala
65 70 75 80
Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys Leu Gly Ser Lys
85 90 95
Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly Arg Gly Lys Gly
100 105 110
Thr Phe Glu Ser Gly Leu Lys Gly Gly Val Lys Ile Val Phe Ser Pro
115 120 125
Glu Glu Ala Lys Ala Val Ser Ser Gln Met Ile Gly Lys Lys Leu Phe
130 135 140
Thr Lys Gln Thr Gly Glu Lys Gly Arg Ile Cys Asn Gln Val Leu Val

145		150		155		160
Cys Glu Arg Lys Tyr	Pro Arg Arg Glu Tyr Tyr	Phe Ala Ile Thr Met				
	165		170			175
Glu Arg Ser Phe Gln Gly	Pro Val Leu Ile Gly	Ser Ser His Gly Gly				
	180		185			190
Val Asn Ile Glu Asp Val	Ala Ala Glu Ser Pro	Glu Ala Ile Ile Lys				
	195		200			205
Glu Pro Ile Asp Ile Glu	Glu Gly Ile Lys Lys	Glu Gln Ala Leu Gln				
	210		215			220
Leu Ala Gln Lys Asn Gly	Ile Ser Pro Asn Ile	Gly Ile Ser Ser Arg				
	225		230			235
Lys Thr Trp Ser Ser Phe	Thr Phe Leu Lys Tyr	Asp Ala Thr Leu Asp				
	245		250			255
Arg Lys Leu						

<210> 167
 <211> 5307
 <212> DNA
 <213> Homo Sapiens

<400> 167

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<211> 1148

<212> PRT

<213> Homo Sapiens

<400> 168

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 Gly Arg Lys Pro Pro Leu Leu Lys Lys Lys Leu Arg Ser Ser Val Ala
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 Glu Ser Asp Thr Ser Pro Val Leu Glu Lys Glu His Gln Pro Asp Val
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 260 265 270
 Ser Leu Val Glu Ile Thr Glu His Lys Asp Phe Thr Leu Lys Thr Glu
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 Glu Leu Ile Glu Ser Pro Lys Leu Glu Ser Ser Glu Gly Glu Ile Ile
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Arg Lys Ser Gln Ser Pro	Ser Pro Lys Asn Glu Ser	Ala Arg Gly Arg		
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Thr Arg Asn Pro Glu Lys	Leu Lys Glu Ser His Trp	Glu Glu Asn Arg		
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<212> DNA

<213> Homo Sapiens

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<212> DNA

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 agagctcttc atctgctaca agaacatttg aatcttggga ccttttaaaga gccctccta 3120
 acccagcagt aactggaaca cacttgggag cagtcctatg tctcagtgcc ccttaaattt 3180
 ctgccctgag cctccacgt cagtgccatc ggtctagaac cactaaccoc gcattgctgt 3240
 tgatcgtcac gctcgcctct atagataacg gctctccaga cctgagcttt ccgcgtcagc 3300
 aagtaggaat cgtttttgct gcagagaata aaaggaccac gtgc 3344

<210> 171
 <211> 1004
 <212> PRT
 <213> Homo Sapiens

<400> 171
 Tyr Ser Cys Ala Ser Ala Gly Ile Gly Ala Ala Gly Pro Trp Arg Gly
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 Thr Leu Arg Glu Glu Leu Gly Thr Ala Thr Leu Gly Glu Phe Phe Gly
 20 25 30
 Val Thr Phe Lys Met Asp Ser Thr Leu Thr Ala Ser Glu Ile Arg Gln
 35 40 45
 Arg Phe Ile Asp Phe Phe Lys Arg Asn Glu His Thr Tyr Val His Ser
 50 55 60
 Ser Ala Thr Ile Pro Leu Asp Asp Pro Thr Leu Leu Phe Ala Asn Ala
 65 70 75 80
 Gly Met Asn Gln Phe Lys Pro Ile Phe Leu Asn Thr Ile Asp Pro Ser
 85 90 95
 His Pro Met Ala Lys Leu Ser Arg Ala Ala Asn Thr Gln Lys Cys Ile
 100 105 110
 Arg Ala Gly Gly Lys Gln Asn Asp Leu Asp Asp Val Gly Lys Asp Val
 115 120 125
 Tyr His His Thr Phe Phe Glu Met Leu Gly Ser Trp Ser Phe Gly Asp
 130 135 140
 Tyr Phe Lys Glu Leu Ala Cys Lys Met Ala Leu Glu Leu Leu Thr Gln
 145 150 155 160
 Glu Phe Gly Ile Pro Ile Glu Arg Leu Tyr Val Thr Tyr Phe Gly Gly
 165 170 175
 Asp Glu Ala Ala Gly Leu Glu Ala Asp Leu Glu Cys Lys Gln Ile Trp
 180 185 190
 Gln Asn Leu Gly Leu Asp Asp Thr Lys Ile Leu Pro Gly Asn Met Lys
 195 200 205
 Asp Asn Phe Trp Glu Met Gly Asp Thr Gly Pro Cys Gly Pro Cys Ser
 210 215 220
 Glu Ile His Tyr Asp Arg Ile Gly Gly Arg Asp Ala Ala His Leu Val
 225 230 235 240
 Asn Gln Asp Asp Pro Asn Val Leu Glu Ile Trp Asn Leu Val Phe Ile
 245 250 255
 Gln Tyr Asn Arg Glu Ala Asp Gly Ile Leu Lys Pro Leu Pro Lys Lys
 260 265 270

Ser Ile Asp Thr Gly Met Gly Leu Glu Arg Leu Val Ser Val Leu Gln
 275 280 285
 Asn Lys Met Ser Asn Tyr Asp Thr Asp Leu Phe Val Pro Tyr Phe Glu
 290 295 300
 Ala Ile Gln Lys Gly Thr Gly Ala Arg Pro Tyr Thr Gly Lys Val Gly
 305 310 315 320
 Ala Glu Asp Ala Asp Gly Ile Asp Met Ala Tyr Arg Val Leu Ala Asp
 325 330 335
 His Ala Arg Thr Ile Thr Val Ala Leu Ala Asp Gly Gly Arg Pro Asp
 340 345 350
 Asn Thr Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Val
 355 360 365
 Arg Tyr Ala His Glu Lys Leu Asn Ala Ser Arg Gly Phe Phe Ala Thr
 370 375 380
 Leu Val Asp Val Val Val Gln Ser Leu Gly Asp Ala Phe Pro Glu Leu
 385 390 395 400
 Lys Lys Asp Pro Asp Met Val Lys Asp Ile Ile Asn Glu Glu Glu Val
 405 410 415
 Gln Phe Leu Lys Thr Leu Ser Arg Gly Arg Arg Ile Leu Asp Arg Lys
 420 425 430
 Ile Gln Ser Leu Gly Asp Ser Lys Thr Ile Pro Gly Asp Thr Ala Trp
 435 440 445
 Leu Leu Tyr Asp Thr Tyr Gly Phe Pro Val Asp Leu Thr Gly Leu Ile
 450 455 460
 Ala Glu Glu Lys Gly Leu Val Val Asp Met Asp Gly Phe Glu Glu Glu
 465 470 475 480
 Arg Lys Leu Ala Gln Leu Lys Ser Gln Gly Lys Gly Ala Gly Gly Glu
 485 490 495
 Asp Leu Ile Met Leu Asp Ile Tyr Ala Ile Glu Glu Leu Arg Ala Arg
 500 505 510
 Gly Leu Glu Val Thr Asp Asp Ser Pro Lys Tyr Asn Tyr His Leu Asp
 515 520 525
 Ser Ser Gly Ser Tyr Val Phe Glu Asn Thr Val Ala Thr Val Met Ala
 530 535 540
 Leu Arg Arg Glu Lys Met Phe Val Glu Glu Val Ser Thr Gly Gln Glu
 545 550 555 560
 Cys Gly Val Val Leu Asp Lys Thr Cys Phe Tyr Ala Glu Gln Gly Gly
 565 570 575
 Gln Ile Tyr Asp Glu Gly Tyr Leu Val Lys Val Asp Asp Ser Ser Glu
 580 585 590
 Asp Lys Thr Glu Phe Thr Val Lys Asn Ala Gln Val Arg Gly Gly Tyr
 595 600 605
 Val Leu His Ile Gly Thr Ile Tyr Gly Asp Leu Lys Val Gly Asp Gln
 610 615 620
 Val Trp Leu Phe Ile Asp Glu Pro Arg Arg Arg Pro Ile Met Ser Asn
 625 630 635 640
 His Thr Ala Thr His Ile Leu Asn Phe Ala Leu Arg Ser Val Leu Gly
 645 650 655
 Glu Ala Asp Gln Lys Gly Ser Leu Val Ala Pro Asp Arg Leu Arg Phe
 660 665 670
 Asp Phe Thr Ala Lys Gly Ala Met Ser Thr Gln Gln Ile Lys Lys Ala
 675 680 685
 Glu Glu Ile Ala Asn Glu Met Ile Glu Ala Ala Lys Ala Val Tyr Thr
 690 695 700
 Gln Asp Cys Pro Leu Ala Ala Ala Lys Ala Ile Gln Gly Leu Arg Ala

705 710 715 720
 Val Phe Asp Glu Thr Tyr Pro Asp Pro Val Arg Val Val Ser Ile Gly
 725 730 735
 Val Pro Val Ser Glu Leu Leu Asp Asp Pro Ser Gly Pro Ala Gly Ser
 740 745 750
 Leu Thr Ser Val Glu Phe Cys Gly Gly Thr His Leu Arg Asn Ser Ser
 755 760 765
 His Ala Gly Ala Phe Val Ile Val Thr Glu Glu Ala Ile Ala Lys Gly
 770 775 780
 Ile Arg Arg Ile Val Ala Val Thr Gly Ala Glu Ala Gln Lys Ala Leu
 785 790 795 800
 Arg Lys Ala Glu Ser Leu Lys Lys Cys Leu Ser Val Met Glu Ala Lys
 805 810 815
 Val Lys Ala Gln Thr Ala Pro Asn Lys Asp Val Gln Arg Glu Ile Ala
 820 825 830
 Asp Leu Gly Glu Ala Leu Ala Thr Ala Val Ile Pro Gln Trp Gln Lys
 835 840 845
 Asp Glu Leu Arg Glu Thr Leu Lys Ser Leu Lys Lys Val Met Asp Asp
 850 855 860
 Leu Asp Arg Ala Ser Lys Ala Asp Val Gln Lys Arg Val Leu Glu Lys
 865 870 875 880
 Thr Lys Gln Phe Ile Asp Ser Asn Pro Asn Gln Pro Leu Val Ile Leu
 885 890 895
 Glu Met Glu Ser Gly Ala Ser Ala Lys Ala Leu Asn Glu Ala Leu Lys
 900 905 910
 Leu Phe Lys Met His Ser Pro Gln Thr Ser Ala Met Leu Phe Thr Val
 915 920 925
 Asp Asn Glu Ala Gly Lys Ile Thr Cys Leu Cys Gln Val Pro Gln Asn
 930 935 940
 Ala Ala Asn Arg Gly Leu Lys Ala Ser Glu Trp Val Gln Gln Val Ser
 945 950 955 960
 Gly Leu Met Asp Gly Lys Gly Gly Lys Asp Val Ser Ala Gln Ala
 965 970 975
 Thr Gly Lys Asn Val Gly Cys Leu Gln Glu Ala Leu Gln Leu Ala Thr
 980 985 990
 Ser Phe Ala Gln Leu Arg Leu Gly Asp Val Lys Asn
 995 1000

<210> 172

<211> 659

<212> DNA

<213> Homo Sapiens

<400> 172

gcctgagcaa	cgtctccgag	caggcgctgg	gctagaggcg	ggtctcaacc	agctactcat	60
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gaaccaaccg	agtcggatcc	tgaccctaaa	acctagtatt	ttccacttgt	tcatcaatat	180
ggaaaactca	gattccaatg	acaaaggaag	tggtgatcag	tctgcagcac	agcgcagaag	240
tcagatggac	cgattggatc	gagaagaagc	tttctatcaa	tttgtaaata	acctgagtga	300
agaagattat	aggcttatga	gagataacaa	tttgctaggc	accccagggtg	aaagtactga	360
ggaagagttg	ctgagacgac	tacagcaaat	taaagaaggc	ccaccaccgc	aaaactcaga	420
tgaaaataga	ggaggagact	cttcagatga	tgtgtctaat	ggtgactcta	taatagactg	480
gcttaactct	gtcagacaaa	ctggaaatac	aacaagaagt	gggcaaagag	gaaaccaatc	540
ttggagagca	gtgagtcgga	ctaataccaaa	cagtgggtga	tttcagattc	agtttagaga	600
taaatgttaa	cccgtataaa	tgggagccaa	aattcagaga	atgaaaatga	gccatctgc	659

<210> 173
 <211> 192
 <212> PRT
 <213> Homo Sapiens

<400> 173
 Pro Glu Gln Arg Leu Arg Ala Gly Ala Gly Leu Glu Ala Gly Leu Asn
 1 5 10 15
 Gln Leu Leu Ile Gly Gly Gly Leu Glu Ser Gly Gly Gln Gly Gly Ala
 20 25 30
 Glu Gln Pro Arg Arg Arg Arg Pro Asn Gln Pro Ser Arg Ile Leu Thr
 35 40 45
 Leu Lys Pro Ser Ile Phe His Leu Phe Ile Asn Met Glu Asn Ser Asp
 50 55 60
 Ser Asn Asp Lys Gly Ser Gly Asp Gln Ser Ala Ala Gln Arg Arg Ser
 65 70 75 80
 Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe Tyr Gln Phe Val Asn
 85 90 95
 Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg Asp Asn Asn Leu Leu
 100 105 110
 Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu Leu Arg Arg Leu Gln
 115 120 125
 Gln Ile Lys Glu Gly Pro Pro Pro Gln Asn Ser Asp Glu Asn Arg Gly
 130 135 140
 Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp Ser Ile Ile Asp Trp
 145 150 155 160
 Leu Asn Ser Val Arg Gln Thr Gly Asn Thr Thr Arg Ser Gly Gln Arg
 165 170 175
 Gly Asn Gln Ser Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Ser Gly
 180 185 190

<210> 174
 <211> 610
 <212> DNA
 <213> Homo Sapiens

<400> 174
 gtactggcat cagtcaatgt tctggagtga tttggggcccc gatgttggct atgaagctat 60
 tggctctgtg gacagtagtt tgcccacagt tgggtgtttt gcaaaagcaa ctgcacaaga 120
 caaccccaaa tctgccacag agcagtcagg aactgggtatc cgatcagaga gtgagacaga 180
 gtccgaggcc tcagaaatta ctattcctcc cagcaccocg gcagttccac aggctcccgt 240
 ccagggggag gactacggca aaggtgtcat cttctacctc agggacaaag tggtcgtggg 300
 gattgtgcta tggaacatct ttaaccgaat gccaatagca aggaagatca ttaaggacgg 360
 tgagcagcat gaagatctca atgaagtagc caaactattc aacattcatg aagactgaag 420
 ccccacagtg gaattggcaa acccactgca gcccttgaga ggaggtcgaa tgggtaaagg 480
 agcatttttt tattcagcag actttctctg tgtatgagtg tgaatgatca agtcctttgt 540
 gaatattttc aactatgtag gtaaattctt aatgttcnca tagtgaaata aattctgatt 600
 cttctaaaaa 610

<210> 175
 <211> 138
 <212> PRT
 <213> Homo Sapiens

<400> 175

Tyr Trp His Gln Ser Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly
 1 5 10 15
 Tyr Glu Ala Ile Gly Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val
 20 25 30
 Phe Ala Lys Ala Thr Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln
 35 40 45
 Ser Gly Thr Gly Ile Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser
 50 55 60
 Glu Ile Thr Ile Pro Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val
 65 70 75 80
 Gln Gly Glu Asp Tyr Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys
 85 90 95
 Val Val Val Gly Ile Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile
 100 105 110
 Ala Arg Lys Ile Ile Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu
 115 120 125
 Val Ala Lys Leu Phe Asn Ile His Glu Asp
 130 135

<210> 176
 <211> 805
 <212> DNA
 <213> Homo Sapiens

<400> 176
 gggacagcca agtctgtgac ttgcacgtac tcccctgccc tcaacaagat gttttgccaa 60
 ctggccaaga cctgccctgt gcagctgtgg gttgattcca ccccccgcc cggcaccgc 120
 gtccgcgcca tggccatcta caagcagtca cagcacatga cggaggttgt gaggcgctgc 180
 cccaccatg agcgtgtctc agatagcgat ggtctggccc ctctcagca tcttatccga 240
 gtggaaggaa atttgcgtgt ggagtatttg gatgacagaa acacttttcg acatagtgtg 300
 gtggtgccct atgagccgcc tgaggttggc tctgactgta ccaccatcca ctacaactac 360
 atgtgtaaca gttcctgcat gggcggcatg aaccggaggc ccctcctcac catcatcaca 420
 ctggaagact ccagtggtaa tctactggga cggaacagct ttgaggtgcg tgtttgtgcc 480
 tgtcctggga gagaccggcg cacagaggaa gagaatctcc gcaagaaagg ggagcctcac 540
 cacgaagctg cccccaggga gcactaagcg agcactgccc aacaacacca agctcctctc 600
 cccagccaaa gaagaaancca ctggatngag aatatttcac cccttcanat tcgttgggcg 660
 tgagcgcttc cganaatgtt ccgaagagct gnaagaaggc cttgggaact caaaggatgc 720
 ccaaggcttg ggaaaggagc caangggggg gaancaangg gctcaactnc aagccaacct 780
 gaaagttcca aaaaangggc ccagt 805

<210> 177
 <211> 626
 <212> DNA
 <213> Homo Sapiens

<400> 177
 ctaatttgct tgtttattcc cacaaggtag ccaggggtgg gggcgccgag ccaagcccag 60
 caggccatgg gaccttcctc cggcggggtg cagctggat tttcggtct gccccaccag 120
 caggtttgca ggcaggccgt catgagtgc ggtggaaggc tccgagggcg tgggcagggg 180
 ctccggcggg gccacacact tgtggagcta gaaatantgg ggcaggtcct tctctatcac 240
 caggggctcc tccatgggtc cgtagcgctt caccacgcag ccgttcttgt cgatgaggaa 300
 ctgtgganan acggtgtcca aactgtgggg ccaccctgc aaggggctga ggctgccctt 360
 cctgtccgct gcccatctgg gccacggctg tggccagggg aaactggctc cctaccccc 420
 acagccccct tacctttggt gaagttccac ttgatggcac tggaaaanaa gcacatggac 480
 gtgagcgctc ccaggcagcc cccacagtc cccaaagctt gtcctgtctc caaggaggcc 540

anaaagggttg tnagcttccc cgggtnectc cacangccac agtgccccc aanncccccc 600
aanagccatc tttaccccaa ggaggg 626

<210> 178
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 178

gcgcgaggct gctgctgctg cccccggccc gcgcgggttg aaacgggagag gccgagccaa 60
gcggcgggccc ctcttatgct gggaggatgc tggagagtag cggctgcaaa gcgctgaagg 120
agggcggtgct ggagaagcgc agcgacgggt tgttgagct ctggaagaaa aagtgttgca 180
tcctcaccga ggaagggctg ctgcttatcc cgcccaagca gctgcaacac cagcagcagc 240
agcaacagca gcagcagcag cagcaacaac agcccgggca ggggcccggc gagccgtccc 300
aaccagtggt ccccgctgtc gccagcctcg agccgcccgt caagctcaag gaactgcact 360
tctccaacat gaagaccgtg gactgtgttg agcgcaagg caagtacatg tacttcactg 420
tggtgatggc agagggcaag gagatcgact ttgggtgccc gcaagaccag ggctggaacg 480
ccgagatcac gctgcagatg gtgcagtaca agaatcgta ggccatcctg gcggtcaaatt 540
ccacgcgga gaagcagcag cactgtgtcc agcancagcc cccctcgag ccgcagccgc 600
agccgcagct ccaagcccca accccagcct tcagcctcaa gccngcaacc ccaagcccca 660
attcacaac ccaagccct caagcccca cccaaagccc tcangcccca ngcaagntcc 720
aaccggttat ncggccatcc aacattcaan atccaanact ctcaangcct taactnccn 780
accaanaac nct 793

<210> 179
<211> 786
<212> DNA
<213> Homo Sapiens

<400> 179

aatatcagag ttttaatttc aaccagctgg cacaacaatg aaagtgtcag actttctgaa 60
agtaactcgag aaataatgaa taaattctta atgttttccc ctccaccgcc cttttttatt 120
actccaagatt aggaattact acggattagg tttttgaaaa taaagtttcc tttttgaaa 180
atggtctaca ttcagaaatg tcttagaaca agcattttaa aaaaactaat aaataatcat 240
aaatcaaaat acattaaaat aaaattacag tacatcatcg ctctagaaa attcaccata 300
caagacgac ctttcaaagg ttcataaata aaagtcttct tgactcgaaa tcgtttcctg 360
catcgtgatg aaaagtatgc agaaaactaa gaagaatcgc aagttttcag taggggtgatg 420
tccaaactac ttgatctggt gcggggcgga gagactgtt tgcttttgat ccaagtgaag 480
acaatagaaa tgtgctcgtc ccacttcctc aagtcctcaa aacctgtct tgcggggag 540
ctgcccctt cangcagagt tgggaggtgc tgcgganaaa ccggtgccc tgccgctgcc 600
aatgcggctg tgggtgtggg tgcngtattt ggtgccgat gonggtgcc ggtnaagggt 660
tggggtgcc antnaaggat gaaaatgtgg atnttngnat nttgattccg gatacgggg 720
gggaacctng cngggggccn naaggcttgg ggttggggct naanggtgg ggttttttaa 780
ttgggg 786

<210> 180
<211> 791
<212> DNA
<213> Homo Sapiens

<400> 180

aggacctcag agaccaggc tctgtgattg tggccttcaa ggaaggggaa cagaaggaga 60
aggaggggat cctgcagctg cgtcgacca actcagccaa gccagtcca ctggcaccat 120
ccctcatggc ctcttctccg acttctatct gtgtgtgtgg gcaggtgcca gctgggggtg 180
gagttctgca gtgtgacctg tgtcaggact ggttccatgg gcagtgtgtg tcagtgcacc 240

atctcctcac	ctctccaaag	cccagttctca	cttcattctcc	actgctagcc	tgggtgggaat	300
gggacacaaa	attcctgtgt	ccactgtgta	tgcgctcacg	acggccacgc	ctagagacaa	360
tcttagcctt	gctggttgcc	ctgcagaggc	tgcccgtgcg	gctgcctgag	ggtgaggccc	420
ttcagtgtct	cacagagagg	gccattggct	ggcaagaccg	tgccagaaaag	gctctggcct	480
ctgaagatgt	gactgctctg	ttgcgacagc	tggctgagct	tcgccaacag	ctacaggcca	540
aacccanacc	agaggaggcc	tcagtctaca	cttcagccac	tgctgtgac	cctatcagag	600
aaggcagtgg	caacaatatt	tcnaangtcc	aagggtgctg	ggagaatgga	gacantgttg	660
accagtcttg	agaacatggc	tccaggaaaag	ggctctgacc	tggagctacn	gtcctcactg	720
ttgccgcaat	ttgactggnc	ctgttttttg	ganctgcctg	aaggcaatcc	cggggctccc	780
cctggaggga	g					791

<210> 181
 <211> 747
 <212> DNA
 <213> Homo Sapiens

<400> 181						
agtatccaaa	catactcatt	gttttatttt	taacaaaaga	aatgaaatta	aagatagacc	60
acaggtagag	tcatgaaatt	cttgtttttc	cctattcttt	ttggtaatta	caacgtacat	120
tgtcttcttt	tataataaga	cccaagggga	gaaaagaaaa	ggatgtacaa	tgaagggtaca	180
agtthtgaag	cacaaaaata	ttttatgaca	gggacaaaaa	aacaaaaaac	aaacaaaaat	240
tgaagtacag	aaagaggggtg	gtggggggcaa	aaataaagggt	acgcacttgg	gcttcctcaa	300
gatttgtttg	tcctatttca	gactagaatg	aaactggttt	aggaaatcac	tcctgtatgc	360
tagcaggaat	gttgctggca	agacacttct	gagcatcggg	gtgtggactt	tacgaaccaa	420
ccttttaaca	gtaactctag	gagagaggat	atcaaaaatt	ggcagtgaag	aattatagat	480
aggcaaaaag	ctccttctga	ggtccaggcc	aggagatagt	angatttaag	aaacaaacaa	540
acaataacaa	ccacaaatgg	acctttgggtg	ccactgtcac	aactgttgct	catcagagta	600
ggagaattgt	ancaaaggca	ttaaagaagg	gacaagcaag	ctgaagagcc	tgaatccttg	660
gggttgtaag	ccnatttttg	gnttcctttc	aagaaaagggt	ctgttggnctg	gtggaanggg	720
tcanggaaca	ntattttcacg	ggtcngc				747

<210> 182
 <211> 909
 <212> DNA
 <213> Homo Sapiens

<400> 182						
aaacagagag	ccaaatcatg	agtgaactcc	cattcacaaat	tgcttccaag	ataataaaaat	60
acctaggaat	ccaacttaca	aaggatgtga	aggacctctt	caaggagaac	tacaaaccac	120
tgctcaatga	aataaaaagag	gatacaaaca	aatggaagaa	cattccatgc	tcattgggtag	180
gaagaatcaa	tatcgtgaaa	atggccatac	tgcccaagggt	aatgtataga	ttcaatgcca	240
tcccatcaa	gctaccaatg	actttcttca	cagaatttga	aaaaactact	caaaagttca	300
tatggaacca	aaaaagagcc	cacattgcca	agtcaatcct	aagccaaaag	aacaaagctg	360
gaggcatcac	gctacctgac	ttcaaactat	actacaaggc	tacagtaacc	aaaacagcgt	420
ggtactggta	ccaaaacaga	gatataaatc	aatgcaacag	aacagagccc	tcagaaataa	480
tgccacatat	ctacaactat	ctgatctttg	acaaacctga	gaaaaacaag	caatggggaa	540
aggattccct	atttaataaa	tgggtgctggg	aaaactggct	agccatatgt	agaaagctga	600
aactggatct	cttctttata	ccttatacaa	aaattaattg	aagatggntt	aaaggactta	660
aacgttagac	ctaaaaccat	aaaaacctta	gaagaaaaac	ctaggcatta	ccattcangg	720
acataggctt	gggcaaggac	ttcctgtcta	aaacaccaan	agcaatggga	ncaaaagcca	780
aaattgcaaa	tggggattct	aattaactaa	agggcttttg	cacagcnaag	aagctccatc	840
agagngaaca	ggaacntcaa	antggggagaa	attttgaacc	taccatcnga	naaggctaata	900
nccagaatc						909

<210> 183

<211> 708
 <212> DNA
 <213> Homo Sapiens

<400> 183

attatcatta	tactttaagt	tttaggttac	atgtgcacaa	tgtgcagggt	agttacatat	60
gtatacatgt	gccatgctgg	tgtgctgcac	ccattaactc	gttatttagc	attaggtata	120
tctcctaata	ctatccctcc	cgcctcccc	caccccacaa	cagtccccag	agtgtgatgt	180
tcccccttct	gtgtccatgt	gttctcactg	ttcaattccc	acctatgagt	gagaatatgc	240
gggtgtttgg	ttttttgtcc	ttgccatagt	ttactgagaa	tgatgatttc	caatttcac	300
cctgtcccta	caaaggacat	gaactcatca	ttttttatgg	ctgcatagta	ttccatgggtg	360
tatatgtgcc	acattttctt	aatccagctc	atcattgttg	gccatttggg	ttggttccaa	420
gtctttgcta	ttgtgaatac	tgccgcaata	aacatacgtg	tgcatgtgtc	tttatagcag	480
catgatttat	antcctttgg	gtatatactc	agtaatggga	tggctgggtc	aaatggnatt	540
ccaantccan	atcccttang	aattgccaca	cggactccac	aanggttgaa	ctantttaca	600
gtcccancaa	cagngtnaaa	gggtccnaan	tcnccaaaat	cctctccaag	caccngttgt	660
tcccggactt	tttaanggat	tncaattcc	aaccggngnt	caaaaggg		708

<210> 184
 <211> 855
 <212> DNA
 <213> Homo Sapiens

<400> 184

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taatcaaatg	caaagcagct	gtgctatggg	aggtaaagaa	acccttttcc	attgaggatg	120
tggagggttg	acctcctaag	gcttatgaag	ttcgatttaa	gatgggtggc	gtaggaatct	180
gtcgcacaga	tgaccacgtg	gttagtgcca	acctggtgac	cccccttct	gtgattttag	240
gccatgaggc	agccggcatc	gtggagagt	ttggagaagg	ggtgactaca	gtcaaaccag	300
gtgataaagt	catcccgctc	tttactcctc	agtgtggaaa	atgcagagtt	tgtaaaaacc	360
cggagagcaa	ctactgcttg	aaaaatgatc	taggcaatcc	tcgggggacc	ctgcaggatg	420
gcaccaggag	gttcacctgc	agggggaagc	ccattcacca	cttccttggc	accagcacct	480
tctcccagta	cacggtgggtg	gatgagaatg	cagtggccaa	aattgatgca	gcctcgcccc	540
tggagaaagt	ctgcctcatt	ggctgtggat	tctcgactgg	gttatgggtc	tgcatgtaac	600
gttgccaagg	tcaccccagg	ctctacctgt	gctgtgtgtg	gcctgggaag	ggtcggccta	660
tctgctgtta	tgggctgtta	aagcaactgg	aggcanccag	aatcaattgc	ggtggacatc	720
aacaaggaca	aattttgcaa	agggcaaaag	agttgggtgc	caatgaatgc	catcaaccct	780
caagnctnca	ngnaaaccca	tccaggnaag	tgctaaaang	gaatttaccg	attggaggggt	840
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<210> 185
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 185

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ctggtaacac	agtgaatttc	cggaaactgc	tactgaaccg	ttgccagaag	gagtttgaaa	240
aagataaagc	agatgatgat	gtctttgaga	agaagcagaa	agaacttgag	gctgccagt	300
ctccagagga	gaggacaagg	cttcatgatg	aactggaaga	agccaaggac	aaagcccggc	360
ggagatccat	tggcaacatc	aagttttattg	gagaactctt	taaactcaaa	atgctgactg	420
aagccatcat	gcctgactgt	gtgggtgaagc	tgctaaagaa	ccatgatgaa	gaatccctgg	480
agtgcctgtg	tcgcctgctc	accaccattg	gcaaagactt	ggactttgaa	aaagcaaagc	540

cacgtatgga ccagtacttt aatcaagatg gagaaaattg tnaaagaaag aaaaacctca	600
tctagggatt cggttcatgc ttcaaagatg ttatanacct aaggctgttg caattgggggt	660
atctcgaaaag agcagatnaa gggcctnaan ctatcgaaca gattcacaaa ganggctaaa	720
attgaaanaa caagaatagc caaagggaag gnccaacaac tcatggacca anggagaaat	780
agaataccaa ggtgttccaa aaanttggcc aaangnnggt tggaaanaen gttcaaaggg	840
ggccangaaa aantccgggt actgg	865

<210> 186
 <211> 736
 <212> DNA
 <213> Homo Sapiens

<400> 186	
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agagtacttt tctcagggtg gcaacttngt ttttttaaac aattcttggg gttctgtgggt	120
ccacagcatt tccttctgtt tcaatgttat gtatgttttg attactattg tgatttttta	180
aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaaatc	240
tttcttacct tgttcacccc aaactttctc aaatctggac taaatgctat accttaaaac	300
aaacatgagg tgcattctga aggggaggga aatttatttc tctgcttttc tattatacaa	360
gttgtttaca gaaactgcaa attaaaaaat tacactggca tttgcagtcc ttaaaataaa	420
ttaaaagttc tcaacttttt tttttttttg ctaaaccatt ttttaagtat gagtccttgt	480
ttaaaagaaa aagattaaaa cagaaaatat tttctataaa taatacatgt attttggttt	540
tagtgctccc gccctaaggt ttgaagttaa cttttancca ngtaaccttt tccctccatga	600
tcaccttttt ttctcttttc cctctcccaa ntccgtgcac acgtgggggt ttccggcaan	660
aattggcctt gctgnactgt gattgggcca anaacgttga aaaacctttt taaaaaaaaa	720
tacttaaaat tggggt	736

<210> 187
 <211> 946
 <212> DNA
 <213> Homo Sapiens

<400> 187	
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tcgggttggg gcatgacgtg aacatccagt ttcttgataa ggacgatggg aaccagcccc	180
aggaccaaat taccatcaca gggtagcaaa agaacacaga agctgccagg gatgctatac	240
tgagaattgt ggggtgaact gagcagatgg tttctgagga cgtcccgtg gaccaccg	300
ttcacgccc catcattgggt gcccgcggca aagccattcg caaaatcatg gacgaattca	360
aggtggacat tcgcttccca cagagcggag cccagacccc caactgcgtc actgtgacgg	420
ggctcccaga gaatgtggag gaagccatcg accacatcct caatctggag gaggaatacg	480
tgagtctctg tgggccttgg agccctgagg cgccttgcca cgtccaccgg cctgaggccc	540
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ggtgagcaag cnggcgggat gctgggggtg ctggggcaaa ctgacctgt cttcctgtct	660
tcgcctgca gctagcctga cgttggtggac agtnaangcg cctgcangtt atacatgaaa	720
ccccagcac acgaanaagc caangnacc tttcaaaagg ctttnttggg gccgggacca	780
acctgggacc gccagcaacc aatnaaaaaa ggcnetgacn ttaaccaagc tcngagggaa	840
tttccancc tttgggggcc caaggtggct cccaaagaac cctccccntt nggggcccc	900
aaacnaatna ttgttcaaaa anggaacaaa aaccctctc aagccc	946

<210> 188
 <211> 802
 <212> DNA
 <213> Homo Sapiens

<400> 188

aaagtcaagg	ncgtttat	ccngaggnc	tgacacanga	agtggaa	naaccacggn	60
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ggagtcngt	atcntaac	gaatgccc	gacctgtg	taatgttaa	cantggagca	180
ngtcctganc	gggcacggc	angcctgg	gancggccg	acacacahc	angcgcnagg	240
ctccctgcg	gacctcng	aggggga	gcgtcaaca	tttacggng	gtccaaccgc	300
tgggtcaa	tgagacaa	cantgtgtg	ttgggttcg	gtcancang	tggananggt	360
tcngttctt	ttgatcant	ncntttggg	ccccaaagg	nggtcntgg	anccacctga	420
nccccaaag	tgggaaatt	ctcaaagct	cncatgtca	gagccttcn	antgctgtg	480
gcggtcca	gtgcgtccc	caccacaa	cctctgga	gngcctggc	ctcttctgt	540
gccgggggt	tcatgtnta	ctgcancgc	tactgtcca	ccaangtc	ctaactgc	600
gcnaagaca	ggaatnac	ggtcagtct	ccaacaacc	ccancatcc	ggcccgccct	660
ggctcaaacc	ctgcaacct	gcctgcctt	cgggaanc	aatttccac	ccttgtnccc	720
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gggntccca	angggccac	aa				802

<210> 189
 <211> 807
 <212> DNA
 <213> Homo Sapiens

<400> 189

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agcggcctt	gagctgtgg	gaggttccg	cagcagctac	agtgacgact	aagactccag	120
tgcatttcta	tcgtaacgg	gcgcggggg	gcgcagatcg	gcgccagca	atcacagaag	180
ccgacaagg	gttcaagcg	aaacatgacc	gctgagccca	tgagtgaag	caagttgaat	240
acattggtgc	agaagcttc	tgacttcctt	gcacactcat	cagaagaatc	tgaagaaaca	300
agttctctc	cacgacttg	aatgaatcaa	aacacagata	aaatcagtgg	ttctggaagt	360
aactctgata	tgatggaaaa	cagcaaggaa	gagggaaact	gctcttcaga	aaaatccaag	420
tcttcaggat	cgtcacgatc	aaagaggaaa	ccttcaattg	taacaaagta	tgtagaatca	480
gatgatgaaa	aacctttgga	tgatgaaact	gtaaatgaag	atgcgtctaa	tgaaaattca	540
gaaaatgata	ttactatgca	nagcttgcca	aaaggtacag	tgattgttca	gccagagcca	600
gtgctgaatg	aagacaaaga	tgatttttaa	ggggcctgaa	tttagaagca	gaagttaaaa	660
tgaaaactga	naatctcaaa	aaacgcggga	gaanatgggc	ttcatgggga	ttgtgangcc	720
tgactggcn	tggtggacaa	caaggtcaat	caatttcaaa	aaggttccat	ttatagacaa	780
cccttcaatg	caaggtcnta	tttgta				807

<210> 190
 <211> 608
 <212> DNA
 <213> Homo Sapiens

<400> 190

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agattggctt	taattttctt	taaaagcatc	ttcttgga	ttctattctc	aggatcattg	120
tcgtcatcat	catcatccac	tgtgacaggc	actgatttag	ataaggcttc	atctcctgaa	180
gattggcaaa	atccagtatg	tgaagacagc	actaaatfff	cagtcacagg	cttaattttc	240
tgttcatcgc	tgcctccctc	acctatagaa	ttctgatcat	catcttctat	atcagaagaa	300
gatgaggatg	taatgtcagc	ttgcttcctt	ttagtgcttg	ttcttaggga	gtttctcttt	360
ttctccttga	caatgactgc	cttcttttta	gatgaagttc	tttgcttctt	ctttttacta	420
tcttcangaa	ctttcctcag	catcagatga	tgatgangcc	actttgtatt	tccttagtat	480
ttctctttga	acttaaattt	cttctttccc	tcaattcgag	tcttttcagt	caccttatca	540
gaagagttac	aancatcttc	tttcatggga	agtatcaaga	tgatgaacaa	tcttgtcnct	600
tccttgaa						608

<210> 191
 <211> 786
 <212> DNA
 <213> Homo Sapiens

<400> 191
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 ggagggacgt ggacaacggc ctctcgctcg tcatcttcag tgactgggtac aacactttctg 120
 ttatgagaaa agtgaagttt tatgatgaaa acacaaggca gtggtggatg ccggataccg 180
 gaggagctaa catcccagct ctgaatgagc tgctgtctgt gtggaacatg gggttcagcg 240
 atggcctgta tgaaggggag ttcaccctgg ccaaccatga catgtattat gcgtcagggg 300
 gcagcatcgc gaagtttcca gaagatggcg tcgtgataac acagactttc aaggaccaag 360
 gattggagggt tttaaagcag gaaacagcag ttgttgaaaa cgtccccatt ttgggacttt 420
 atcagattcc agctgagggt ggaggccgga ttgtactgta tggggactcc aattgcttgg 480
 atgacagtca ccgacagaag gactgctttt ggcttctgga tgccctcctc cagtacacat 540
 cgtatgggggt gacaccgctt agcctcagtc actctgggaa ccgccagcgc cctcccantt 600
 ggagcaagct cagtcaactcc agagaggatg gaaggaaacc atctcatcgg tactccaagg 660
 ttctggangg ccatttgga aaacaaaaac ctcgggctcn acaaccctgt ccangcctgt 720
 nctgggcca gccaanagcc tttaaaccan aacggngccc aattaaccct ttggaaaaca 780
 tcagaa 786

<210> 192
 <211> 819
 <212> DNA
 <213> Homo Sapiens

<400> 192
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 aaattacaaa acatggtggc aggtgatact taaaaaata aagcgaagggt ctatgtttta 120
 cagattttgt catgtttcct taaaatctca gtctgtactg tcattaaaaa gatcatggaa 180
 tctatgttgt tctcatgat ggaatagtaa aaaaactgca ttcactgac aaaaaaata 240
 gctttgcttc caaatagcac aagtctttta agtgaacttt cccaacaata aatatagaaa 300
 atagccttta acaagcgtct tttagcttgg tcagggttgt atcatttggt tggaaagtac 360
 atccttcccc tgcagtcaga agacccaga cagcctttcc agttctcccg agtctttggg 420
 gcgcacagct gcggcgaggga agtctcactg gcggcagagc cactaagtc cctctgacgg 480
 gatccacagg aatcttctcg atgtaccagg agcctctgcc catcacagga gggcaggccc 540
 atgtagaaca agactctaac aaacctgcag ctggaaactg gattcctttt aaaccaaccc 600
 gccaacacag ctcggnctac ccaccancgc cgtccgtnaa aggggctctc tgggcctcac 660
 gggtcagcca ggttgccggg cacaccgaaa ggggtccttg ggcgggtgaa cctgctgcat 720
 gaantggcg gggngcttca acctgggct tctccgggt ttgggcctgg nctggggcct 780
 tgttgaantt gntccacaaa agaaaggcca ggagcaaca 819

<210> 193
 <211> 744
 <212> DNA
 <213> Homo Sapiens

<400> 193
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 tgtctgctgt acctactggc agtcagattg caaatattgg tcagcaagca aacataccta 120
 ctgcagtgca gcagccctct acccagggtc cacttctcag tattcagcag ggtgctcctc 180
 catcttcgca agtggttcca cctgctcaaa ctgggattat tcatcaggga gttcaaacta 240
 gtgctccaag ccttctctca caattgggta ttgcatccca aagttccttg ttaactgtgc 300
 ctccccagcc acaaggagta gaatcagtag ctcaaggaaat tgtttcacag cagttgctg 360
 cagttagttc tttgccctct gctagtagta tttctgttac aagtcagggt agttcaactg 420

gtccttcttg	aatgccttct	gccccaaaca	acttggttcc	accacaaaat	atagcaca	480
ccctgtctac	ccaaaatggt	aatttggttc	aaagtgttaa	gtcaacctcc	cttgatagca	540
actaatacaa	atttgccttt	ggcacaacag	ataccactaa	gttctaccca	agttctccgc	600
acaatcatta	gctcaggcaa	ttggaagcca	aattgaagat	gccaggcggt	gcagcggagc	660
cctccttaag	ttggcttacc	tcaagactaa	tcagttggtg	acaattgggg	ggaatgttca	720
gcaagtttca	agattgggaa	gtta				744

<210> 194
 <211> 567
 <212> DNA
 <213> Homo Sapiens

<400> 194						
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ttacaattgt	gtagagaaca	tgcaacagaa	catatgcata	taactactat	acaggtgata	120
tgcaaaaacc	cctactggga	aatccatttc	attagttaga	actgagcatt	tttcaaagta	180
ttcaaccagc	tcaattgaaa	gacttcagtg	aacaaggatt	tacttcagcg	tattcagcag	240
ctagattttca	ggattacaca	aagtgcagtaa	ctgtgccaaa	ttcttaaaat	ttcttttaggt	300
gtggtttttg	tcagttagca	gtttttatgt	agatcnatat	ntaaaagtcc	acacctcttc	360
agacangcca	atgaaacnac	taaatttcaa	tctgtacaan	ctaaatagta	attacagtcc	420
tctangtgnn	caangatact	tacaccacat	anacaaatnt	acnntacgca	naacaacctt	480
catggggaag	gatagcccta	gggtccccagc	tancctgtca	ccatttttgt	cactctcata	540
gttttgggtg	ccaatccatt	gggttttg				567

<210> 195
 <211> 771
 <212> DNA
 <213> Homo Sapiens

<400> 195						
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tagttgacaa	tgcatcacagc	tgtgatccaa	ggataaaaaa	gttcaaggaa	gaagaaaaag	120
ccaagaaaga	ancanaaaaag	aaagcaaaaag	cagaagctaa	acggaaggag	caagaagcta	180
aagaaaaaca	aagacaagct	gaattagaag	ctgctcggtt	agctaaggag	aaagaagagg	240
aggaagttag	acagcaagca	ttgctggcaa	agaaggaaaa	agatatccag	aaaaaagcca	300
ttaagaagga	aaggcaaaaa	tttcgaaact	catgcaagac	ctggaatcat	ttttctgata	360
atgaggcaga	gcgggttaaa	atgatggaag	aagtggaaaa	actttgtgat	cggcttgaac	420
tggcaagctt	acagtgcctg	aatgaaacac	tcacatcatg	cacaaaagaa	gtnggaaagg	480
ctgctttgga	aaaacagata	gaagaaataa	atgagcaaat	cagaaaagag	aaagaggaag	540
ctgaggctcg	tatgcgacaa	gcattctaaga	acacagagaa	atcaactggg	ggaagggtgga	600
aatggaagt	aaaaattggg	cacaaagatg	ntctacaatt	actaatttna	aagctgtgaa	660
tcctgttncc	tgctggaaca	aantcaagat	gggaagttat	tgccaantac	atgaacatac	720
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<210> 196
 <211> 561
 <212> DNA
 <213> Homo Sapiens

<400> 196						
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ctacttgc	atcagcacttg	ttcttgagca	gctttctttg	cttttaccat	ctcgacaagt	120
tccttgtatc	gtttcatgca	gtccttcttt	gtcctgccag	gcaccgcttc	tgctattttt	180
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gcgttgctctg cttgaggtac cactccatgt tcttttttga acttatcaaa tgccttttta 360
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 tctttggnan gttcttttga ctccaagagg aagaangtnt ngttcatgtn antangcaan 480
 aacgtcccat ctggaanttt tgttcnacca gggaacanac tcacaagctt taactaagta 540
 antgtngnat naccgncngn c 561

<210> 197
 <211> 691
 <212> DNA
 <213> Homo Sapiens

<400> 197
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 cacagtgtan tatgaataac agttttcacc- cagctcctat gatcatggag ataccagaat 180
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 gtgtttctct gtccaatata ggactggctc agctggctcc atctcatccc ttagctggga 420
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 aggagattgc aaggggcaaat gccagtgaag gggcacattt ccacccgctc caagtttggc 600
 ggcactgccc tctgcnctg ctcaccanna ngcagctggg atggggcctn tccccaatcg 660
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<210> 198
 <211> 646
 <212> DNA
 <213> Homo Sapiens

<400> 198
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 cctactgtgc tgggtgctcg tctgtccctc ttctcattag ccactcacag gagagggtgt 180
 tgtgactct gattcacagg ggatgaactc aggatctcaa aagacataca aaaactanag 240
 gtatgtatca cttaagtagc tacgaaactc acaccgtgat ctcccttctg acacacatct 300
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 gggactgcta tttgagtttt atcagtcaaa ggctcaagca tcaanaccct cagttancat 480
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 tctcnattc ctccaaaagg gctgggattt ggatttggca aagtca 646

<210> 199
 <211> 811
 <212> DNA
 <213> Homo Sapiens

<400> 199
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 gatgaaatta tttctaagac aaagcaagta attcaggggc tgggaagcttt gaagaatgag 180
 cacaattcca ttttacaag tttgctggag acactgaagt gtttgaagaa agatgatgaa 240
 agtaatttgg tggaggagaa atcaaactg atccggaagt cactggagat gttggagctc 300
 ggcctgagtg aggcacaggt tatgatggct ttgtcaaact acctgaatgc tgtggagtcc 360

gagaagcaga aactgcgtgc gcaggttcgt cgtctgtgcc aggagaatca gtggctacgg 420
 gatgaactgg ccaacacgca gcagaaactg cagaagagt agcagtctgt ggctcaactg 480
 gaggaggaga agaagcatct ggagtttatg aatcagctaa aaaaatatga tgacgacatt 540
 tccccatccg aggacaaaga cactgattct accaaagagc ctctggatga ccttttcccc 600
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 gccagcaag gcnctacna agattccgc gcggctgcgg acgctccaca acctgggtga 720
 ttcagttcgc ctcnncangg ggccgctacc aaggtaacct gttgccccct cctggcaaag 780
 caaggncctt gggaagggan cctgggagga a 811

<210> 200
 <211> 763
 <212> DNA
 <213> Homo Sapiens

<400> 200
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 agttcacaga gaggtgcagc tctgacaaga tcctagaggc tgctagacac agcgggcagc 180
 actggagaga gaagggaagc tgcgggaggc gccaccgctc atgcaggaga cagtgtgaga 240
 gtcacgggag gctaggccat gggacgctga gcaagtcagt taaccagccc gagcttcatt 300
 ttcctcattt cctccccctc gtcaggggcca ctctcgtact tgaccacgct cacgttgagg 360
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 tgtttgtgaa cattgtcaag accctgttta cgagacctca tagcagcttc ttctaactgt 480
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 gtaacagttg gncatcaac tttgcanget ttgtaccaac cgcatactc tccaaaaaga 600
 tgtcccatcc ttttgctttc ctttgcattc ttctctttcc tcaacaatgc atccaaatgg 660
 gtttaatttc aacatctaca gaaccaaact ccttttcattg tgcacaagtg agaatcnctt 720
 tgtacantgt ttccgccttc cttgaacntt cctgttttca aaa 763

<210> 201
 <211> 717
 <212> DNA
 <213> Homo Sapiens

<400> 201
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 agaatganca caattccatt ttacaaagtt tgctggagac actgaagtgt ttgaagaaag 180
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 gacgacattt ccccatccga gggacaaaga cactgattct accaaagagc ctccggatga 540
 ccttttcccc aatgatgaag acgacccag ggcaaggga tccancagca gcacagcaan 600
 ttgcagccgc ggctgcccga gcaaggcggc tacgagattc ccgccgaggc tgccggacgc 660
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 <211> 647
 <212> DNA
 <213> Homo Sapiens

<400> 202
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tactggggca	tatcctaggg	agaccgggag	tccgagcggg	gccccaggg	ctctaagtac	180
cacggagcac	gtgcggcaca	tgccttgctg	taaggcttag	ttacgtcaac	aggtcaccgt	240
catgccattg	caacaacacc	ttgtgtgaca	cttaactacc	tgttaccaa	gtgaacagct	300
aatcgctctt	aattttttaa	ctcgtgtatt	acacagtaaa	tggattttan	taatacagtt	360
tatattacta	agtacatatc	tggcaaagct	acatgtatac	agaaatcagg	aaccccccca	420
aaaaggacag	cagcaccgaa	aggaatggcc	agttcacaga	nangtgcagc	tctgacaaga	480
tcctagangc	tgctagacac	agcgggcagc	actggganaa	gagaagggaa	gctgcgggag	540
gcgccaaccc	gtcatgccag	gggacagtgt	ganagtcacg	ggncgggcta	ngccaatggg	600
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<210> 203

<211> 786

<212> DNA

<213> Homo Sapiens

<400> 203

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tggaggagga	gcagcaggcc	ctccagaaga	agctgaaggg	gacagaggat	gaggtggaaa	180
agtattctga	atccgtgaag	gaggcccagg	agaaactgga	gcaggccgag	aagaaggcca	240
ctgatgctga	ggcagatgtg	gcctccctga	accgcgcgat	tcagctgggt	gaggaggagc	300
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ccatggacca	ngccctcaag	tcctgatgg	cctcanagga	ggagtattcc	accaaagaag	660
attaatatga	agaggagatn	aaactgttgg	anggagaagc	tgaanggagg	ctganacccc	720
aagcaaaaagt	ttgccnaaaa	ggtctgtggg	caaaaatttg	gngaaaaaac	catcnaatga	780
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<210> 204

<211> 738

<212> DNA

<213> Homo Sapiens

<400> 204

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cgttctcttc	cttggcactg	gccaaggctc	cttctaggtc	atcgatggtt	ttctccaact	180
ttgccacaga	cctctcgga	aactctgctc	gggtctcagc	ctccttcagc	ttctctcca	240
acagtttgat	ctcctcttca	tatttatctt	ctttggtgga	atactctctc	tctgaggcca	300
tcagggaact	gagggcctgg	tccatggttc	gaagttcttc	ctccagctgt	ctggctcggc	360
tctcgccac	ctcagccctc	tcctccgagc	gtctcagctc	tccttcagg	atcaccagct	420
tcctggccac	ctcttcatat	ttgcggtctg	aatctcagc	gatgtgcttg	gcctcttca	480
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tanccaangc	gctcctgggc	ccggtcaanc	tcctctctca	caagctgaat	gcggcggttc	660
aaggaaggca	anatctgcct	caacaacaat	tggccttctt	cncggccngc	tccaattttc	720
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<210> 205

<211> 818

<212> DNA

<213> Homo Sapiens

<400> 205

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gttctcctcc	ttggcactgg	ccaaggtctc	ttctaggtca	tcgatggttt	tctccaactt	180
tgccacagac	ctctcggcaa	actctgctcg	ggtctcagcc	tccttcagct	tctcctccaa	240
cagtttgatc	tcctcttcat	atztatcttc	tttgggtgaa	tactcctcct	ctgaggccat	300
cagggacttg	agggcctggt	ccatgggtcg	aagttectcc	tcagctgtc	tggctcggct	360
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cctggccacc	tcttcatatt	tgcggtctga	atcctcagcg	atgtgcttgg	cctccttcag	480
ctgcatctcc	tgcagttcca	tcttctcctc	atccttcaag	gcccggtttt	cgatganctt	540
tcattcctct	ctcggtctct	atcagccgcc	ttctcgggct	cntccaagct	tctgcaaggc	600
tgtanncann	ggctcctggg	gcccgggtnc	aagntcctcc	tcaaacangc	tnaaatncca	660
gagggtttca	nggaagggcc	aaaatctggc	ctnnagnatc	aattggcttt	cttnccgggg	720
nctngcncca	atcttctccn	ggggcctncc	tttcangggg	tnaagaanaa	atctcaaatt	780
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<210> 206

<211> 927

<212> DNA

<213> Homo Sapiens

<400> 206

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tcgaccgcgc	cgagcaggcc	gaagccgaca	agaagcaagc	tgaggaccgc	tgcaagcagc	120
tggaggagga	gcagcaggcc	ctccagaaga	agctgaaggg	gacagaggat	gaggtggaaa	180
agtattctga	atccgtgaag	gaggcccagg	agaaactgga	gcaggccgag	aagaaggcca	240
ctgatgctga	ggcagatgtg	gcctcctga	accgcgcgat	tcagctgggt	gaggaggagc	300
tggaccgggc	ccaggagcgc	ctggctacag	cctgcagaa	gctggaggag	gccgagaagg	360
cggctgatga	gagcgagaga	ggaatgaagg	tcacgaaaa	ccgggccatg	aaggatgagg	420
agaagatgga	actgcaggag	atgcagctga	aggaggccaa	gcacatcgct	gaggattcag	480
accgcaaata	tgaagaggtg	gccaggaagc	tgggtgatcct	ggaaggagag	ctggagcgct	540
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tggaactcaa	caacctgtga	gggccagccc	cacccccagc	caggctatgg	ttgccacccc	900
aaccaataa	aactgatgtt	actagcc				927

<210> 207

<211> 910

<212> DNA

<213> Homo Sapiens

<400> 207

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cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
tggttacagc	ctataacat	ctttttgaaa	ctaagcgttt	taagggtact	gaaagtataa	240
gtaaagtgtc	tgagcaagta	aaaaatgtga	agcttaatga	agataaacc	aaagaaacca	300
agtctgaaga	gaccctggat	gagggccac	caaaatatac	taaatctgtt	ctgaaaaagg	360
gagataaaac	caactttccc	aaaaaggagg	atgttggttc	ctgctgggat	acaggaacac	420
tacaagatgg	gactgttttt	gataactaata	ttcaaacaag	tgcaaagaag	aagaaaaatg	480

ccaagccttt	aagttttaag	gtcggagtag	gcaaagttat	cagaggatgg	gatgaagctc	540
tcttgactat	gagtaaagga	gaaaangctc	gactggagat	tgaaccagaa	tgggcttacg	600
gaaagaaagg	acagcctgat	gccaaaattc	caccaaatgc	aaaactcact	tttgaagtgg	660
nantatggga	tattgattga	aatagcagtg	cntcagctcn	aggntattag	caacaatgat	720
taaaacntgg	ncttgaaaga	aaatttcaca	actagttnag	aaacttggtta	ccaaatggta	780
aaggaaaaag	tcaactggga	aaaattcaag	ggngttaana	aaaanttggt	ttacctgggg	840
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tccnaaaacc						910

<210> 208
 <211> 745
 <212> DNA
 <213> Homo Sapiens

<400> 208

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ttctccttga	ccagtatttt	acacagctgt	aggaaagtat	tttagaccag	ggattcataa	120
gggattttatc	tctcaaaagc	tgggaccaag	taaacaaatt	ttattaactc	cttgaatttt	180
ccagttgact	cttcctttac	aatagtaaca	agttctaact	agttgtgtaa	atttcttcaa	240
ggccaagttt	tatcattggt	gctaatatcc	ttagagctga	agcactgcta	tttcaatcaa	300
tatccactaa	ttccacttca	aaagtgagtt	ttgcatttgg	tgggaattttg	gcatcaggct	360
gtccttttctt	tccgtaagcc	cattctgggt	caatctccag	tcgagccttt	tctcctttac	420
tcatagtcaa	gagagcttca	tcccatectc	tgataacttt	gcttactccg	accttaaaac	480
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gttggttttaa	cccccttttt	cagaacagat	ttaagtanat	tttgggggac	cctcanccaa	660
ggggtcnctt	canaactggg	tttcttgggg	gtttaacctt	cattnagcct	canaattttt	720
tacntggccn	cagacacttt	tactt				745

<210> 209
 <211> 965
 <212> DNA
 <213> Homo Sapiens

<400> 209

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agctgcccaa	gaaggacatt	atcaagtttc	tgcaggaaca	cggttcagat	tcgtttcttg	120
cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
tggttacagc	ctataaccat	ctttttgaaa	ctaagcgttt	taagggtact	gaaagtataa	240
gtaaagtgtc	tgagcaagta	aaaaatgtga	agcttaatga	agataaaacc	aaagaaaacca	300
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tacaagatgg	gactgttttt	gatactaata	ttcaaacaag	tgcaaagaag	aagaaaaatg	480
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tcttgactat	gagtaaagga	gaaaaggctc	gactggagat	tgaaccaaga	atgggcttac	600
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gaatttagtg	atattgattg	aaatagcagt	gcttcagcct	ccaagggata	ttagcaacaa	720
tgaataaaaac	tttggncttg	angaaaattt	acacaacctt	gtttagaacc	ttgttactat	780
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ggncccagcc	ttttgagaga	taaatccctt	angaaancct	ggtccnaaaa	tactttccta	900
aagnctgtgt	taaataccng	ggncaagggn	gaaacttttt	ccctttaccn	caagggtggt	960
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<210> 210
 <211> 867

<212> DNA

<213> Homo Sapiens

<400> 210

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taagggattt	atctctcaaa	agctgggacc	aagtaaacia	atatttattaa	ctccttgaat		180
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caatatccac	taattccact	tcaaaaagtga	gttttgcaat	tgggtggaatt	ttggcatcag		360
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aacttaaagg	cttggcattt	ttcttcttct	ttgcacttgt	ttgaatatta	gtatcaaaaa		540
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aagtttgggt	tttaactccct	tttttcagaa	caagatttag	taaaattttg	gnnggaccct		660
caatccaagg	gtctcttcaa	nacttgggtt	cctttggggg	ttaancctca	attaagcctc		720
acaatttttt	acttggctca	agaaancntt	tacttaaacc	tttcagggtac	ccttttaaaaa		780
nccttangtt	ttaaaaaaa	tgggttataa	gggctggtaa	ccnaagggtg	ggcccttggt		840
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<210> 211

<211> 972

<212> DNA

<213> Homo Sapiens

<400> 211

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cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
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gtaaagtgtc	tgagcaagta	aaaaatgtga	agcttaatga	agataaaccc	aaagaaacca	300
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gagataaaa	caactttccc	aaaaaggagg	atgtttgttc	ctgctgggtat	acaggaacac	420
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<210> 212

<211> 817

<212> DNA

<213> Homo Sapiens

<400> 212

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tctcgcaaag	agcgggaagc	tgagcttggg	gccaaagcca	aggaattcac	caatgtttat	180
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<210> 213
 <211> 756
 <212> DNA
 <213> Homo Sapiens

<400> 213						
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ggcactttat	gatacttttt	ctgcttttgg	aaacatactg	tcttgcaagg	tggtgtgtga	180
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<210> 214
 <211> 728
 <212> DNA
 <213> Homo Sapiens

<400> 214						
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cagaacccaa	agaacatatt	cgtataattg	aaaaattcta	ggtgcttcat	aattgacctt	180
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acaagctagg	aagtcttcaa	accttgagtt	gaattccata	aggggttatt	tggcttttga	300
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ctttcttggc	atgatgagcc	tgtagaactg	ctacagcttc	atccaccttg	gagcggagag	420
actcggggga	ctctaacatg	tgcagcagct	canagttgtc	tatctccagc	agcattcccc	480
tgatcttccc	agccagattt	gaatgcattg	tttggatgan	tgggaacaag	cgttctccca	540
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gccttgcaaa	tggaccgcaa	ggctgggggtg	cctgcaaaan	gctgtatggc	aaggatgaag	660
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caacaaca						728

<210> 215
 <211> 710
 <212> DNA
 <213> Homo Sapiens

<400> 215

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canaacccaa	agaacatatt	cgtataattg	aaaaattcta	ggtgcttcan	aattgacctt	180
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ctgcccctgc	acaatggacc	gcaaggctgg	gggggtgctg	canaaggctg	tttgggcaag	660
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<210> 216

<211> 824

<212> DNA

<213> Homo Sapiens

<400> 216

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ccgtcccttg	ggctatgect	acgtcaactt	ccagcagccg	gccgacgctg	agcgggcttt	180
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ttggaaagaa	atgaatggga	aaagaaataa	antggtaaaa	tcataatttg	tagggccgtn	780
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<210> 217

<211> 749

<212> DNA

<213> Homo Sapiens

<400> 217

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cagaacccaa	agaacatatt	cgtataattg	aaaaattcta	ggtgcttcat	aattgacctt	180
ttgatacaaa	atgacctatt	aaatttgcaa	tttgtaatcc	ttggtgttga	ggtccatagg	240
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tgatcttccc	agccaagatt	tgaatgcatt	gtttggatga	gtgggaacaa	gcgttctccc	540
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ctgcccctgc	acatgggacc	gcaaggctgg	ggtgcctgca	naggctgtat	gggaaggatg	660
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nccagcagca	acancaacng	cttggcgcc				749

<210> 218
<211> 600
<212> DNA
<213> Homo Sapiens

<400> 218
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anatttgaat gcattgtttg ggatgangtg ggganaaagc gttctcncag canncngctt 540
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<210> 219
<211> 1077
<212> DNA
<213> Homo Sapiens

<400> 219
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ccgctccctg ggctatgect acgtcaactt ccagcagccg gccgacgctg agcgggcttt 180
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tggaagaagc aaagggtttg gcttcgtctg cttctcatct cctgaagaan caaccaagc 1020
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<210> 220
<211> 1007
<212> DNA
<213> Homo Sapiens

<400> 220
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tctgtcacc ttccctacag cctgaggagt acatggccta cgttcagagg caagccgact 180
caaagcagta tggagataaa atcatagagg agctgcaaga tctaggcccc caagtgtgga 240
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acagtaagga ctcagatttc tggaagatgc ttaatgagc agaggaccag gcccaggag 360
gggaggaggt gccggctgag gagcaggacc caagccctga ggcagcagat tcagcttctg 420

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gtgatccaga	acggcagaga	gagatggaag	aagaggagga	tgaggatgag	gatgaggatg	660
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aagactggag	ggaaaaacaa	gagttccaaa	ncctggtgaa	nnaagcncat	aaaaaagaag	960
gttgtcccaa	aaaagntccc	cccatcaanc	caaccctnca	gggaaaaa		1007

<210> 221

<211> 833

<212> DNA

<213> Homo Sapiens

<400> 221

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cttctgggtg	tcccaatgat	tttcagaaca	acgtgcaggt	caaagtcatt	cgaagccctg	300
cggatttgat	tcgattcata	gaggagctga	aaggtggaac	aaaaaagggg	aagccaaata	360
taggccaaaga	gcagcctgtg	gatgatgctg	cagaagtccc	tcagagggaa	ccagagaagg	420
aaaggggtga	tccagaacgg	cagagagaga	tggaagaaga	ggaggatgag	gatgaggatg	480
aggatgaaga	tgaggatgaa	cggcagttac	tgggagaatt	tgagaangaa	ctggaaggga	540
tcctgcttcc	gtcagaccga	gaccggctcc	gttcggaggt	gaangctggc	atggagccgg	600
gaactggnaa	acatcatcca	ggagacanga	gaaaganctg	ggacccanat	ggggctgaag	660
aanggatcag	aatccgggat	cgggcaatgc	tggctctcaa	aatcaactct	caacaaantc	720
attaaaaaga	ctggagggga	aaacaagagt	tccaaancct	ggtgaannaa	gcncataaaa	780
aagaaggttg	tcccaaaaaa	gnctccccc	tcaanccaac	cctncaggga	aaa	833

<210> 222

<211> 745

<212> DNA

<213> Homo Sapiens

<400> 222

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cacacctttt	tactgggat	tgtgctggag	gtgataggca	gcattctacc	atttccctcag	120
caacagaggt	gaaggctcct	caactcagaa	gcacaaattg	taggggacag	ggtgggcagg	180
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cactaagggc	aggtgggggc	ctgcttgctc	agtgcctgct	aagtgtcctg	ccctccttgc	300
tctctctacc	cacctccact	caaaagatcc	tactgaatct	ccaggtaggc	agcagggaat	360
atcctatcat	taggggacaa	taacaggaaa	agccacagag	gagaggaaga	ggattgagtg	420
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gcagcaagca	ttcaccacag	gccccacac	ccacagagtt	gcccagagang	tccacaagct	540
cagctccact	ctgctgtttg	gccctcaagg	gttccagggt	ggggaagtgg	ggaagaggca	600
ngccagtcca	ggaagatctg	gattccgtga	angggccaag	tgtagtgttg	gtctcagaag	660
tcaaattntc	caagtccctt	gttgcctccc	ccactggag	aagccccana	cccggnggta	720
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<210> 223

<211> 747

<212> DNA

<213> Homo Sapiens

<400> 223

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tctgtcaccc	tccctacag	cctgaggagt	acatggccta	cgttcagagg	caagccgact	180
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acagtaagga	ctcagatttc	tggagatgc	ttaatgagcc	agaggaccag	gccccaggag	360
gggaggagggt	gccggctgag	gagcaggacc	caagccctga	ggcagcagat	tcagcttctg	420
gtgctcccaa	tgattttcag	aacaacgtgc	aggtcaaagt	cattcgaagc	cctgctggatt	480
tgattcgatt	catagaggag	ctgaaagggtg	gaacaaaaaa	ggggaagcca	aatataggcc	540
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gtgatccaga	acggcagaga	gagatgggaa	ngaagangan	gatgaggatg	aggatgaggg	660
atgaaagann	aaggatgaaa	cgggcaagtt	actgggggaan	aatttttgana	aagggaactg	720
ggaaagggat	tcttggcttt	ccgttca				747

<210> 224

<211> 618

<212> DNA

<213> Homo Sapiens

<400> 224

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ctttttcgct	gggattgtgc	tggagggtgat	aggcagcatt	ctaccatttc	ctcagcaaca	120
gaggtgaagg	ctcctcaact	cagaagcaca	aattgtaggg	gacaggggtg	gcagggaaag	180
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agggcagggtg	ggggcctgct	tgctcagtg	ctgctaagt	tcctgccttc	cttgctctct	300
actacccacct	ccactcaaaa	gacctaactg	aatctccagg	tangcancan	ggaatatcct	360
atcatttaggg	gacaatanca	ggaaaagcca	cagaggagag	gaagaggatt	gagtganaag	420
attcangacag	caaattatca	caggccccgt	gaggtctcaa	ngtngngctg	caacaagggg	480
caancagcat	tcacccangg	gccccacacc	cacnnnagtt	gccccagagg	tcacancctc	540
ancctccan	ctgcengttt	ggccctcaag	gggttccaan	gttcngnaaa	gtgggggagg	600
aaggcanccc	antcccag					618

<210> 225

<211> 765

<212> DNA

<213> Homo Sapiens

<400> 225

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ggatgaggag	cttagaaaaag	agcagagAAC	tcaccaggaa	aagaaagttt	attgggtgtaa	120
tcagtgtagt	aggaccttcc	agggcagctc	agatctcatc	agacatcagg	taactcatac	180
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gagagaaact	tgaagaatgt	gagaaaacct	tcagcaagga	tganggagct	taggggagag	660
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caagggcagc	tcangacctc	atcggggccat	caggtaactc	aatac		765

<210> 226
<211> 791
<212> DNA
<213> Homo Sapiens

<400> 226

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tgcaacgtcc	ctgaacacca	taacttagag	aatgaagttt	ctagattaga	agacataatg	180
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angatcaagc	aagaagaaat	cttgaaaaga	aattaacnaa	aattntnca	gcaaaaagact	780
cagacttcaa	a					791

<210> 227
<211> 687
<212> DNA
<213> Homo Sapiens

<400> 227

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<210> 228
<211> 810
<212> DNA
<213> Homo Sapiens

<400> 228

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anctnaagct	gggccaatgg	ctccaaagtt	ccaacnaaag	gttaaaanat	cccagctcaa	780
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<210> 229

<211> 552

<212> DNA

<213> Homo Sapiens

<400> 229

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<210> 230

<211> 842

<212> DNA

<213> Homo Sapiens

<400> 230

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aaaaggagtc	ttgtataaca	cagttgaaga	aagagttatc	tgaaaacatc	aatgctgtca	180
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atcaaaacac	tgttaaagaa	ttgcagatcc	agcttgagtt	aaaatcaaag	gaagcttatg	540
aaaaggatga	gcagataaat	ttattgaagg	aagagcttga	tcagcaaaaat	aaaagatttg	600
attgttttaa	gggtgaaatg	gaagacgaca	agagcaagat	gggagaaaaa	ggagtctaatt	660
ttagaaacag	agttaaagtc	tcaaacagca	agaattatgg	gattagagga	ccatattanc	720
caagaaaact	atgttgaaat	tagagtcctt	aaatngaaag	ttccttaaaa	aattacaatc	780
aacaaaaagg	atattggacc	acaaagnaat	tgggtcaaaa	aaccttcaac	aantttcaag	840
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<210> 231

<211> 781

<212> DNA

<213> Homo Sapiens

<400> 231

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gaaaaatata	agtacaaaag	ctaagtaaac	aatgaggtag	tgccatttgg	gatttttttac	180
atgtcttagc	ttaaagaact	ggtcttttagc	aaatattcaa	cagatcaacc	tgaataaaat	240

agtcaattaa	atgctcta	at	ttatcagaaa	aaatccacta	agttttcacct	caaaatgtat	300
tgcacaagtc	tttttaaaaa	at	caccctaa	aaataaatag	gaaaggtaag	ccgttcttta	360
aaaagaatgg	atgaaaggaa	tattatgtaa	gcccataaag	cagggttaagt	tatcaaaaata		420
tcttttaaac	aacataaaac	tcttcccaag	agaaaactga	agaaaaaact	atcaccatttt		480
ctccactgat	aaaatctatt	ttaaaggcag	tctgcaactt	atctgtgggc	cagattttttc		540
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agtgtggaca	agttttccaa	gcagcangtc	acccaatgtc	actcttcctc	aagatgaagg		660
atcggagcca	tgacacatgt	ttaactaagc	acagaccgga	tgggtttacc	cagaagatac		720
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<210> 232

<211> 767

<212> DNA

<213> Homo Sapiens

<400> 232

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tctgaaaaat	ataagtacaa	aagctaagta	aacaatgagg	tactgccatt	tgggattttt	180
tacatgtctt	agcttaaaga	actggctctt	agcaaatatt	caacagatca	acctgaataa	240
aatagtcaat	taaatgctct	aatttatcag	aaaaaatcca	ctaagtttca	cctcaaaaatg	300
tattgcacaa	gtctttttta	aaaatcacc	taaaaataaa	taggaaagg	aagccgttct	360
ttaaaaagaa	tggatgaaag	gaatattatg	taagcccata	aagcagggtta	agttatcaaaa	420
atatctttta	aacaacataa	aactcttccc	aagagaaaaac	tgaagaaaaa	actatcacca	480
tttctccact	gataaaatct	attttanagg	cagtctgcaa	cttatctgtg	ggccagattt	540
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caagtgtggg	acagttttcc	aagcagcagt	cacccaatgt	cactcttctt	caagatgaaa	660
gatcggagnc	atgacacatg	ttaacctaag	nacangactg	gagggtttac	ncangaagat	720
acactgcgaa	ggtgaaagt	aaacatcaag	ccgaggaacc	tccctt		767

<210> 233

<211> 879

<212> DNA

<213> Homo Sapiens

<400> 233

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atcagttact	taaaaaaatt	gctgagaaag	atgatgatct	aaaacgaaca	gccaaaagat	180
atgaagaaat	ccttgatgct	cgtgaagaag	aatgactgc	aaaagtaagg	gacctgcaga	240
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gcaatgataa	tgtaacaatt	atggagctac	agacacagct	agcacagaag	acgactttaa	360
tcagtgattc	gaaattgaaa	gagcaagagt	tcagagaaca	gattcacaat	ttagaagacc	420
gtttgaagaa	atatgaaaag	aatgtatatg	caacaactgt	ggggacacct	tacaaagggtg	480
gcaatttgta	ccatacggat	gtctcactct	ttggagaacc	taccgaattt	gagtatttgc	540
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ccaccgtact	gaagttccct	gatgatcaga	ctcagaaaaat	tttgggaaaa	gagaagatct	660
cggctgatgt	ttacttcacc	tcgcagtggg	atcctcngag	taaacatca	gtcgtgccta	720
agtttacatg	tgatcatggg	ccgattcttc	atcctttgaa	gaaagagtgg	acattgggggt	780
naccggctgc	cttgggaaaa	ctgtccanac	nttgcnacn	ccttgggggaa	atggaagnnt	840
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<210> 234

<211> 780

<212> DNA
<213> Homo Sapiens

<400> 234

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gtacaaaagc	taagtaaaca	atgaggtact	gccatttggg	atttttttaca	tgtcttagct	180
taaagaactg	gtcttttagca	aatattcaac	agatcaacct	gaataaaaata	gtcaattaaa	240
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aagttaaaca	tcaagnccgag	catnctctc	tttccaaaaa	ttttccggng	tccggattca	780

<210> 235
<211> 780
<212> DNA
<213> Homo Sapiens

<400> 235

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ctttagagga	gaaagatcag	tatatcagtg	ttctccaaac	tcaggtttct	ctactgaaac	180
aacgattacg	aaatggcccc	atgaatgttg	atgtactgaa	accacttcct	cagctggaac	240
cacaggctga	agtccttcaact	aaagaagaga	atccagaaag	tgatggagag	ccagtagtggt	300
aagatggaac	ttctgtaaaa	acactggaaa	cactccagca	aagagtgaag	cgtcaagaga	360
acctacttaa	gcgttgtaag	gaaacaattc	agtcacataa	ggaacaatgt	acactattaa	420
ctagtgaaaa	agaagctctg	caagaacaac	tggtatgaaag	acttcaagaa	ctagaaaaga	480
taaaggacct	tcatatggcc	gagaagacta	aacttatcac	tcagttgcgt	gatgcaaaga	540
acttaattga	acagcttgaa	caaggataag	ggaatggtaa	tcgcagagac	aaaacgtcag	600
atgcatgaaa	ccctggaaat	gaaagaagaa	gaaattgctc	aactccgtag	tcgcatcaaa	660
cagatgacta	cccaagggag	aggaattacg	ggaacaagan	agaaaagtcc	gaaagaactg	720
cntttgaggg	aacttgaaaa	agccttgagt	acagnccaaa	aanacagnng	aagccaccgg	780

<210> 236
<211> 711
<212> DNA
<213> Homo Sapiens

<400> 236

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tcatatcttc	cttttccacc	aagatttgct	ttgtctgttc	ctgttctttg	ttaccatctt	180
caagtttgga	ctcatagact	tggtttaaag	attttacttt	ttgtctcatt	tcactatctt	240
gtttttcaag	ttgtctgcat	aagtcttgca	cctggatttt	gtgagcatct	aactcagtac	300
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tttccaaatc	caacaacttc	tgctgcaatt	gggccaactg	ttctcctat	gcttttgtct	420
gctcatgtgt	ggcactctgg	taagactgaa	aaacgtccag	cttagcagat	gcctgctgga	480
gttcccttcc	agacctttta	atatctgcct	ccaaattttc	tacatgagcc	tgatgctctt	540
tcaaatgctt	gtccctttcc	ttcaagagaa	gctcaagttg	nttaanttga	tcttttaaaag	600
ccttctcaan	tcctccggga	tanaaaacnt	cgtgttcttt	naatgagaac	ggtcaacntg	660

ccggctgggt gataantttt ccgttcance anccttgggg ctccaaattc c

711

<210> 237

<211> 658

<212> DNA

<213> Homo Sapiens

<400> 237

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aaaatataag tacaaaagct aagtaaaca tgaggtactg ccatttggga ttttttacat	180
gtcttagctt aaagaactgg tctttagcaa atattcaaca gatcaacctg aataaaatag	240
tcaattaaat gctctaattt atcagaaaaa atccactaag tttcacctca aaatgtattg	300
cacaagtctt tttaaaaaat caccctaaan ataaatagga aaggtaagcc gttctttaa	360
aagaatggat gaaaggaata ttatgtaagc ccataagagc aggttaagtt atcaaaatat	420
cttttaaaca ncataaaact cttcccanga gaaaactgaa gaaaaaacta tcaccatttc	480
tccactgata aaatctattt taaaggcagt ctgcanttta tctgtgggccc aagatttttc	540
ttggnctttt ggctacatga gggggccctg gaatgaaaaa cttcattccc aanggagttt	600
gcnaggtgtg ggacagggtt tccaaggcaa gcaagtnagc caaatngtca gctcttcc	658

<210> 238

<211> 678

<212> DNA

<213> Homo Sapiens

<400> 238

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ttctgaaaaat ataagtacaa aagctaagta aacaatgagg tactgccatt tgggattttt	180
tacatgtctt agcttaaaga actgggtctt agcaaatatt caacagatca acctgaataa	240
taaatgctct aatttatcag aaaaaatcca ctaagtttca cctcaaaatg	300
gtcttttttaa aaaaatcaccc taaaaataaa taggaaaggt aancogttct	360
ttaaaaagaa tggatgaaag gaatattatg taagcccata aagcaggtta agttatcaaa	420
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ncatttcnnc actgataaaa tctantttaa agggngagtc gcaacttanc tgtggggccag	540
atctttccgt ggggcttttg ggctacantn agggggccct gaatgaaaaa nttcaattcc	600
ncaaagtngg tagcaaatg tgggncangt ttttccaaag cagncaantt cancccnana	660
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<210> 239

<211> 1402

<212> DNA

<213> Homo Sapiens

<400> 239

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atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat	180
atgaagaaat ccttgatgct cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga	240
ctcaacttga ggagctgcag aagaaatacc agcaaaagct agagcaggag gagaacctg	300
gcaatgataa tgtaacaatt atggagctac agacacagct agcacagaag acgacttta	360
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gcaatttgta ccatacggat gtctcactct ttggagaacc taccgaattt gagtatttgc	540
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ccaccgtact	gaagttccct	gatgatcaga	ctcagaaaat	tttggaaaga	gaagatgctc	660
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taaagtttat	ttactatata	ac				1402

<210> 240
 <211> 760
 <212> DNA
 <213> Homo Sapiens

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gtctggacaa	tagaataaat	gaagtcaata	aaaccattct	tttaacaacc	ttaataccat	300
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<210> 241
 <211> 745
 <212> DNA
 <213> Homo Sapiens

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ctataatgac	atgggaaatg	ttcatgaact	gtgaggtgaa	aagatacaga	aatgacttat	180
gcctacngat	actacctttg	aaaaaggatc	cataaaaaat	acattgaata	taagttggct	240
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tcaatatgta	ctaaaattca	catgcattta	ttttataatc	agaatgtcat	tataattaaa	360
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aangtttncc	tttggttaacc	ngaag				745

<210> 242
 <211> 818
 <212> DNA
 <213> Homo Sapiens

<400> 242

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<210> 243
 <211> 799
 <212> DNA
 <213> Homo Sapiens

<400> 243

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atacatttaa	aaaatacngg	ttaaaccngg	tgagggaatt	ccacatttgg	cctatttaac	720
aaaaatttta	aaccaatttt	caaaaggggc	tttggggtaa	aaagtngatt	cccaagcaac	780
ntcaancant	ttaaccttc					799

<210> 244
 <211> 726
 <212> DNA
 <213> Homo Sapiens

<400> 244

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aatatgaaaa	tgaagatctg	atcaagcatg	gctggcctga	agatatctgg	tttcatgtgg	180
acaaactctc	ttcggtcat	gtataccttc	gattacataa	gggagagaat	atagaagaca	240
tcccaaagga	agtgtgatg	gactgtgccc	accttgtgaa	ggccaatagc	attcaaggct	300
gcaagatgaa	caacgttaat	gtggtatata	cgccgtggtc	taacctgaag	aaaacagctg	360
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agaagaaagt aaatgagatc ctgaaccgat tagaaaagac caaagtcgag cggttcccag 480
acctancagc agagaaagaa tgcagagatc gtgaagagag gaatgagaaa aaagcccaaa 540
ttcaggaaat gaaaaagaga gaaanagaag aaatgaagaa gaanaggga atggatgaac 600
ttangagcta ttcactacta atgaaagttt gaaaatatgt cttcanatca ggatggcaat 660
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aatggt 726

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<210> 245
 <211> 592
 <212> DNA
 <213> Homo Sapiens

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<400> 245
ccagattaaa aaaatggtat tttattataa cttttaaaat tgcggaacat cagactgaat 60
atcatcagac acatacaca aaccactcat ctctaaagtc attttctata ccctctcaaa 120
atctggccag tgagttttgc ctcagggaat tttccagttc aaccccatac accaactggt 180
aataaatgga aacactagcc ttttggtttt gccanagtt ccaaagtgtc attacaggtg 240
gaatatctgc tgcaggaagt cattcttgct gctgtgggtg tgagtaaaat gcttagttcc 300
ttctaaaatc ataattgcaa tatggacttc tgcttcacgc tgcactcctaa ggcacaaatc 360
aggtaacctc catctcccaa atgatcaaca ggagcactcc atcctatctt accctcaatg 420
cnganaaatt acnccctgggc ccanaagttg tcacataggt ggcttgggtt acttggggct 480
caggcaacaa ctgccacagg cccagcttg atgaanacca tcnatttctt taaaatatgt 540
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<210> 246
 <211> 821
 <212> DNA
 <213> Homo Sapiens

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<400> 246
aggatgaaga gctggagagc gccgaggacg acgagcgcag ctgtcggggc cgcgagtcgg 60
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tagaaatgaa ggaacagatg tatcaggaca aactggcttc tctcaagagg cagttgcaac 180
aactgcaaga aggtacatta caggaatatc agaagagaat gaaaaaacta gatcagcagt 240
acaaagagag gatacggaat gcagaactct tctccagct ggaaactgaa caagtggaa 300
gaaattacat taaagaaaag aaggcagcag tgaagaatt tgaagacaag aaggttgagc 360
tgaaagagaa cctgattgct gagctagaag aaaagaagaa aatgattgaa aatgaaaagc 420
tgacaatgga actgactgga gattctatgg aggtgaaacc tatcatgacc agaaagttgc 480
ggaggcgacc aaatgatccc gtcccatcc cagacaagag gaggaacact gctccagccc 540
agctaaacta tttgttaaca ggatgaacag atcatggagg atctgagaac attaaataag 600
cttaagtcac ccaagagacc agcatctcca tctctcctg agcacttgcc tgcaacacccc 660
gccggaatct ccaagcccca gaggttcnaa agccccggat anaagaatgg caaacctggt 720
actatgacaa aaagatgggt accacaagag ccaaggccat cctatcctgg angtc aaagg 780
gacaaaccan gaaactgaag cctgcctnat taagtttccg t 821

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<210> 247
 <211> 639
 <212> DNA
 <213> Homo Sapiens

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<400> 247
gttacacaaa gcatttattt ctctgagaag gccgagagcc acgagaattc atcatctcct 60
gctaggacct ctgcccacag cttctgggca aatagtgaat tggacgcgac agggaaagta 120
gctacgtgat ccactaatca gattcaaaac atgaaaatgc actggagagt gtatcccttc 180
ctgctcttct ccatggtaga gagacttaaa gataatcaat aaaaatagct gtcccttcaa 240

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actcagagga	ggtttttcaaa	aacaagtata	agcaaaaaat	aaagaaataa	aaggaaagta	300
aatcaaacc	cccaatacgc	ctgaaagtaa	aacagtctca	tggtagactga	tgtctggaan	360
aagttgagc	agaaaagact	gacaaagttg	gaangcatcc	cggccacaaa	agtgccnaa	420
aagaattcan	tgcagtgtc	tccatttcca	aggetgagta	actattccca	gntaagttaa	480
catttttcna	nttaaggana	nancgaanac	anntncatnt	ctanatccca	ctccagaaat	540
anggtcaatg	agaangangc	actgtannna	aagtcaagna	gctggancnc	cggggcggnt	600
tnacccaaga	gcccggcgct	nnaagcctgg	gccaagct			639

<210> 248

<211> 846

<212> DNA

<213> Homo Sapiens

<400> 248

aacaggatgt	caaaaattaa	actgcgcttt	ccatcacaaat	agaggacgat	atgttgatgg	60
ccttttctta	cctccgagca	aaactgtgtt	gcccactgtg	cctgagtcac	cagaagagga	120
agtgaaggct	agccaacttt	cagttcagca	gaacaaattg	tctgtccagt	ccaatccttc	180
ccctcagctg	cggagcggtta	tgaaagtaga	aagttccgaa	aatgttccta	gccccacgca	240
tccaccagtt	gtaattaatg	ctgcagatga	tgatgaagat	gatgatgatc	agttttctga	300
ggaaggtgat	gaaaccaaaa	cacctaccct	gcaaccaact	cctgaagtgc	acaatggatt	360
acgagtgact	tctgtccgga	aacctgcagt	caatataaag	caaggtgaat	gtttgaattt	420
tggaataaaa	actcttgagg	aaattaagtc	aaagaaaatg	aaggaaaaat	ctaagaagca	480
aggtgagggg	tcttcaggag	tttccagttc	tttactccac	cctgagcccg	ttccaggtcc	540
tgaaaaagaa	aatgtcagga	ctgtggtgag	gacagtaact	ctctccacca	aacaaggaga	600
agaacccttg	gttagattga	gtcttactga	gagactgggg	aaacgaaaat	tttcagcagg	660
cggtgacagt	gatcctccat	taaagcgtag	cctggcacan	aggctaaggg	aagaaagttg	720
aagctccaga	aactaacant	gacaaaacac	caangaaagc	tcaagtttcc	aagtccccct	780
aaaggggcga	atttaggcag	tcagccngga	ttcaagataa	tnagggatgc	aacaagatta	840

<210> 249

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 249

gacttttcta	catcagtttt	atttaaaaca	caaacaagta	tttctctttc	tgtaagggca	60
aatggttcaa	ataatgcgga	acacgaaaca	ttgactaata	caagtgcctt	aaatatgaaa	120
caaaattatt	ttttaaaaaa	gcaaaagaat	aaagaatata	tacaaaaggg	acctggaatc	180
tgtaagctga	ttccaaaaat	gaaataagta	gaaaatccat	ggtgaaacct	gaacattcta	240
cctctgcttt	ggagaagggc	tatcatataa	cattcagtc	gctgaagatg	gattggtaga	300
ggtgtgtcta	tacataaaact	tcagtcattt	ttgcttgtgc	agaatcatcc	caatcttccc	360
aagactgaat	gggcagtcct	gtggctttct	tcctttttcca	tattcccaac	aaggctacgt	420
gaagttcaac	tcttgatgag	ccgcttataa	cagcagttcc	ttaggagcca	acatgacagg	480
tgggtcagat	ttccctatga	gaaacaaaac	tggccaccta	cagcaaaaata	tcaaaatggg	540
taagtccttc	cttctctctc	ctcctgatta	tatacaacat	atctcctttc	aagactatta	600
tttccatcat	gccttattcc	ttcacaaatc	taaaccttga	ngtgatatga	angaaaccaa	660
catcaagaaa	agaaaactca	attcagaaat	gaanaaaacg	ggcaggtata	caatacaccc	720
cagagcatct	caatatcccc	tgggacagnt	acaattcagt	gtt		763

<210> 250

<211> 899

<212> DNA

<213> Homo Sapiens

<400> 250

attcaagtca	agagatgtga	gaccatgaga	gagaagcaca	tgcagaaaca	gcaggagagg	60
gaaaaatcag	tcttgacacc	tcttcgggga	gatgtagcct	cttgcaatac	ccaagtggca	120
gagaaaccag	tgctcactgc	tgtgccagga	atcacacggc	acctgaccaa	gcggcttccc	180
acaaagtcat	cccagaaggt	ggaggtagaa	acctcagggg	ttgggagactc	attattgaat	240
gtgaaatgtg	cagcacagac	cttggaaaaa	aggggtaaag	ctaaacccaa	agtgaacgtg	300
aagccatctg	tggttaaagt	tgtgtcatcc	cccaaattgg	ccccaaaacg	taaggcagtg	360
gagatgcacg	ctgctgtcat	tgccgctgtg	aagccactca	gctccagcag	tgtcctacag	420
gaacccccag	ccaaaaaggg	agctgtggct	gttgtcccg	ttgtctctga	ggacaaatca	480
gtcactgtgc	ctgaagcaga	aaatcctaga	gacagtcttg	tgctgcctcc	aaccagtc	540
tcttcagatt	cctaccccc	ggagggtgtc	ggcccttcct	catcccaaat	gagcatgaaa	600
actgcgcgac	tcagctctgc	ctcaacaagg	aaagccccca	ctctctgtgg	aggatgattt	660
tgagaaacta	atatggggaga	tttcaaggag	gcaaaattgg	naactganat	tgacctggat	720
tctgggaaaa	gatgaagatg	acccttccgg	cttngngcct	atcaannaaa	ngattgntan	780
cctgaaaggg	tggttaattga	nggacncctt	naaaaaaaaa	atccnccaaa	aaaactnggg	840
ccttaanttc	naccaaattg	taacaatttn	acctgagaat	gnttaatttc	ctttaggcc	899

<210> 251

<211> 755

<212> DNA

<213> Homo Sapiens

<400> 251

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tcaaataatg	cggaacacga	aacattgana	nagacaagt	ctttaaatat	gaaacaaaat	120
tattttttta	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatgggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tagagggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcagaatc	atcccaatct	tccaagact	360
gaatgggcag	tcctgtggct	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaacatga	cagggtgggtc	480
agatttccct	atgagaaaca	aaactggcca	cctacagcaa	aatatcaaaa	tgggtaagtc	540
cttcttctct	cttctctctg	attatatata	acatatctcc	tttcaaagac	tattattttcc	600
atcatgctta	ntccttcaca	aatctaaaac	ttgagggtgat	atgaaggaaa	ccaacatcan	660
gaaaagaaaa	ctcaattcag	aaatgaagaa	aacgggcang	tatacaattc	anccccagag	720
caacccaata	atccctgggc	aaaagttcaa	ttcaa			755

<210> 252

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 252

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tcaaataatg	cggaacacga	aacattgact	aatacaagt	ctttaaatat	gaaacaaaat	120
tattttttta	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatgggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tagagggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcagaatc	atcccaatct	tccaagact	360
gaatgggcag	tcctgtggct	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaacatga	cagggtgggtc	480
agatttccct	atgagaaaca	aaactggcca	cctacagcaa	aatatcaaaa	tgggtaagtc	540
cttcttctct	cttctctctg	gattatatac	aacatatctc	ctttcaagac	tattattttcc	600
atcatgcnta	atccttcaca	aatctaaaac	cttgagggtg	atatgaaagg	aaaccaacat	660
canagaaaag	aaaactcaat	tcaagaaaaat	taagaaaacc	tggcaaggta	tacaaatata	720

<210> 253
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 253

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aatgggtcaa	ataatgcgga	acacgaaaca	ttgactaata	caagtgcctt	aaatatgaaa	120
caaaattatt	ttttaaaaaa	gcaaaagaat	aaagaatata	tacaaaaggg	acctggaatc	180
tgtaaggnga	ttccaaaaac	gaaataagta	gaaaatccat	ggtgaaacct	gaanattcta	240
cctctgcttt	gganaagggc	tatcatataa	cattcagtc	gctgaanatt	gattggtaaa	300
ggtgtgtcta	tacataaact	tcagtcattt	ttgcttgtgc	anaatcatcc	caatcttccc	360
aagactgaat	gggcagtcct	gtggctttct	tccttttcca	nattcccaac	aaggctacgt	420
gaagttcaac	tcttgatgag	ccgcttataa	cagcagttcc	ttaggagcca	acatgacagg	480
tgggtcagat	ttccctatga	gaaacaaaa	tggccacctc	cagcaaaata	tcaaaatggg	540
taagtccttc	cttctctctc	cncctgatta	tatacaanat	atctcctttc	aagactatta	600
tttccatcat	gcttattcct	tcacanattc	aaaccttgan	gtgatattga	nggnaaccaa	660
catcangaaa	agaaaactca	attcagnaat	gaangaaaac	tgggaggtat	ttaatanacc	720
cccangnnga	atccaaatac	cctggnaana	gttcaattca	antgtacngc	naaagnccat	780
aantaantat	tgg					793

<210> 254
<211> 625
<212> DNA
<213> Homo Sapiens

<400> 254

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tcaaataatg	cggaacacga	aacattgact	aatacaagtg	ctttaaatat	gaaacaaaat	120
tattttttta	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tanagggtgtg	300
tctatacata	aacttcagtc	attttttgctt	gtgcagaatc	atcccaatct	tcccaagact	360
gaatgggcag	tctgtgggt	ttcttctctt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacancaa	gttccttang	agccaacatg	acaggtgggg	480
tcangatttc	cctatgagaa	acaanactgg	ccacctacag	caaaaatatn	aaaatgggg	540
aagtccttcc	ttctcttctc	tctgaatta	tatncaacat	ntctcctttt	caagacnatt	600
anttccatca	gggcttaatc	cttca				625

<210> 255
<211> 907
<212> DNA
<213> Homo Sapiens

<400> 255

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ctgcccagca	gactaetcat	cctggcgggc	ggaagcgcaa	aggcaaggct	cagtatgtgc	120
tggccaagcg	cgctcgggcg	tgogacgctg	gcgggccccg	tcagctagag	cccgggctac	180
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agccctcttg	aagtgaggga	gaggatgatg	atgcggaggc	tgcccttgaag	aaagaagttg	360
gtgacattaa	ggcatctaca	gagatgaggt	taagaagatt	ccagtcagtg	gaaagtgagg	420
caaataacgt	tgtcttcac	aggacacttg	ggatagagcc	tgagaaattg	gtgcatcata	480

ttctccagga	tatgtacaaa	accaagaaaa	agaagactcg	agttattttg	cgaatgttac	540
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tggaaccctg	gtttaaagct	ccaaacaaag	ggacatttca	gatttgtgtac	aaaatctcga	660
nataacagtc	atgtnaatag	agaagaagtt	atcaagagaa	tttgcangga	atagtgtgca	720
acctcaattc	agnaaataaa	gtgggtntca	acaatccaca	agtacacaat	ngtaatanaa	780
atcatcaaan	ctgtcngttc	cctganngtt	tgttaaagga	ttacaagggt	ggtttannaa	840
aattcaatcn	ccaagaaggt	tggtnaanaa	nccccctaang	ggntccttca	naggcnttaa	900
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<210> 256
 <211> 794
 <212> DNA
 <213> Homo Sapiens

<400> 256						
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gacctctggt	tatcagatat	gatgtcacia	aanagagata	ttggcctttg	ttctggcagg	120
ctcctagcaa	tagaaaaagt	tttctttgaa	tttcatcatt	tacaaatctt	acaaatgcta	180
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ttttcagtta	atgacacaaa	accttttttg	catcatatga	catatcatca	gtaaatcaac	300
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tttgcttctt	aaaccttttg	actaaagggt	attttctgaac	aaaagcctta	ctgtttttga	480
tagtccaaaa	gccatttgaa	aataatgaat	atcctttctt	gtcaagtggc	tgtgatttat	540
tgttacaatt	gctaagtttt	gtaagttgca	tgtcacagac	aatgcacaat	gggacaagan	600
aaccttggac	ctgagtcac	ataaataccc	cttgagaagt	taccttttcc	ttaatgaaga	660
caagaatttc	ctttgggtgc	cccttgggtg	cactaagtat	acttgaaagt	ntnctccagn	720
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<210> 257
 <211> 885
 <212> DNA
 <213> Homo Sapiens

<400> 257						
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tacctctctc	aggcacatgc	aaggcttttt	tagaagatat	gaaaaaatat	gcagaaacat	600
ttttggaacc	ctgggtttta	agctccaaac	aaagggacat	ttcagattgt	gtacaaatct	660
cgaataaaca	gtcatgtgaa	tngagaaaga	agttatcaga	gaaattggca	aggaatagtt	720
gtgcaccctc	aattcagaaa	attaaagggt	ggntctcaac	caatccacag	ttcacagntg	780
gtagttagaa	atcaatcaaa	acctgtcngt	ttgcccgaan	ttgnttgta	aaagaattca	840
angttggttt	tanaanaaat	naaatcccca	aagaagggtg	gtgaa		885

<210> 258
 <211> 798
 <212> DNA

<213> Homo Sapiens

<400> 258

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cttcactgta	tcttcaagtt	tttgatatca	gnagcactgt	ggagaaaagca	gtgtgctata	120
atgtcaacat	caggattttct	tttttttttt	ttaataacgc	aaaatgactt	atggagacaa	180
ccactgatgg	ggcaccagga	gtgtagatac	cagacctctg	gttatcagat	atgatgtcac	240
aacattatat	attggccttt	gttctggcag	gctcctagca	atagaaaaag	ttttccttga	300
atttcatcat	ttacaaatct	tacaaatgct	acagcatgac	aaatattagt	gaaacctgtt	360
gactcatcat	cctggataga	gaagctgcta	cttttcagtt	aatgacacaa	aacctttttt	420
gcatcatatg	acatatcatc	aagtaaataca	acttattgag	aataaagtct	cttcaacttt	480
gtactgcac	ttgccccagc	attttaaatgt	tattaagatt	ctcaccaacc	atgcataatt	540
tcctttcctg	agataagttc	tgctactaaa	taatttgctt	cttaaacctt	ttgactaaag	600
gtgatttctg	aacaaaagcc	ttactgtttt	tgataagtcc	caaaaagcca	tttgaaaaat	660
aatgaatatc	ctttcntgtc	aagtggctgt	gaatttaatg	ttacaattgc	caagttttgt	720
aagttgcatn	gtcacangac	aatgcacaat	ggggacaagg	agaaccttgg	gcttgagtcc	780
acaataanta	ccccttga					798

<210> 259

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 259

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ggcaaggctc	agtatgtgct	ggccaagcgc	gctcggcgct	gcgacgctgg	cgggccccgt	180
cagctagagc	ccgggtctaca	gggcatcctc	atcacctgca	atatgaacga	gcgcaagtgc	240
gtggaggagg	cctacagcct	cctcaacgaa	tacggcgacg	acatgtatgg	gccagaaaaag	300
tttacagaca	aggatcagca	gdcctctgga	agtgaggagg	aggatgatga	tgccggaggct	360
gccttgaaga	aagaagtgtg	tgacattaag	gcactctacg	agatgagggt	aagaagattc	420
cagtcagtgg	aaagtggagc	aaataacgtt	gtcttcatca	ggacacttgg	gatanagcct	480
gagaaattgg	tgcatcatat	tctccaggat	atgtacaaaa	ccaagaaaaa	gaagactcga	540
gttattttgc	gaatgttacc	catctcaggc	acatgcaang	cttttttaga	agatatgaaa	600
aaatatgcan	aaacattttt	ggaancctgg	tttaaagctc	caaacaaagg	gacatttcag	660
attgtgttca	aatctcgaaa	ataacagtca	tggtgaatag	aagaagaagt	tatcagagaa	720
nttggcaagg	aataatgntg	caacctcaat	tcagaaaata	aaagtggatt	tcaccaattc	780
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<210> 260

<211> 772

<212> DNA

<213> Homo Sapiens

<400> 260

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tttcagttaa	tgacacaaaa	ccttttttgc	atcatatgac	atatcatcag	taaatcaact	300
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tagatttctca	ccaaccatgc	atattttcct	ttcctgagat	aagttctgct	actaaataat	420
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agtccaaaag	ccatttgaaa	ataatgaata	tcctttcttg	tcaagtggcn	gtgattttatt	540
gttacaattg	ctagttttgt	nagttgcatg	tcacagacaa	tgacacaaatg	gacangagag	600

cctgggactg agtccacata ataccntga gaagtannct ttctttatta agacagaant	660
ttttgtgtc ccttggtgca caagtntact gaagtntcnc aagaaggact ggangtcntc	720
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<210> 261
 <211> 753
 <212> DNA
 <213> Homo Sapiens

<400> 261	
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cagtatgtgc tggccaagcg cgtcggcgc tgcgacgtg gcgggccccg tcagctagag	180
cccggggtac agggcatcct catcacctgc aatatgaacg agcgcaagtg cgtggaggag	240
gcctacagec teeteaaega atacggcgac gacatgtatg ggccagaaaa gtttacagac	300
aaggatcagc agccctctgg aagtgagggg gaggatgatg atgcggaggc tgccctgaag	360
aaagaagttg gtgacattaa ggcattctaca gagatgaggt taagaagatt ccagtcagt	420
gaaagtggag caaataacgt tgtcttcac aggacacttg ggatagagcc tgagaaattg	480
gtgcatcata ttctccagga tatgtacaaa accaagaaaa agaagactcg agttattttg	540
cgaatgttac ccatctcagg cacatgcaag gcttttttag aaagatatga anaaatatgc	600
anaaaacatt tttggaaccc tgggttttaa gctccaaaca aaggacatt tcagaattgt	660
ggtacaaatc tcgaaatanc agtcatgtta antagagaan naagtttttc agaagaattt	720
ggcaaggaat nagtnttgca accctcaatt tca	753

<210> 262
 <211> 659
 <212> DNA
 <213> Homo Sapiens

<400> 262	
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tcctagcaat agaaaaagtt ttctttgaat ttoatcattt acaaacttta caaatgtac	180
agcatgacaa atattagtga aacctgttga ctcatcatcc tggatagaga agctgctact	240
tttcagttaa tgacacaaaa ccttttttgc atcatatgac atatcatcag taaatcaact	300
tattgagaat aaagtctctt caacttttga ctgcatcttg cccagcatt ttaatgttat	360
tagattctca ccangccatg catattttcc ttctctgaga taagtctctg tactaaagaa	420
tttgcttctt aaaccttttg actaaagggt atttctgaac aaaagcctta ctgtttttga	480
nnagtccana agccatttga aaaataatga atatcctttc cttgtcaagt ggcngtgatt	540
tantgttaca atttgcnagg ttttgtaagt tgcatggtca cagnanaatg cacantnggg	600
acannagan cntgggncng aagtccacat tatanccctt tgagnaangt agctttccc	659

<210> 263
 <211> 673
 <212> DNA
 <213> Homo Sapiens

<400> 263	
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tttaaggggt ctgtcatgga aggtgctctt ccaggaacct ctgtgatgga ggtcacagcc	120
acagacgagg acgatgatgt gaacacctac aatgccgcca tcgcttacac catcctcagc	180
caagatcctg agtccctga caaaaatatg ttcaccatta acaggaacac aggagtcac	240
agtgtggtca ccactgggct ggaccgagag agtttcccta cgtataccct ggtggttcaa	300
gctgctgacc ttcaagggtg ggggttaagc acaacagcaa cagctgtgat cacagtcact	360
gacaccaacg ataatcctcc gatcttcaat cccaccacgt acaagggtca ggtgcctgaa	420

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ccagcggttg	gaggctgtat	acaccatatt	gaatgatgat	ggtgggacaa	tttgtcgtca	540
ccacaaatcc	agtgaacaac	gatggcattt	tgaaaaacag	caaagttgaa	gtcaagtgat	600
tttgcgtggt	cngaatacat	tgttgccctn	ggtgggagaa	aggtntocaa	cacatacccc	660
gggattngtt	att					673

<210> 264
 <211> 661
 <212> DNA
 <213> Homo Sapiens

<400> 264

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gctcctcatt	ttcctgaaga	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	ccgcttctcc	tcaagttcca	anagagtggg	caattagtga	aattccatca	240
gtcatgttaa	aatatacttt	caccaggtan	acatccttct	ttcaatgcta	gaggacagtg	300
aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
aacgcgggag	tgctgaacac	atgccctcgg	aagggaacct	gaagacccaa	gtgacctgca	420
ccataaaacc	accccgaggg	tcagccatgc	tgccagcact	caagaagcag	cagggccacc	480
tgctggaaaa	ctgggacacg	ctctgggtgc	ctggccctgc	ctgcccctc	cacgtccttg	540
gagccagggt	tacggcaggg	aacatgatct	tcttctccag	cttctgtgga	aggaacanga	600
aatttttcat	gatgtcntcc	agctcttcta	nggccaactg	ggcatgganc	ttggccacgt	660
c						661

<210> 265
 <211> 659
 <212> DNA
 <213> Homo Sapiens

<400> 265

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gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatanagcta	ggtgacatat	180
gggtggccaa	ccgcttctcc	tcaagttcca	anagagtggg	caattagtga	aattccatca	240
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aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
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ccataaaacc	accccgaggg	tcagccatgc	tgccagcact	caaaaagcag	cagggccacc	480
tgctggaana	actgggcacg	gctctgggtg	cctggccctg	cctgcccctc	ccacgtcctt	540
gganccaggt	ctacggcnagg	accatgatct	tcttctccan	cttctgtgga	aggaacanga	600
antttttcat	gatgtcntcc	actcttctag	ggccaactgg	gcatggactt	ggccacgtc	659

<210> 266
 <211> 620
 <212> DNA
 <213> Homo Sapiens

<400> 266

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gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	ccgcttctcc	tcaagttcca	anagagtggg	caattagtga	aattccatca	240
gtcatgttaa	aatatacttt	caccaggtan	acatccttct	ttcaatgcta	gaggacagtg	300
aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360

aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
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ntttttcatg	atgtcatcca					620

<210> 267
 <211> 745
 <212> DNA
 <213> Homo Sapiens

<400> 267						
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gcactactac	aagtcagaaa	tctggaagcg	taaccacaga	acagctccaa	gaggttcttt	120
tgtcagctta	tgaccctcaa	attccaacac	gggtgctgc	cctgcgtact	ctttccact	180
ggatagagca	gagagaagca	aaagcccttg	agatgcaaga	gaagcttctc	aagatattct	240
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tgctgtcaga	cgtctatcct	gagaaaatct	tgccggactt	gttggctcaa	tatgacagca	360
gcaaagacaa	gcacacacca	gagaccaaga	atgaaagtcg	gggaagtcct	tatgcgaatc	420
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attgctgtgg	ccaaaaacat	tntntgaaag	ttcaagttcg	cannagctgg	ccaanacaat	660
gtggggttgt	gcctgcnngc	tttcggggga	actcaacca	agaaaaagct	tantgtaagg	720
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<210> 268
 <211> 676
 <212> DNA
 <213> Homo Sapiens

<400> 268						
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acctccaact	gcattctccta	ctctgaaatg	cctcttgagc	agccaagggg	ggccagttct	120
gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
gggtggccaa	cgccttctcc	tcaagttcca	ananagtggg	caattagtga	aattccatca	240
gtcatgttaa	aatatacttt	caccaggtag	acatccttct	ttcaatgcta	gaggacagtg	300
aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
ccataaaaacc	accccgaggg	tcagccatgc	tgccagcact	caagaagcag	cagggccacc	480
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gtcatcgggc	tccaaa					676

<210> 269
 <211> 737
 <212> DNA
 <213> Homo Sapiens

<400> 269						
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cctgttggtg	tctttattat	tgaaagagaa	acaggatggc	tgaagctctt	ctctcacgct	120
gtgtcatcca	acgggaatgc	agttgaggat	ccaatggaga	ttttgatcac	ggtaaccgat	180
cagaatgaca	acaagcccga	attcaccacg	gaggtcttta	aggggtctgt	catggaaggt	240

gctcttccag	gaacctctgt	gatggaggtc	acagccacag	acgcggacga	tgatgtgaac	300
acctacaatg	ccgccatcgc	ttacaccatc	ctcagccaag	atcctgagct	ccctgacaaa	360
aatatgttca	ccattaacag	gaacacagga	gtcatcagtg	tggtcaccac	tgggctggac	420
cgagagagtt	tccctacgta	taccctgggtg	gttcaagctg	ctgaccttca	aggtgagggg	480
ttaagcacia	cagcaacagc	tgtgatcaca	gtcactgaca	ccaacgataa	tcctccgata	540
ttcaatccca	ccacgtacaa	gggtcangtg	cctganaaag	aaggctaacg	tcgttatcac	600
caacactgaa	aagtgactga	tgctgatgc	cccccaatta	nccanccgt	gggaagctgt	660
ntacaccata	tngaaatgat	gatgggtggg	cnaatttgn	cgttcaccaa	caaatanccan	720
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<210> 270

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 270						
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gctcctcatt	ttcctgaana	anaatctcag	cctgaaagaa	tatanagcta	ggtgacatat	180
gggtggccaa	ccgcttctcc	tcaagttcca	ananagtggg	caattagtga	aattccatca	240
gtcatgttaa	aatatacttt	caccagggtan	acatccttct	ttcaatgcta	gaggacagtg	300
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aacgcgggag	tgctgaacac	atgccctcgg	aagggaccct	gaagacccaa	gtgacctgca	420
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ggagccaggt	ctacggcagg	aacatgatct	tcttctccac	ttctgtggaa	ggaacangaa	600
atctttcatg	atgtctccan	ctcttctagg	gccactgggc	atggancttg	ggcnentcat	660
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<210> 271

<211> 814

<212> DNA

<213> Homo Sapiens

<400> 271						
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gctcctcatt	ttcctgaaga	agaatctcag	cctgaaagaa	tatagagcta	ggtgacatat	180
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gtcatgttaa	aatatacttt	caccaggtag	acatccttct	ttcaatgcta	gaggacagtg	300
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gaagtttttc	aatgatgtca	tccagctcct	cctanggccca	actgggcaag	ggagcttggg	660
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gaaggacggg	ggctcaacaa	cccaagtanc	ctttccnggg	ctgaatcccc	ngaagcaagc	780
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<210> 272

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 272

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cccagacagg	cctgcagtca	aatgctccaa	tcattcctca	aggagtcaat	gagcccagca	180
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<210> 273

<211> 677

<212> DNA

<213> Homo Sapiens

<400> 273

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aaaaaaggaa	ntttttcaag	gnngtcatcc	nangctcctc	caaggggnca	aaatgggggc	660
antggaacct	tgggcaa					677

<210> 274

<211> 863

<212> DNA

<213> Homo Sapiens

<400> 274

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anggcattag	ggagacatgg	tctcaaagta	accgagaacc	tttgattcat	accttctctga	780

aggggaatta gagattctga atggtgctca cagggccaac aaccttggen aaccttgggg 840
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<210> 275
<211> 821
<212> DNA
<213> Homo Sapiens

<400> 275
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ccataaaacc accccgaggg tcagccatgc tgccagcact caagaggcag cagggccacc 480
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<210> 276
<211> 722
<212> DNA
<213> Homo Sapiens

<400> 276
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tgatgtgat gcccccaata cccagcgtg ggaggctgta tacaccatat tgaatgatga 180
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aaagttgaag tcaagtgatt ttgctgttct gaagcagttg ttgcctctgt tggagaagggt 300
atccaacaca taccctgatc cgggtcatcca agaactcgtt gttgatctcc gcacaccat 360
ctctacccat ggagcctttg ccactgaggg cgtcagcatg gctgccccaa gtacactgaa 420
cagaaaagat ctggaaggga aaatagaaga gcagcaacaa accagtcctg aaagaccac 480
tgatgtagct catagccacc ttgaacaaca gcagagccat gaagacagcc cccagacag 540
gctgcagtc aaatgtctca atcattcctc aaggagtcaa tgagcccagc actactacaa 600
gtcagaaatc tggaagcgtt accacagaac agctccaaga ggttcntttg tcagctttat 660
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ca 722

<210> 277
<211> 805
<212> DNA
<213> Homo Sapiens

<400> 277
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gctcctcatt ttctgaaga agaattctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgtttctcc tcaagttcca agagagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtag acatccttct ttcaatgcta gaggacagtg 300

aaaaatgtag	attaatgaga	tctgtaactg	tcttctctta	actgtacacc	cctcaggctg	360
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ngaagttttt	caagatgtca	tccaactcct	ccaagggcca	actggggcat	gggagccttg	660
gcacgtcatn	cggtctccag	acacactacg	gtgcttcaac	aagggnggta	nagattcttg	720
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<210> 278
 <211> 1358
 <212> DNA
 <213> Homo Sapiens

<400> 278						
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aatttaagtc	tatccgtgag	accatgaagg	agaagggctt	gctgggggag	ttcctgagga	180
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ccatggccta	catggatgct	gcctactttg	gtgagatcag	catcgggact	ccaccccaga	300
acttctgtgt	cctttttgac	accggctcct	ccaacttgtg	ggtgccctct	gtctactgcc	360
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ccaatgggca	aaccttctcc	ctgcagtatg	gcagtggcag	cctcaccggc	ttctttggct	480
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aatnagcctg	ggtaccaact	tcgtctaagc	gcagtttgat	ggcatcatgg	gcctggcctt	600
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cggttgctct	ttgggggtgt	ggatagcage	ntgtacacgg	ggcagatcta	ctggggcgnt	780
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ctgcaccctc	ctagggcatt	gtatctgtct	ttccactctg	gattcagcct	tctttttctg	1320
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<210> 279
 <211> 702
 <212> DNA
 <213> Homo Sapiens

<400> 279						
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gataatgtta	aaaaactaca	agaagagatt	gagaaaatta	ggccaggctt	tgaggagcaa	120
attttatatc	tgcaaaagca	attagacgct	accactgatg	aaaagaagga	aacagttact	180
caactccaaa	atatcattga	ggctaattct	cagcattacc	aaaaaaatat	taatagtttg	240
caggaagagc	ttttacagtt	gaaagctata	caccaagaag	aggtgaaaga	gttgatgtgc	300
cagattgaag	catcagctaa	ggaacatgaa	gcagagataa	ataagttgaa	cgagctaaaa	360
gagaacttag	taaaacaatg	tgaggcaagt	gaaaagaaca	tccagaagaa	atatgaatgt	420
gagttagaaa	atttaaggaa	agccacctca	aatgcaaacc	aagacaatca	gatatgttct	480
attctcttgc	aagaaaatac	atttgtagaa	caaagtagta	aatgaaaaag	tcaaacactt	540

agaagatacc ttaaaaagaa cttgaatctc aacacagtat cttaaaaaaga tgagggttaac 600
 ttatatgaat aatccttaag tttaaaactt gaaaatggga tgccctcaacc atttttaaagg 660
 gtnagaggttt tttccangna accgggggaa gaccttaaaa gg 702

<210> 280

<211> 874

<212> DNA

<213> Homo Sapiens

<400> 280

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 aacagtgaga tctctgagca catgggtctgt acctcaacca cttttctatc accagggtct 120
 agaatagttg ggcatthtaa taaaatttgc taaatgaatg aaaaatccaa aataaatcat 180
 gaagccattt ataaatcaca ccaatcttgc ttgggttaaa caatagaaaag taacactttt 240
 gaaagagaag gcaaacaggt gttagagggg caagaatgtg agctcgagga aaagacagct 300
 acgaactgtg tttttaacaa ctcattatct ggctactata tttcccaatc tattctaaca 360
 ctaagaagaa tctgtctaata taattgtgac aacatctgca aaaccatagt tacctatttt 420
 ttcttccaac tcttttactg aagacagagg atcatttttt acagaagggtg attttgctaa 480
 ggaatcctan attttacagg ggggaaaaaa aaacacnaaa caaaacaaaa accagaatca 540
 gaattcattt tccataatga actggccatc ntgttaagca taanaaaatc actatcaaag 600
 anaattccta cagaaaccaa tttggtcaca gaatttcocct tggttanacca gaaaattaat 660
 actgaactta ctatgcatat ggcattttact attaaaaaaa aaaaagtant aaccaaggcc 720
 aaganaaaca acctgaaaca ttaaatatcat ntttataagg aaaaantaaa tgaattttta 780
 tcttaatttt aaanaaaaac cnaaaatttt nncatacccc cccgctctta cttaaaaaant 840
 gncttaccaa aataactaanc ctttcccaa aacc 874

<210> 281

<211> 730

<212> DNA

<213> Homo Sapiens

<400> 281

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 ggcccaggct ctgccacac atcctggganaaactgccata ggccctagaa ggagggatga 180
 aaggcgtatg ggagggaana cagcgggtccc cggatcagca gcagcaccac catcctctga 240
 tggcccctgg gcagtcgcc agctcggaag cactcagggc tggagcctgg gctctaagca 300
 tgggccccag gagccanaca ggaggagggc agcaggaang gctggcatgg aagggtctgag 360
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 agcttcttca ggaagcctcc aactgatcct catccttgat gccacaaaac ttgtccacca 480
 cgtccccatt cttcatggcc agcacagtgg gcaccgctga cacctcatac tcaatggcga 540
 agtctgtgtg gtentcaata tccaccttgg ccatcaccac cttcccgctg tgcttggcca 600
 ccattcttct taacctccgn cccangatct tcagggtcca caccactgtg cgtggaaatc 660
 cacaaccact ggtgtctcct gtttgaacac tccgtcttga aantcngtcc ntcctgnata 720
 ttaaagggtg 730

<210> 282

<211> 699

<212> DNA

<213> Homo Sapiens

<400> 282

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 aatttaagtc tatccgtgag accatgaagg agaagggtt gctgggggag ttctgaggag 180

cccacaagta	tgatcctgct	tggaagtacc	gcttttggtga	cctcagcgtg	acctacgagc	240
ccatggccta	catggatgct	gcctactttg	gtgagatcag	catcgggact	ccaccccaga	300
acttctcgtt	ccttttttgac	accggctcct	ccaacttgtg	ggtgccctct	gtctactgcc	360
agagccaggc	ctgcaccagt	cactcccgtc	tcaaccccag	cgagtcgtcc	acctaactcca	420
ccaatgggca	aaccttctcc	ctgcagtatg	gcagtggcag	cctcaccggc	ttcttttggt	480
atgacaccct	gactgtccag	agcatccaan	gtccccaacc	aggagtccgg	cttgagtggg	540
aatnagcctg	ggtaccaact	tcgtctaagc	gcanttttga	tgggatcaag	ggcctggggc	600
taacctgggt	ctgtcccgtt	ggattaaggc	caccacaagc	tatntagggc	nattnggntc	660
aaggatgggt	gtcnctttat	nnagcccccg	tnctttcaa			699

<210> 283

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 283

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tgtgagaacg	tgatgaaaga	cgatatcccc	gtttacacac	aaattcaact	gattcacctg	180
ttctcgaata	aagcttctgt	ttggctgtcc	accttaatgc	tatgttataa	ttttccataa	240
tttctcggga	tattacacac	ggatgtaagc	attttgggtg	ttctgaccat	tgtccatttc	300
tacatgttat	tcgcttggtt	ccctcaagtt	gatacaagtt	ctggcattgg	tactcaactg	360
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gagggggccc	acatttttct	gtagaatctt	tgcattgagg	tggttccgtc	cagtttccat	480
ttaaacacat	cacttcttca	ttccccaaaca	tttcataagg	gtccctacat	tgataacgta	540
ctctctcacc	agatggatat	ttactcatct	gtctcgacac	tatataagca	ttttgtactg	600
tgggcggtat	ccacangang	tgtctctgca	tgttgggctt	cctgtccact	gctattaatg	660
catgtttacat	tactgggtcc	accattttgt	aatatgttgc	acaagtttta	gtccttgctc	720
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<210> 284

<211> 764

<212> DNA

<213> Homo Sapiens

<400> 284

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agttccaaca	tggaatgaag	gacagtctct	tttctcttca	ggatgcagaa	tggtactggg	180
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gcaataataa	gttaataaag	atctatcacc	gggatggtaa	atatggcttt	tctgatcctc	360
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aaggaaatac	agatgaagag	gactgcaata	gaaagctttt	aatgaaaaca	ttaaaatatt	660
tggaaagagca	ntgtcacaca	caaggaacca	acattnccaa	agaatataat	gagnggattt	720
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<210> 285

<211> 586

<212> DNA

<213> Homo Sapiens

<400> 285
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atccccacaa aaagaatgct attccncatc tcagagaaac aggcaggaag gacanaaggg 180
gttagttaca gtgatcaatt ttagcgtttg ctaaaacnca caaattcnag nctttttaag 240
ttcaagtttt ggtacagaag tatacattca actatgagtg ccacgttttc ccatcaaaca 300
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gctggtgaaa tgctgaancc taaattatgt tggnaagaaa caaagtacct tcanttgaag 420
gtttttttta acanctnngc ttaaattatt taaatgaaan cccaagcctc ccnatttncc 480
tttggtngcc ttttncanaa aatcccatc natcacaaa cctaaaaag ccttcttcgt 540
nggggggaaa aaananactg ccaaangcaa aaacaaaaac ncccaa 586

<210> 286

<211> 666

<212> DNA

<213> Homo Sapiens

<400> 286
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agttagcgag ccaatgagag accaagtcgc acggactcat ttgacagagg acactcccaa 180
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gcagtgccat gtcactcttg agggcgctga tatcaagaat ggaactgaaa gaccttcct 600
nagccattga aaccaattga cctactacac aaganactaa agatcttaca ngagaaggca 660
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<210> 287

<211> 782

<212> DNA

<213> Homo Sapiens

<400> 287
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catgaaggaa gaaatgtctg tttttgccgc cctcatcgtc acggaaagag taggggtgcgc 120
tctctgccta gcagaaggag tcacaggctc agagcaaact cattcaaagg atgttatttc 180
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agtggaatgt gccagccagt gcgaccgcga tgggtgtgaa ggtgggctgc agctggatga 420
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gaaagtccac caagttcctc ccaatttcca atcacgaaac ttcaacctg cgttctctgg 720
ctgcctccat gaaggatggg ttacaaactg ccgggttccc tttggggccg aaaaattgcc 780
aa 782

<210> 288

<211> 707

<212> DNA

<213> Homo Sapiens

<400> 288

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gagggaaaga	ctgtgcagta	attgtcacac	agaagaaagt	acctgacaaa	ttattggatt	180
ccagcacagt	gactcaactta	ttcaagataa	ctgaaaacat	tggttgtgtg	atgaccggaa	240
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acaagtatgg	ctatgagatt	cctgtggaca	tgctgtgtaa	aagaattgcc	gatatttctc	360
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ctactgttcc	atcaattgan	ttcaaacctt	cagaaataga	aattgggagt	aatgaacgtt	660
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<210> 289

<211> 673

<212> DNA

<213> Homo Sapiens

<400> 289

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acttccccnn	atttttgact	atgatggcta	gaaaaatgaa	agatacagat	agtgaagaag	180
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aactacgtca	cgtcatgaca	aacttaggag	aaaaactaac	agatgaagaa	gtagatgaaa	300
tgatcagaga	agcagatatt	gatggagacg	gacaagtcaa	ctatgaagaa	ttcgtacaga	360
tgatgactgc	aaaatgaaga	cctactttca	actccttttt	ccccctcta	gaagaatcaa	420
attgaatctt	ttacttacct	cttgcaaaaa	aaaaaaaaat	aagncanaaa	annataaaaa	480
aaaaaaaaacnc	gagagtactt	ctaaagcggc	cgcgggccna	tcgattttcc	acccgggtgg	540
gggtaccagg	aagtgtccca	attcgcccta	taggggagtc	gtattacaat	tcacggggcc	600
gtcgttttta	aaacgtcntg	acgggggaaa	accctggngt	taccaactta	atcccccttg	660
caacaaatnc	ccc					673

<210> 290

<211> 573

<212> DNA

<213> Homo Sapiens

<400> 290

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ccatcaatat	ctgcttcnct	gatcatttca	tctacttctt	catctgttag	tttttcnccn	180
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aagactcgga	atgcctcaag	gatttcttct	tcactatctg	tatctttcan	ttttcnagcc	300
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atcatatcct	gnaattcaan	cttctgttgg	gtnttgacct	antgaccnca	nggacaagtt	420
ccaagttccc	tttggttgtg	aagggtgcca	nctcgtgccc	gaattccttt	gggntccnac	480
ganggggtcna	accctgcana	ggngccgcga	ancctccaan	cttttggttc	ccctttanat	540
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<210> 291

<211> 819

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<211> 762
<212> DNA
<213> Homo Sapiens

<400> 294

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<210> 295
<211> 708

<212> DNA
<213> Homo Sapiens

<400> 295

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gtcctggatg	ataaccatgt	tccaaatgac	taagtgaaga	gacactgtgg	gttcctgcct	660
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<211> 652
<212> DNA
<213> Homo Sapiens

<400> 296

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tggtcctcag	atcaagtgat	tctacggnat	anacgacaag	ctgccctatt	tacacagaag	540
ctgcangaac	tcaagaggga	atgtgggatt	gcccctgggg	agttcaatgg	ttgcangggg	600

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652

<210> 297
<211> 879
<212> DNA
<213> Homo Sapiens

<400> 297

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gaaagacatt cagactgggtc cacgtgggct tgtagcagg cagaggaacc ctgctttcca	240
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gtcttgatg ataaccatgt tccnaaatga ctagtgaaga gacactgtgg tttctgtcct	660
ttaacaaant ggtgtactcc ttgccctcct ccaatantgt ccaaagggt ggtaaaaacc	720
ctttgattaa aggcgtgctg cctgttgagt tccccangg nacttgggac anggganccg	780
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<210> 298
<211> 697
<212> DNA
<213> Homo Sapiens

<400> 298

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aaggacatag ctttggaaacc taaggaacaa aaacatgaag acaggcagag caatacacct	180
tctctcctg ttagtacctt ttcacaggt acttctacca ccagtgatat tgaagtttta	240
gatcatgaaa gtgtaataag tgagagctca gcgagctcga gacaagagac tacagattca	300
aatcaagtc ttcacttgat gcagacatct tttcagcttc tctctgcac tgcttgctcct	360
gaatataatc gtttagatga tttccaaaaa ctactgaga gttgctgttc atctgatgct	420
tttgaaagaa tagactcatt tagtgtacag tcattagata gccggagtgt aagtgaatc	480
aattcaagat gatgaattgt caggcaaggg gatatgcttt agtgcctatt ataagttaat	540
tcttcaactc caaaagtcta aaacagttga atctgccgaa ggaaaatctg aagaagtaaa	600
tgaacatta agttatacca ctgaggaagc agaaatggga agaaaagtgg gcgaaagtgg	660
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<210> 299
<211> 510
<212> DNA
<213> Homo Sapiens

<400> 299

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ttttncctt tatccaanct catcnanaaa acattgaata tgttcagggt tcnnggann	180
ggtncnnaaa ggnncnctt tttatacnga ctttaattgt aaagcngggg gaaataaatt	240
ttcnatcna aatttttttt aagtttaaat cnttccnctt tttaatttct nanagtgtcc	300
gtgtactcc tacttttaaa ggaaaaaat tanttttaaa ttttaatancc cccgatttaa	360

taatttttta	ctttaacnnc	taatgttont	tttcoctgaac	nntaattaan	aatgtttgaa	420
attttaaatg	tnaaanantc	caanttttccg	tntgttaaca	ttacnccctcc	aatgtttcnta	480
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<210> 300
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<400> 300						
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tgaaggaaaa	tctgaagaag	taaattgaaac	attagttata	cccactgagg	aagcagaaat	180
ggaagaaaag	ggacgaagt	caactcctgt	taactgtgaa	cagcctgata	tcttggttct	240
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tgctgaaagt	cagccanaan	cactttctga	caaggaanat	gtttgcaata	cagttgaatt	360
tctgaatgaa	aaagcnggaa	aaaagggang	ctcagttatt	atctcttagt	aaggaaaaag	420
cactttctag	aagaagcttt	ttgatacctg	aananatgaa	atgttcacag	tngaaaggaa	480
naanngcagt	ancattttccn	tccttgaaan	gatttngttt	actcaaagga	attngnnnaa	540
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<210> 301
 <211> 792
 <212> DNA
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tncaaatcaa	aatttttttt	aanttttaaa	catncactct	ttaaatttca	aacagtgtca	300
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taatttttta	ctttaacact	taatgtacat	tttcatganc	agtaattaaa	atatnttgaa	420
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tntgaacacc	attcttcttc	tctagccatn	tttatntgan	gataaagtaa	taaattctctg	600
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aaaataaagt	tcaaatattg	cacaaaaata	atttaactgt	aaatattact	nontagtgtg	720
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 <212> DNA
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ttcagatcaa	aatttttttt	aagttttaa	cattcactct	ttaaatttca	gacagtgtca	300
gtgtgactct	tactttttaa	ggaaaaaaat	tagttttaa	tttaatagcc	acagatttaa	360

taatttttta	ctttaacact	taatgtacat	tttcatgagc	agtaattaag	atatgttgaa	420
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ctggtgctat	tcaaggnaaa	aaaatggaat	gccttaaaaa	aataaaatcc	ttaaagaata	660
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cgtatggaga	gccgggaata	agttcccctg	tcagtggagg	atgggatact	tcaacctggg	360
ggttgaaatc	aaacactgaa	cctcagagtc	caccaatagc	ctctcctaaa	gcaatcacia	420
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aacnaccang	nagaangaan	tgaaaancan	cttacatgaa	tccttgacac	ttggncaant	600
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 <212> DNA
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 <211> 767
 <212> DNA
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<400> 305

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<211> 1659

<212> DNA

<213> Homo Sapiens

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<210> 307

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 307

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<210> 308

<211> 833

<212> DNA

<213> Homo Sapiens

<400> 308

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<210> 309

<211> 1320

<212> DNA

<213> Homo Sapiens

<400> 309

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<210> 310
 <211> 1030
 <212> DNA
 <213> Homo Sapiens

<400> 310						
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ccaaaatgac	aggttcagca	ccacccctt	ctccaacacc	taacaaagag	atgaagaaca	180
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atagattttc	ccagagctgc	tgaggagctt	gatatggaaa	atgaattttt	attaccacct	720
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<210> 311
 <211> 546
 <212> DNA
 <213> Homo Sapiens

<400> 311						
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gctaaaataa	aaagcacaga	aggaaaaaat	aattgatttg	tacataagct	aaattataat	180
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gtttatatga	atatgtttgt	aacagtgaga	tttctgatat	ggtataacaa	agtatatgat	300
tgaggacct	gcaaaatgta	tactcgggtt	gtttttcttt	ttaaaaatat	tgtnaaacag	360
gcaagtgagg	cttaacagca	ttatggttca	ttacnggggt	tgggntatat	acctttttca	420
gcttctgtna	tgagcaagtt	gtgttttcaa	tccccacttt	caatgtctat	gggaagggcg	480
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ccggcc						546

<210> 312
 <211> 518
 <212> DNA
 <213> Homo Sapiens

<400> 312

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ctgggaaana	attgggggtct	ggaataaanc	tncaaattggg	tnccngctt	cactaaaacc	180
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ctnctgctgc	tgttgctgct	gggcantnca	agggaaaacc	cccccgacaa	actgggataa	360
ngtgacctgn	ttgcnacant	ctngggccct	attnccntac	ctgnccctgna	aatncttccc	420
nctctgcccc	ctttactnnt	gccaanncct	tcccccccg	ttaggataaa	aattccccctn	480
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<210> 313

<211> 660

<212> DNA

<213> Homo Sapiens

<400> 313

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gtgcttcaga	agctgctgca	tttgacagt	acgaatcgga	agcagtgggt	gcgacccgaa	180
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tgagtaacct	ttctgctctg	ttgcagcaac	aagaccagaa	agtgaatata	cgcgtggctg	300
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gtacaacctt	ctcagctaca	aatacttgaa	gaaacaagac	aangggactc	aagccantgg	600
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<210> 314

<211> 516

<212> DNA

<213> Homo Sapiens

<400> 314

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aggctgctta	gcccacccag	cctatcacac	tgcccgtccc	acgttgggca	gccacataaa	180
aacacgtcac	agctcaanaa	natccgtgga	tgcacctctg	aatccccccc	aatggtttct	240
gtgcattttt	ttaatatgtt	acaaaatatg	ttaactagga	aaaattagct	gtactgtgac	300
aagtgcggga	cgtcctatta	ggattaccgt	ccccaggca	ttactttctta	ttgcagtaag	360
acctctaaaa	ggtggagctg	tncaaaccac	aaaaaatcta	aacgatttta	agaanagcag	420
caactcaata	ctgctttagt	tcattttaat	tttctttccc	aaaaatacac	tcctaaatat	480
acaaactata	caatcttatt	attttaatgc	tggtttt			516

<210> 315

<211> 677

<212> DNA

<213> Homo Sapiens

<400> 315

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aaatttgctt	tcaaaacaaa	tatactcatt	tcaaagaact	tccaactctt	ctccactgtg	180
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gggcatctaa gatgaaaaat atggagggtt cagacccac acatattgct gaaaggcatg 300
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 cacagaacc agcatttcat catgaaagca ggaagacata cgggcaagag tgcaaatgga 480
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 acacagccca ctaagagggt ggcaagtga gttctgaaag accagtatga tgacttgtan 600
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<210> 316

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 316

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 ggcaatccaa attcaacttg ctacactgaa acaaaaatgt ccgtanatcg tgagttcata 720
 taataacctc cttaatgatc ttctgcaca naaaccaat tcttttcaac ttggggtcaa 780
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<210> 317

<211> 835

<212> DNA

<213> Homo Sapiens

<400> 317

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<210> 318

<211> 582

<212> DNA

<213> Homo Sapiens

<400> 318

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canagctcac caagttcncn ccgtatcaaa ttccanaat acccacaaga tttcttcacc	180
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<210> 319

<211> 827

<212> DNA

<213> Homo Sapiens

<400> 319

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atggaaataa ttaagcttat taaagacaaa agaaaggatg ttagttttcg aaacattggc	180
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<210> 320

<211> 598

<212> DNA

<213> Homo Sapiens

<400> 320

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acacaaactc cttacaaaaa acaagcttat ctataggttc ccacgagctg gtcattctca	300
gtttacaata tgctgtggct gctggcccat gtcactgggc tttcctataa aagctttctt	360
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tggtgtgatg ggtctcgaa ccacacttct cctgtcccc ttcactgaaa gccttggeet	480
ctctcctgtg acagagctcc tcttccgggt catcacattt gctctgacac gtgggnagcc	540
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<210> 321

<211> 808

<212> DNA

<213> Homo Sapiens

<400> 321

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ccgtgcagag	actgggtgct	tcagaagctg	ctgcatttga	cagtgacgaa	tcggaagcag	480
tgggtgcgac	ccgaattcag	attgccctga	agtatgatga	gaagaataag	caatttgcaa	540
tattaatcat	ccagctgagt	aacctttctg	ctctgttgca	ncaacaaaga	ccagaaagtg	600
aatatccgcg	tggctgtcct	tccttgctct	gaaaagcaca	aactgcctgt	tccgggaccc	660
gggctctgga	cgcctcaaac	actccaagt	ttcaatgaag	gtgttctggg	tatccatgg	720
ccctatccaa	accnttaac	aagaaagacc	tttaanaag	tccaatgtcc	ngtnaccaac	780
cggacaaggg	agccaatctt	gggaaaaa				808

<210> 322

<211> 629

<212> DNA

<213> Homo Sapiens

<400> 322

agcaaaataa	atgtcactat	atcaagataa	agaataacat	taggtgtgaa	ctagcatagg	60
tgattcatgg	gaaacgaat	ggcaaattcg	aaaggaatc	tgggaaccat	cgtactagg	120
tacattgctt	ttttgctgt	agagaaccca	tgaggagagg	ggttctcagc	cttcccagtg	180
gaacccttct	cttagttgca	ctggcattgg	gggatctcat	tgtctggcct	aggtccaggc	240
agggcagctc	ctggggccca	agggcgggct	cactcaccag	ctgtcttcca	gtgtctgtgt	300
gctgtcctg	ccctcctgcc	tcttctccaa	ctccactgct	gtctgttcca	acagagcaag	360
acacagcgct	cgtgctggca	ngccctgaag	caagggccat	gactcccact	ggcttgagct	420
ccctgctctg	tttcttcaag	tattttgtan	ctgagaaagt	tgtaccaanc	gaatcnacct	480
ctccccaaga	cggggaagac	ctcccgcaca	ggctgatttg	gggcgcctcc	caagcactct	540
tccaaaatgg	ctcccgctcg	ttgggacana	catccnactt	tttaangcct	tccggggnaa	600
agggctgggn	taaggacatt	gggtncccc				629

<210> 323

<211> 798

<212> DNA

<213> Homo Sapiens

<400> 323

aacatttctg	tgatcaacat	tgttactg	gtttctactg	toaacaaaat	gagcccaaca	60
tgacaactca	gaaaggacct	gaaaacttac	attatgatca	gggttgctag	acatctcgaa	120
ccaaaatgac	aggttcagca	ccacccctt	ctccaacacc	taacaaagag	atgaagaaca	180
aagcagttct	ttgcaaacct	ttaacaatga	caaaagctac	ttactgtaaa	cctcacatgc	240
agaccaaato	ttgtcagaca	gatgatactt	ggaggacaga	atatgttcca	gtgcctatcc	300
ctgtgcctgt	gtatatccca	gttctatgc	acatgtacag	tcagaatatt	cctgttcccta	360
ctacagttcc	tgttcctgtg	ccagttcctg	ttttctgccc	tgtccatttg	gacagcagtg	420
agaagattcc	tgcagcaatt	gaggagctaa	aaagcaagg	ttcttcagat	gctcttgata	480
cagagttgct	tacaatgacg	gatatgatga	gtgaagacga	ggggaaaaca	gagacaacca	540
acatcaacag	tgtaattatt	gaaacagata	taattgggtc	agaccttttg	aagaactctg	600
accagagac	acagtcacgc	atgcctgatg	taccatata	accagatttg	gatatcgaa	660
tagattttcc	cagagctgct	gaaggagcct	tgatatggga	aatgaattt	ttattaccaa	720
ccngtttttg	ggcgaaagaa	tatgaaggaa	caagcccaaa	cctcgattct	aaaaaaaaag	780

<210> 324
 <211> 754
 <212> DNA
 <213> Homo Sapiens

<400> 324

aaaaggacac	taagggtttta	ataaggggaa	caaaaaattg	ttttcaccag	catagattca	60
cattacagta	caccaatatt	gacagcattc	tcttgtctat	ttttggtaca	gaagatggta	120
tctctctaca	taaccttgta	aggcttcagt	aactaaaatg	taaaaccaa	caaaacaaaa	180
ccccaaaaca	aaacaaaaac	cccagcctat	tagtttacag	tttattttta	aaattccgaa	240
agacactgca	agttctaaac	ttttagtagt	gctaccata	cacaaccatc	tggttaagaa	300
cccagtaaaa	gagccccctt	ccaaggaagc	tttgcaacag	tagagttgtg	caatatggat	360
gttcttact	acaagaaaaa	aattatacat	ggcacattct	cattcatatt	ctgtaatgta	420
aaaagttaca	aacataccta	atcaataaaa	taataataaa	aaaagaattt	gaatgtattt	480
gttaagtatc	ctaaaaccac	tacatagaat	aatggcaact	ttcactcaca	gattattttac	540
atggtaatac	ccagcgtggg	tacactgcta	caaaactcaa	aacagaagga	gtaaacttga	600
aatgttttcc	ataataaaga	tctagcanca	tgactatcct	aatgccgttt	tatcccgaat	660
gcttctggca	acgttccctt	ttaatccggt	gtctcatcca	attcaaaaan	tggcctttac	720
caaaaaatat	cctttttaca	gaaagaaacc	cggt			754

<210> 325
 <211> 854
 <212> DNA
 <213> Homo Sapiens

<400> 325

ggtcaggggt	gagagctgga	atctctgcac	gggccttgga	aaacgactgt	cttcttctgc	60
caaaatgtca	ggaattggaa	ataaaagagc	agctggagaa	cctggcacct	ccatgcctcc	120
tgagaagaag	gcagctgttg	aagattcagg	gaccacagtg	gaaacaatta	agctaggagg	180
tgtctcttca	acggaggaac	tagacattag	aacactgcaa	accaaaaaatc	gcaagctggc	240
agaaaatggt	gatcagcggc	aggccattga	agatgaactt	cgtgagcaca	ttgaaaaact	300
ggaacgacga	caggccactg	atgatgcctc	actattgatt	gtcaaccgat	actggagtca	360
gtttgatgaa	aacatccgta	tcatccttaa	acgttatgat	ctggagcagg	gcttgggaga	420
cctactcaca	gaacgaaaag	cccttggttg	gcctgaacca	gaaccagact	ctgatagcaa	480
tcaggagcgt	aaagatgacc	gagagagagc	agttccagtg	aagagatgga	gtctcagctg	540
caggaacgtg	tggagtcttc	ccgccgagcc	gtgtcccaga	ttgtgactgt	ttatgataaa	600
ttgcaagaaa	aagtggagct	cttatcccgg	gaagctaaac	agtgaggagat	aatctgatag	660
tggaggggaag	canttgaag	gagctgaact	ctttcctcgc	acaaggagaa	tattaaggct	720
acanggaatt	gacaagatct	tcctcaggaa	aaagcatcgc	aaccatggtc	tcaaggngtt	780
cctccaaagt	tgcaagaggt	aaaattgggg	naaaagccga	attcaccaan	tttccgggtcc	840
tggaaagtcca	anga					854

<210> 326
 <211> 760
 <212> DNA
 <213> Homo Sapiens

<400> 326

caaactgaat	cctgctttta	ttcaagcttg	tggagaacaa	agtcctacag	aaacattcca	60
cagaattttc	tggaaaagag	ggatcacaa	aacctgtaa	aaaggagact	gagagtaatt	120
catagctcac	caagttctct	ccgtatcaaa	tttcagaaat	acccacaaga	tttcttcacc	180
agctcagtc	tgactcaacc	tcttcaatct	ttatttcatt	agaagacaaa	gggtcatatt	240
atttaaaatt	attctagtct	caagaaattt	aaagacttga	agtagtagag	cattcaaaac	300

ttaaataact	ttaacaagaa	agccagctga	tottaacaag	ttactctgct	agtaaattggg	360
aaatagactg	aatcatccta	gacataatTT	cattagggct	gcaaaccacc	caggggagag	420
tagcacaatt	ataccatttt	gtaatccaca	ttcacaagaa	gtttgctaca	caaatagaaga	480
aaactttgtg	cccatagaca	acttattttt	taaaatatca	ctccccaaaa	gtagccatgt	540
ttccactttt	gttccctttt	ccacatcaaa	aataccaact	tgattttctt	aggaggaatg	600
gacaatccaa	gtttatacaa	gtgggctggg	aaaaagaaaa	cactgaaaag	tctaaaagca	660
caagataaaç	aaagcctggg	aagggaagac	agttaagagt	tatttgtttc	caantcaatc	720
cnaaaaccca	anggcttgta	attaacaagt	cctttccggc			760

<210> 327

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 327

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gcagacccaaa	tcttgtcaga	cagatgatac	ttggaggaca	gaatatgttc	cagtgcctat	120
ccctgtgcct	gtgtatatcc	cagttcctat	gcacatgtac	agtcagaata	ttcctgtttcc	180
tactacagtt	cctgttcctg	tgccagttcc	tgTTTTtctg	cctgctccat	tggacagcag	240
tgagaagatt	cctgcagcaa	ttgaggagct	aaaaagcaag	gtttcttcag	atgctcttga	300
tacagagttg	cttacaatga	cggatatgat	gagtgaagac	gaggggaaaa	cagagacaac	360
caacatcaac	agtgtaatga	ttgaaacaga	tataattggg	tcagaccttt	tgaagaactc	420
tgaccagag	acacagtcca	gcatgcctga	tgtaccatat	gaaccaagat	ttggatatcg	480
aaatagatTT	tcccagagct	gctgaggagc	ttgatatgga	aatgaattt	ttattaccac	540
ctgttttttg	cgaagaatat	gaggaacagc	ccaagacctc	gatctaaaaa	aaaagggagc	600
caagagaaan	gctgtatcaa	ggataccaag	tctcatgatg	ataagtctga	caatttcaga	660
atgcagcTT	cctttcaaat	tatacgatg	ggcgtaaatg	catgggnaac	accgggtcaa	720
aaactaagnn	acttgatga	aagatcTcc	gggnaattag	aatgagttaa	aatccttcca	780
aatccantna	agtttaaaag	agggTntaat	ccctcaaaa	ccanagctgg	ngccttaaca	840
aggggggttaa	cc					852

<210> 328

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 328

aaaaggacac	taaggTTTT	ataaggggaa	caaaaaattg	ttttcaccag	catagattca	60
cattacagta	caccaatatt	gacagcattc	tctgtctat	ttttggtaca	gaagatggta	120
tctctctaca	taaccttgta	aggcttcagt	aactaaaatg	taaaacccaa	caaaacaaaa	180
ccccaaaaca	aaacaaaaac	cccagcctat	tagtttacag	tttattttta	aaattccgaa	240
agacactgca	agttctaaac	ttttagtagt	gctaccata	cacaaccatc	tggttaagaa	300
cccagtaaaa	gagccccctt	ccaaggaagc	tttgcaacag	tagagttgtg	caatatggat	360
gtttcttact	acaagaaaaa	aattatacat	ggcacattct	cattcatatt	ctgtaatgta	420
aaaagttaca	aacataccta	atcaaataaa	taataataaa	aaaagaattt	gaatgtattt	480
gttaagtata	ctaaaaccac	tacatagaat	aatggcaact	ttcactcaca	gattattttac	540
atggtaatac	ccagcgTggg	tacactgcta	caaaactcaa	aacagaanga	gtaaacttga	600
aatgttttcc	ataataaaga	tctagcaaca	tgactatcca	atgotgtttt	atcccagattg	660
cttctgcaac	gttcctttta	atccgtgtct	catccagttc	anaantgtcc	ttatcaanaa	720
taacctttac	tagaagaaac	cgtncagca	tattttcaan	gggtttccgg	tccaattgaa	780
gttanacgtn	taccaaaca					799

<210> 329

<211> 978

<212> DNA

<213> Homo Sapiens

<400> 329

ggaagatggc	ggcggccggt	ccacagcggg	cgtggaccgt	ggagcagctg	cgcagtgage	60
agctgcccaa	gaaggacatt	atcaagtttc	tgcaggaaca	cggttcanat	tcgtttcttg	120
cagaacataa	attattagga	aacattaaaa	atgtggccaa	gacagctaac	aaggaccact	180
tggttacagc	ctataaccat	ctttttgaaa	actaagcgtt	ttaagggtac	tgaaagtata	240
agtaaaagtgt	ctgagcaagt	aaaaaatgtg	aagcttaaata	gaagataaac	ccaaagaaac	300
caagtctgaa	gagaccctgg	atgaggggtcc	cccaaaatat	actaaatcct	gttctgaaaa	360
aggagataa	aaccaacttt	cccaaaaagg	gagatgttgt	tactgctgg	tatacaggaa	420
cactacaaga	tgggactgtt	tttgatacta	atattcaaac	aagtgcagg	aagaagaaaa	480
atgccaaagcc	tttaagtttt	aaggctggag	taggcaaagt	tatcagagga	tgggatgaag	540
ctctcttgac	tatgagtaaa	ggagaaaagg	ctcgactgga	gattgaacca	gaatgggctt	600
acggaaagaa	aggacagcct	gatgccaaaa	tccnccaaa	tgcaaaactc	acttttgaa	660
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tgataaaact	tggccttgaa	gaaatttacn	caactagtta	gaacttgta	ctattgtaaa	780
ggaagagtca	actggaaaat	tcaaggagtt	aataaaattt	gtttacttgg	tcccagcttt	840
tgagagataa	atcccttatg	aatccctggt	ctaaaatact	ttcctacagc	tgtgtaaaat	900
actggtcaag	gagaactttt	tccttttacc	tcattgttga	aacttaagt	gctcaataaa	960
aattgatccn	ctgtcttg					978

<210> 330

<211> 1017

<212> DNA

<213> Homo Sapiens

<400> 330

cgatcggcgg	agctcccacc	tccgcttaca	gctcgtgccc	gccgtcctgc	cccgcgcccc	60
caggagacct	ggaccagacc	acgatgtgga	aacgctggct	cgcgctcgcg	ctcgcgctgg	120
tggcggctgc	ctgggtccgc	gccgaggaag	agctaaggag	caaatccaag	atctgtgcca	180
atgtgttttg	tggagccggc	cggaatgtg	cagtcacaga	gaaaggggaa	cccacctgtc	240
tctgcattga	gcaatgcaaa	cctcacaaga	ggcctgtgtg	tggcagtaat	ggcaagacct	300
acctcaacca	ctgtgaactg	catcgagatg	cctgcctcac	tggatccaaa	atccaggttg	360
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gctatcagtc	caaccgtgat	gagctccgac	gtcgcacatc	ccagtggctg	gaagctgaga	480
tcattccaga	tggctgggtc	tctaaaggca	gcaactacag	tgaaatccta	gacaagtatt	540
ttaagaactt	tgataatggg	gattctcgcc	tggactccag	tgaattcctg	aagtttgtgg	600
aacagaatga	aactgccatc	aatattacaa	cgtatccaga	ccaggagaa	aaagaagttg	660
ttaggggact	ctgtgttgat	gctctcattg	aactgtctga	tgaaaatgct	gattggaaac	720
tcagcttcca	agagtttctc	aagtgcctca	acccatcttt	caaccctcct	gagaagaagt	780
gtgccctgga	ggatgaaacg	tatgcagatg	gagctgagac	cgaagtggac	tgtaacccgc	840
tgtgtctgtg	cctgtggaaa	ttgggtctgt	cagccatgac	ctgtgacnga	aagaatcaga	900
agggggccca	gacccagacn	gaggangaga	tgancngata	tgtccaggag	ctccaaagct	960
taggaaacag	cttgaaaaga	nccagagagg	gagcccccaa	agagattatg	aggaggc	1017

<210> 331

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 331

cccagaaaga	tcatacacagt	ttctgtaaaa	gaagatgtac	acctgaaaaa	ggcagaaaat	60
gcctggaagc	caagccaaaa	acgagacagc	caagccgatg	atcccgaaaa	cattaaaacc	120
caggagcttt	ttagaaaagt	tcgaagtatc	ttaaataaat	tgacaccaca	gatgttcaat	180
caactgatga	agcaagtgtc	aggacttact	gttgacacag	aggagcggct	gaaaggagtt	240

attgacctgg	tctttgagaa	ggctattgat	gaacccagtt	tctctgtggc	ttacgcaaac	300
atgtgtcgat	gtctagtaac	gctgaaagta	cccatggcag	acaagcctgg	taacacagtg	360
aatttcggga	agctgctact	gaaccgttgc	cagaaggagt	ttgaaaaaga	taaagcagat	420
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cagtacttta	atcagatgga	gaaaattgtg	aaaggaaaga	aaaacctcat	ctaggatcgg	780
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<210> 332

<211> 881

<212> DNA

<213> Homo Sapiens

<400> 332

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caggagacct	ggaccagacc	acgatgtgga	aacgctggct	cgcgctcgcg	ctcgcgctgg	120
tggcggctgc	ctgggtccgc	gccgaggaag	agctaaggag	caaatccaag	atctgtgcca	180
atgtgttttg	tggagccggc	cgggaatgtg	cagtcacaga	gaaaggggaa	ccacctgtc	240
tctgcattga	gcaatgcaaa	cctcacaaga	ggcctgtgtg	tggcagtaat	ggcaagacct	300
acctcaacca	ctgtgaactg	catcgagatg	cctgcctcac	tggatccaaa	atccaggttg	360
attacgatgg	acactgcaaa	gagaagaaat	ccgtaagtcc	atctgccagc	ccagttgttt	420
gctatcagtc	caaccgtgat	gagctccgac	gtcgcacatc	ccagtggctg	gaagctgaga	480
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tgtgcccttg	gaggatgaaa	cgtatgcaan	atggagcttg	aaancgaggt	ggactgtaan	840
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<210> 333

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 333

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agaggcctgt	gtgtggcagt	aatggcaaga	cctacctcaa	ccactgtgaa	ctgcatcgag	120
atgcctgcct	cactggatcc	aaaatccagg	ttgattacga	tggacactgc	aaagagaaga	180
aatccgtaag	tccatctgcc	agcccagttg	tttgcataca	gtccaaccgt	gatgagctcc	240
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tgtcagccat	gacctgtgac	ngaaagaatc	agaagggggc	ccagaccag	acngaggang	720
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aggagacccc	caaagagatt	atgaggaggg				810

<210> 334

<211> 808
<212> DNA
<213> Homo Sapiens

<400> 334

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caagttaaat	gcaatataga	agcctactaa	atacaaatac	aagttcacia	acacatatgc	120
aacagaaaact	tgttttagatt	gtttcttgaa	gtttgactac	ttaaaaacat	aggtgtaaag	180
gaaagacatt	cagactgggc	cacgtgggct	tgtagcagg	cagaggaacc	ctgctttcca	240
aaaactgata	tagtccagag	tcacggcatg	tgggaatgtt	tccatggaca	ctggatctta	300
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ctaagcccta	tgtctttaga	gggctgaagg	aaccaaact	agtttaatcc	tgtttgtttg	420
ctccatgcaa	aactttatgg	aagactcccc	agactaggct	atttagcagc	ttccatgaat	480
ggctctcaga	tcattgtgatt	ctacggcata	gacgacagct	gccctattta	cacagaagct	540
gcagaactca	agaggaatgt	ggatttgctc	ttgggaagtt	caatgttgca	gggttaaagta	600
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atttcaaact	ggaccaagtg	gaggtttg				808

<210> 335
<211> 758
<212> DNA
<213> Homo Sapiens

<400> 335

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aggctaaaat	agaagaacaa	gaagagcaaa	ggaaggtcca	gcaactcatg	accaaagaga	120
agagaagacc	aggtgtccag	agagtggacg	aaggtgggtg	gaacactgta	caaggggcca	180
agaacagtcc	ggtaactggac	ccctcaaaat	tcctaaaaat	cactaagcct	acaattgatg	240
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gagcaaaaggc	aagtgtgagact	gatgccttac	ggtcaagtgc	ttccagttta	aacagattct	360
ctgccctgca	actctcagca	ccctcagggt	ccacgccatc	cacgcctgta	gagtttgatt	420
cccgaaggac	cttaactagt	cgtggaagta	tgggcaggga	gaagaatgac	aagcccttc	480
catctgcaac	agctcggcca	aatactttca	tgaggggtgg	cagcagtaaa	gacctgctag	540
acaatcagtc	tcaagaagag	cagcggagag	agatgctgga	gaccgtgaag	cagctnacan	600
gaggtgtgga	tgtggagagg	aacagccttg	agctgaaccg	aaataaacia	gggagtcagc	660
aaaaccccca	aanttcagca	atgtcagctt	attgacaagg	gttgattatc	agaagaggac	720
tgganaggaa	gtccaaatct	atcatggtta	attttttc			758

<210> 336
<211> 785
<212> DNA
<213> Homo Sapiens

<400> 336

aaacttgcaa	tgtttgtctt	tattttgttc	tttatatttt	caaagtgaag	agaaatagta	60
ctgagtcaat	ttctttttgt	tttttttaaa	atttgttcta	tgtattttaca	agccttaaag	120
ttgctctaaa	gattttcaaga	gtattaagag	tactttttct	agggtagcac	tttttttttt	180
tttaaacaat	tcttggagtt	ctgtgggtcca	cagcatttcc	ttctgtttca	atgttatgta	240
cgttttgatt	actattngna	tttttttaaa	tttctgaagc	aagctgagag	gcaggcagaa	300
agatttgatg	ccaaaaaaaa	aaaaatcttt	cttaccttgt	tcaccccaaa	ctttctcaaa	360
tctggactaa	atgctatacc	ttaaaacaaa	catgaggngc	atcttgaagg	ggagggaaat	420
ttattttctc	gctttttctat	tatacaagtt	gtttacagaa	actgcaaatt	aaaaaattac	480
actggcattt	gcagtcctta	aaataaatta	aaagttctca	actttttttt	ttttgctaaa	540

cattttttta agtatgagtc cttgttttaa aagaaaagat taaaacagaa aatattttct 600
 ataaatacnt gnattttggg ttttaagggct cccgccctaa ggnttgaagg ttacttttat 660
 cccaggaccc tttttcctcc atggaacccc tttttttcnc ttttcctttt tcccacttgc 720
 ngccncccnt nggggggttc tggcaaaaaa tggcccttgc tgcncgtggg aattggccaa 780
 aaacc 785

<210> 337

<211> 643

<212> DNA

<213> Homo Sapiens

<400> 337

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 cagaacataa attatttagga aacattaaaa atgtggccaa gacagctaac aaggaccact 180
 tggttacagc ctataaccat ctttttgaaa actaagcgtt ttaanggtac tgaangnta 240
 nntaaagtgt ctgancaagt naaaaatgnn aancttantg aagataancc caaagaaacc 300
 aagtntgang agaccctgga tgaggggtcca ccnaaatata ctaaatctgn tctgaaaaag 360
 ggagataaaa ccaacttttc caaaaaggga gatgttggtc actgctggta tacaggaaca 420
 ctacaagatg ggactgtttt tgatactaat attcaaaca gtgcaaagaa naagaaaaat 480
 gccaaagcctt taagttttaa ggtcggagta cgcaaaagtt atcanaggat ggggatgaag 540
 ctctcttgac tatgagtaaa ggagaaaagg ctngactgga aaatggaccc aaaatggctt 600
 accggaaaaga aagggaacag ctgatnccaa aatttcccca aat 643

<210> 338

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 338

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 taagggattt atctctcaaa agctgggacc aagtaaaca attttattaa ctcttgaat 180
 tttccagttg actcttctt tacaatagta acaagttcta actagttgng taaatttctt 240
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 caatatccac taattccact tcaaaagtga gttttgcatt tggnggaatt ttggcatcag 360
 gctgtccttt ctttccgtaa gccattctg gttcaatctc cagtcgagcc ttttctcctt 420
 tactcatagt caagagagct tcatcccatc ctctgataac tttgcctact ccgaccttaa 480
 aacttaaagg ctgggcattt ttcttctctt ttgcacttgt ttgaatatta gtatcaaaaa 540
 cagtcccatc ttgtagtgtt cctgtatacc agcagtgaac aacatctccc tttttgggaa 600
 agttggtttt atctccctt ttcagaacag gatttagtat attttggggg accctcatcc 660
 agggctctct cagacttggt ttctttgggt ttatcttcat ttaagcttca cattttttac 720
 ttgctcagac actttactta tactttcagt acccttaaaa ccgcttaagt ttcaaaaaag 780
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<210> 339

<211> 758

<212> DNA

<213> Homo Sapiens

<400> 339

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 cagtagctgt cagagggaaa gactgtgcag taattgtcac acagaagaaa gtacctgaca 180
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tgatgaccgg	aatgacagct	gacagcagat	cccaggtaca	gagggcacgc	tatgaggcag	300
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ccgatatttc	tcaggtctac	acacagaatg	ctgaaatgag	gcctcttggt	tgttgatga	420
ttttaattgg	tatagatgaa	gagcaaggcc	ctcaggtata	taagtgtgat	cctgcaggtt	480
actactgtgg	gtttaaagcc	actgcagcgg	gagttaaaca	aactgagtca	accagcttcc	540
ttgaaaaaaa	agtgaagaag	aaatttgatt	ggacatttga	acagacagtg	gaaactgcaa	600
ttacatgcct	gtctactggg	ctatcaattg	atttcaaacc	ttcagaaata	gaagttggag	660
tagtgacagt	tgaaaatcct	aaattcagga	ttottacnng	aagcagagat	tgatgcttac	720
cttgtgnntt	agcngagagg	agacttaacc	attggccg			758

<210> 340

<211> 840

<212> DNA

<213> Homo Sapiens

<400> 340

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ggtaagtggc	atcacggatc	tggtaaacta	acgacaatgt	ttagtctctc	tctgctagag	180
caacaagggtg	agcatcaatc	tctgcttctg	taanaatcct	gaatttagga	ttttcaactg	240
tcactactcc	aacttctatt	tctgaagggt	tgaaatcaat	tgatagaaca	gtagacaggc	300
atgtaattgc	agtttccact	gtctgttcaa	atgtccaatc	aaatttcttc	ttcacttttt	360
tttcaaggaa	gctgggtgac	tcagtttgg	taactccgc	tgcagtggct	ttaaaccac	420
agtagtaacc	tgcaggatca	cacttatata	cctgagggcc	ttgctcttca	tctataccaa	480
ttaaaatcat	acaacaacca	agaggcctca	tttcagcatt	ctgtgtgtag	acctgagaaa	540
tatcggcaat	tctttttacac	agcatgtcca	caggaatctc	atagccatac	ttggatttcc	600
agttagctgc	ctcatagccg	tgccttctg	tacctgggat	ctgctgtcag	ctgcattccg	660
gtcatcacac	aaccaatggg	ttcagttatc	ttggaataag	tgaggctact	gngctggaat	720
nccaataatt	tggcaggnac	actttctttt	gggngacaa	ttactggccc	agtcttttcc	780
tttggacagn	tactggaggt	aaagggccacc	ctgggttaat	agccctttaa	aggcntaatc	840

<210> 341

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 341

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caagttaa	gcaatataga	agcctactaa	atacaaat	aaagttcaca	acacatatgc	120
aacagaaact	tgtttanatt	gtttcttgaa	gtttgactac	ttaaaaaacat	aggngtaaag	180
gaaagacatt	canactggtc	cncgngggct	tgntagcagg	cagaggaacc	ctgctttcca	240
aaaactgnta	tagtccanan	tcncggcatg	ngggaatgnt	tccatggacn	ctggatctta	300
acagatgcta	tagggtttac	aaaactacnc	acncagagaa	agcccaagga	agcctgcagg	360
ctaagcccta	tgctttttaga	gggctgaagg	aaccaaacc	agtttaatcc	tgtttgnttg	420
ctccatgcaa	aacttttttg	aaactcccc	agactaggct	ttttancagn	nttccattga	480
atggggcnnc	aaancnttg	gaattttacg	gntnaaan	aaagntngcc	ttntttnc	540
ccgaaagctt	tgaaaaactt	ttcagnggg	atnggggaat	ttggnttntt	ggggnngttc	600
aattgttncc	ngggtaaaaa	ganacccttg	gggaggnaaa	ccctgngtt	tnaannggcc	660
ttaggggaaa	naaccnttg	gggtntcntt	ggnnttttaa	caaaattggg	gggncntttt	720
ggnccttcc	cccaaaaggg	ggcccanggn	ctngggaaaa	aaccttttgg	antaaggggg	780
gncccnctt	gga					793

<210> 342

<211> 906

<212> DNA

<213> Homo Sapiens

<400> 342

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agggtcggct	ctaccaagta	gaatatgctt	ttaaggctat	taaccagggt	ggccttacat	120
cagtagctgt	cagagggaaa	gactgtgcag	taattgtcac	acagaagaaa	gtacctgaca	180
aattattgga	ttccagcaca	gtgactcact	tattcaagat	aactgaaaac	attggttgtg	240
tgatgaccgg	aatgacagct	gacagcagat	cccaggtaga	gagggcacgc	tatgaggcag	300
ctaactggaa	atacaagtat	ggctatgaga	ttcctgtgga	catgctgtgt	aaaagaattg	360
ccgatatttc	tcaggtctac	acacagaatg	ctgaaatgag	gcctcttggg	tgttgtatga	420
ttttaattgg	tatagatgaa	gagcaaggcc	ctcaggtaga	taagtgtgat	cctgcagggt	480
actactgtgg	gtttaaagcc	actgcagcgg	gagttaaaca	aactgagtca	accagcttcc	540
ttgaaaaaaa	agtgaagaag	aaatttgatt	ggacatttga	acagacagtg	gaaactgcaa	600
ttacatgcct	gtctactgtt	ctatcaattg	atttcaaacc	ttcagaaata	gaagttggag	660
tagtgacagt	tgaaaatcct	aaattcagga	ttnttacaga	agcagagatt	gatgtccacc	720
ttgttgctct	agcagagaga	gactaaacat	tgtcgttagt	ttaccagatc	cgtgatgcc	780
cttacctgtg	tgtttggtta	caacaaacca	acatcatgga	ggcccttgga	ttgaaaaagg	840
agcctctccc	actcctccta	ccaccgaagt	ggtaggact	ctatataaat	aaaacaaggc	900
ttttgg						906

<210> 343

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 343

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tcgaggtgtt	tttaccacca	agactaaaaa	aagataggaa	aaacttggtg	gagacccgat	120
tgcacatcac	tggcagagaa	ctgaggtcca	aaatagctga	aacctttgga	cttcaagaaa	180
attatatcaa	aattgtcata	aataagaagc	aactacaact	agggaaaacc	cttgaagaac	240
aaggcgtggc	tcacaatgtg	aaagcgatgg	tgettgaact	aaaacaatct	gaagaggacg	300
cgaggaaaaa	cttccagtta	gaggaagagg	agcaaaatga	ggccaaaact	aaagaaaaac	360
aaattcagag	gaccaagaga	ggactagaaa	tactggcaaa	gagagcagca	gagacagtgg	420
tggatccaga	aatgacaccg	tacttagaca	tagctaacca	gacaggcaga	tcaatcagaa	480
ttcccccatc	agaaaagaaa	gcccttatgt	tagctatggg	atatcatgag	aagggcagag	540
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tggatatagt	gtgggtgttac	tttcgcctgg	aacagctgga	atgccttgat	gatgcagaaa	720
aaaaattaac	ttggnccaga	aatgctttaa	aaattggtcc	ggagaaatcn	tcgaaactgg	780
tccccntaaa	nggaattgtg	gggaaaagag	aangtctggg	tctaagactn	tacttacttt	840
nagggatccg	aactttttcca	gggggaatga	tgtaa			875

<210> 344

<211> 629

<212> DNA

<213> Homo Sapiens

<400> 344

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cccatcagtc	caaactggac	caccacact	ttgaaaaagt	tggagcattt	cagccggctc	120
cgcgatgacc	atcctgtctt	cagtcagtgc	cttctggaag	ggagggaaag	tcttggtatgc	180
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gccgacacac	agcgaactac	atacttttag	aaagagcctc	tgtcacatgg	ctagaacaac	360
aacaacaaca	aagaaaaccc	acaaaaaacc	tggagaaaat	atatctaaat	ctctgatagg	420

tctcttagct	agcagtgagt	tcagtatgac	agcacagagt	ctaaaaatat	taattaaata	480
taaattgctt	tggtttagcat	ttaaaccctt	cccattcaat	agaagatttc	tgtaatgagg	540
aatgctgaat	atatataaag	cctgccactc	aatctttgaa	tttcnggggg	cgcaatttta	600
ctgaactaag	ancctaaaa	caactggcg				629

<210> 345

<211> 724

<212> DNA

<213> Homo Sapiens

<400> 345

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ctttcatttt	aaaaagttat	atttaatttt	tgggggcctt	aattaaaatt	taacatttta	180
ccatgngtnn	tttttttgta	aacagttctac	atgtcaacaa	atggataagg	gttaacaaaag	240
gcaaatnctg	acttcatttg	tgtttttaac	acgattatat	gaatttttct	tttttaatta	300
aaaaaatgac	ataaaacat	tcatataggt	cctcttctct	caactgcttt	gagatatagc	360
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tcagctccaa	tggaaattnc	tcatagcact	tcttacagac	tggcttcatt	tcaaactcca	540
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accaggcctt	attaagagca	gagaccccca	tcaccttcta	taacacgatt	gcagtgaggaa	660
gcaaacatca	ccaaatatgt	gggttatagn	gagtttcaca	atatgccag	gcctttcctt	720
tcaa						724

<210> 346

<211> 907

<212> DNA

<213> Homo Sapiens

<400> 346

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tactgatgca	gaaagacgat	cagtgatgga	tgcaacacag	attgctggtc	ttaattgctt	180
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tcaagtttct	gtatgtgcat	ttaatatagg	aaaactgaaa	gttctggcca	ctgcatttga	360
cacgacattg	ggaggtagaa	aatttgatga	agtgttagta	aatcacttct	gtgaagaatt	420
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ggagtgtgag	aaactcaaga	aattgatgag	tgcaaatgct	tcagatctcc	ctttgagcat	540
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<210> 347

<211> 711

<212> DNA

<213> Homo Sapiens

<400> 347

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tnaaattcct	ggaaacgtat	nttaatagg	tgacctaaat	tttttaattc	agccaactta	540
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ccagtttcaa	agtaaaactg	ttacgancat	nttcactnnc	aaacttctca	tattcnccac	660
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<210> 348

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 348

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caatttgttt	cttagcttct	tcttggaagg	ctcggtattc	atcctctacc	ttagcaatgg	420
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gctgagcctt	caggcgattc	atctctatct	ggtcactggc	cactgnggcb	ttgnattcct	660
ctaacgtggc	tgncaaaggc	gcttttcctt	tctgctcnac	tcaaataaat	tcgctccata	720
tggngggact	ggcgttcctt	tggagtggcc	cctatcattt	cttggngctb	tccttantgg	780
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<210> 349

<211> 832

<212> DNA

<213> Homo Sapiens

<400> 349

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aacaaaatta	tttttttaaaa	aagcaaaaaga	ataaagaata	tatacaaaaag	ggacctggaa	180
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gaggtgtgtc	tatacataaa	cttcagtcac	ttttgcttgt	gcagaatcat	cccaatcttc	360
ccaagactga	atgggcagtc	ctgtggcttt	cttctttttc	catattccca	acaaggctac	420
gtgaagttca	actcttgatg	agccgcttac	aacagcagtt	ccttaggagc	caacatgaca	480
ggtgggtcag	atttccctat	gagaaacaaa	actggccacc	tacagcaaaa	tatcaaaatg	540
ggtaagtcc	tccttctctc	tcctcctgat	tatatataac	atatctcctt	tcaagactat	600
tatttccatc	atgcttattc	cttcacaaat	ctaaaccttg	aggtgatatg	aaggaaacca	660
acatcangaa	aagaaaactc	aattcagaaa	tgaagaaaac	tggcaggtat	acaatacacc	720
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ggattaaata	attgggcagc	ttgggaataa	agctcatttt	tttnccctca	gg	832

<210> 350
 <211> 782
 <212> DNA
 <213> Homo Sapiens

<400> 350

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tnaaanaang	cgnancacna	ancatngact	aatncaaggg	cttnaaatat	gaancaaaat	120
natttttttaa	aaaagcaaaa	naataaanaa	tatatncaaa	ngggaccngn	aatcngnaag	180
cngatnccaa	aaccnaaata	agtaaaaaan	ccanggggaa	nccngancat	tcnacctnng	240
nttngnaaaa	gggctatcat	ncaacattca	gncagntgaa	nanggatnng	nanaggnggg	300
ncnatncata	anccttcagnc	attttngctn	gggcaaaatc	atcccaatnt	tcccaanact	360
gaanggncag	cccnggggct	ttcttccctt	nccanattcc	caacanggnt	acnggaagtt	420
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aaatttccct	atgagaanca	aaacngggca	cctacagcaa	aatatcaaaa	ggggnaagnc	540
cttcttccct	cttctctcng	attatatnca	ccatatctcc	tttcangact	atnatttcca	600
tcaggctnat	tccttcacaa	atntaaacct	tgaggggata	tgaaggaacc	caacttcngg	660
aaangaaaac	tcaattcana	aattgaagaa	acctggcagg	tatacaatac	ccccccaggn	720
catntcaana	tccttggcac	aagnnccaat	tcagggncct	ggtaccagcc	ccatagaana	780
aa						782

<210> 351
 <211> 775
 <212> DNA
 <213> Homo Sapiens

<400> 351

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tgagaccaca	ggagttgaca	tcaactaaaat	tcaagtcaag	agatgtgaga	ccatgagaga	180
gaagcacatg	cagaaacagc	aggagagggg	aaaatcagtc	ttgacacctc	ttcgggggaga	240
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cacacggcac	ctgaccaagc	ggcttcccac	aaagtcaccc	cagaagggtg	aggtagaaac	360
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gggtaaagct	aaacccaaaag	tgaacgtgaa	gccatctgtg	gttaaagttg	tgtcatcccc	480
caaattggcc	ccaaaacgta	aggcagtgga	gatgcacgct	gctgtcattg	ccgctgtgaa	540
gccactcagc	tccagcagtg	tcctacagga	acccccagcc	aaaaaggcag	ctgtggctgt	600
tgtcccgcct	gtctctgagg	acaaatcagt	cactgtgcct	gaagcagaaa	atcctagaga	660
cagtctttgt	gcttgncttc	aacccagtc	ttnttcagat	tccttaccct	cagaggtgtc	720
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<210> 352
 <211> 865
 <212> DNA
 <213> Homo Sapiens

<400> 352

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tatttttttaa	aaaagcaaaa	gaataaagaa	tatatacaaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacgaaata	agtagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	gatggattgg	tagaggtgtg	300
tctatacata	aacttcagtc	atttttgctt	gtgcagaatc	atcccaatct	tcccaagact	360
gaatgggcag	tcctgtggct	ttcttccctt	tocatatcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaacatga	caggtgggtc	480

agatttccct	atgagaaaca	aaactggcca	cctacagcaa	aatatcaaaa	tgggtaagtc	540
cttccttcct	cttcctcctg	attatatata	acatatctcc	tttcaagact	attattttcca	600
tcatgcttaa	tncttccaaa	tctaaacctt	gaggngatat	tgaanggaaa	cccaccttca	660
nggaaaagaa	aacctcaatt	tcagaaatgg	aagaaaaact	ggcaggggat	accaatacac	720
ccccccagag	cattttttaa	atatccctgg	ncacaagtnc	caattcaagg	gnacctgggt	780
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<210> 353

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 353

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caaaattatt	ttttaaaaaa	gcaaaagaat	aaagaatata	tacaaaaggg	acctggaatc	180
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cctctgcttt	ggagaagggc	tatcatata	cattcagtc	gctgaagatg	gattggtaga	300
ggtgtgtcta	tacataaact	tcagtcattt	ttgcttgtgc	agaatcatcc	caatcttccc	360
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gaagttcaac	tcttgatgag	ccgcttaca	cagcagttcc	ttaggagcca	acatgacagg	480
tggttcagat	ttccctatga	gaaacaaaac	tggccacct	cagcaaaata	tcaaaatggg	540
gtaagtcctt	ccttcctctt	cctcctgatt	atatacaaca	tatctccttt	caagactatt	600
atttccatca	tgcttattcc	ttccaaatct	aaaccttga	ggtgatatga	aggaaaccaa	660
catcaagaaa	aagaaaactc	aattcagaaa	atgaagaaaa	ctggcagggg	tacaatacac	720
ccccagagca	tcttcaatat	ccctggggca	cagtncccaa	ttcagggact	gggtacaggc	780
ccataagaat	naaataattg	ggcagctttg	gaataaagcc	tcattttttt	cccttcaggn	840
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<210> 354

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 354

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caaaattatt	ttttaaaaaa	gcaaaagaat	aaagaatata	tacaaaaggg	acctggaatn	180
tgtaaggtga	ttccaaaaac	gaaataagta	gaaaatccat	ggtgaaacct	gaacattcta	240
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ggtgtgtcta	tacataaact	tcagtcattt	ttgcttgtgc	agaatcatcc	caatcttccc	360
aagactgaat	gggcagtcct	gtggctttct	tccttttcca	tattcccaac	aaggctacgt	420
gaagttcaac	tcttgatgag	ccgcttaca	cagcagttcc	ttaggagcca	acatgacagg	480
tggttcagat	ttccctatga	gaaacaaaac	tggccacct	cagcaaaata	tcaaaatggg	540
taagncttct	cttcctcttc	ctnctgatta	tatacnncat	atctcctttc	aagactatta	600
tttccatcat	gcttattcct	tccaaatcta	aaccttgagg	ngatatgaan	ggaaaccaca	660
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<210> 355

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 355

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accgcaatgg	ggcctctatc	cacgagttct	gcataaacct	gcggcagctc	tacggggaca	180
gccgcaagtt	cctgctgctt	ggtctgaggc	ccttcacccc	tgagaaggac	agccagcact	240
tcgagaactt	cctggagacc	attggcgctga	aggatggccg	cggcatcatc	actgacagct	300
ttggcaggca	cgggcggggc	ctgagcacca	catccagttc	caccaccaat	gggaacaggg	360
ccacggggcag	ctctgatgac	cggtcggcac	cctcagaggg	ggatgagtgg	gaccgcatga	420
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gatggacagt	ggatgggggg	gcacccacac	cttcgcgcga	gtcgtcatag	gccttcccag	540
aaggagctgc	ccagacctgc	gtgtcagccc	ttggtggtgg	ccaggganag	gcgcccgggtg	600
cagatggccc	cgggcggggc	aggtcctnta	ctgtgaagga	gcaggagagct	gccgagggac	660
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tgagtggtgt	ccccgctcgg	ggagggcccc	gccgagcggg	cagggagagc	cagtcctgtc	780
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accttaaaaa	gaagtttact	gc				862

<210> 356
 <211> 750
 <212> DNA
 <213> Homo Sapiens

<400> 356

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accgcaatgg	ggcctctatc	cacgagttct	gcataaacct	gcggcagctc	tacggggaca	180
gccgcaagtt	cctgctgctt	ggtctgaggc	ccttcacccc	tgagaaggac	agccagcact	240
tcgagaactt	cctggagacc	attggcgctga	aggatggccg	cggcatcatc	actgacagct	300
ttggcaggca	cgggcggggc	ctgagcacca	catccagttc	caccaccaat	gggaacaggg	360
ccacggggcag	ctctgatgac	cggtcggcac	cctcagaggg	ggatgagtgg	gaccgcatga	420
tctcggacat	cagcagcgac	attgaggcgc	tgggctgcag	catggaccag	gactcagcat	480
gatggacagt	ggatgggggg	gcacccacac	cttcgcgcga	gtcgtcatag	gccttcccag	540
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cacgaacctc	aatgccgggg	tggaangctc	tttggttgt	ccaccaaggc	ttagcccagc	720
ccttgcaatg	nggccccgct	tcgggggaagg				750

<210> 357
 <211> 725
 <212> DNA
 <213> Homo Sapiens

<400> 357

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acagccgtcc	aaggggcccag	ccgacaggac	tggctctccc	tgcccgtcgc	gccggggccct	120
ccccgagcgg	ggacacactg	cagggcttgg	ctganccctg	gtggacaagg	caaagagcct	180
tccaccccgc	actgaggctc	gtgtccctcg	gcagctccct	gtccttcac	agtanaggac	240
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atgtcgctgc	tgatgtccga	natcatgcgg	tcccactcat	ccccctctga	gggtgccgac	480
cggtcatcag	agctgcccg	ggccctgttc	ccattggtgg	tggaactgga	tgtggtgtc	540
agggcccgc	ggtgcctgcc	aaagctgtca	gtgatgatgc	cgcggccatc	cttnacgcca	600
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accaagcagc	anggaacttg	cggnttntcc	ccgaaaanct	tgccncaggt	tgatgcaaaa	720
acttc						725

<210> 358
 <211> 813
 <212> DNA
 <213> Homo Sapiens

<400> 358

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cattatggca	agaagggcgc	tgttttcgac	aggtgtgcag	gtttcggcac	atggagattg	120
ataaaaaacg	cagtgaatt	ccttggttatt	gggaaaatca	gccaacagga	tgtcaaaaat	180
taaactgcgc	tttccatcac	aatagaggac	gatatgttga	tggccttttc	ctacctccga	240
gcaaaactgt	gttgcccact	gtgcctgagt	caccagaaga	ggaagtgaag	gctagccaac	300
tttcagttca	gcagaacaaa	ttgtctgtcc	agtccaatcc	ttccctcag	ctgcgagagcg	360
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atgctgcaga	tgatgatgaa	gatgatgatg	atcagttttc	tgaggaaggt	gatgaaacca	480
aaacacctac	cctgcaacca	actcctgaag	ttcacaatgg	attacgagtg	acttctgtcc	540
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atgagtctta	ctgagagact	ggggaaacca	aaa			813

<210> 359
 <211> 756
 <212> DNA
 <213> Homo Sapiens

<400> 359

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gggccagggc	agaggaggaa	gagaaggcta	aggtagaaga	gcagaaacgt	aacaagcagc	120
tagaagagaa	aaaacgtgcc	atgcaagaga	caaagataaa	aggggaaaag	gtagaacaga	180
aaatagaagg	gaaatgggta	aatgaaaaga	aagcacaaga	agataaactt	cagacagctg	240
tcctaaagaa	acagggagaa	gagaagggaa	ctaaagtgc	agctaaaaga	gaaaagctcc	300
aagaagacaa	gcctaccttc	aaaaaagaag	agatcaaaga	tgaaaagatt	aaaaaggaca	360
aagaacccaa	agaagaagtt	aagagcttca	tggatcgaaa	gaagggtttt	acagaagtta	420
agtcgcagaa	tggagaattc	atgaccaca	aacttaaca	tactgagaat	actttcagcc	480
gccttgagg	gagggccagc	gtggacacca	aggaggctga	gggcgcccc	caggtggaag	540
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gagaagctca	aacagaagca	gcaggaggcg	gctttggagc	tggaggaaact	caaggaaaaa	660
ganggaggag	agaaggaagg	tcctgganga	ggaagagcag	aggaaggaac	aggaggaaag	720
ccgatcggaa	aaccttcaag	aggaggaaga	agaaga			756

<210> 360
 <211> 706
 <212> DNA
 <213> Homo Sapiens

<400> 360

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gatcttctgt	tgacttcana	tgnggttggt	atcactgctc	aaatacagag	ttatgatgat	180
cagtanaaaa	gtctntattt	cacagcatgg	gtttctttan	aaacaggctc	ctgngcaaaag	240
gcagtacttt	taccatgaac	atctntanac	tgggattatt	aaatatagny	ataatataca	300
tgggtttact	gggatattga	aaaataaaag	ataatgaacc	caatttagta	aatcaacata	360
aatacaaaac	agagcgaatt	agccctntac	aactgagctc	gtcctgcgtc	ttgagcttgg	420
gttctttctg	gaactgtctc	aaaccttagt	gggggaagtg	accttatcca	canattgctt	480

ttcccagagg ttccgcttgc tggataccgt ctctgggnet caagtcanaa ggtttgggag 540
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cctaccttta agccagcagt ttnccttatt tggggnggcc ctgctgcant ggggggatga 660
aaacncattt cctttntcca catactcttg aaggttgccg tacacc 706

<210> 361
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 361
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gagcgagtga acatgccgcc cgcggtggac cctgcggagt tcttcgtgct gatggagcgt 180
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gcattggact cccggaagaa ctacaactgg gccatcacca gagaggggct ggtggtcagg 600
ccacaacgca nggacttcta agggcccagt aaggacagtg cccggcaggg accatgtatg 660
tatcatggcg gaagagttgc ccttgactgg aattaaagca attggtgttg cttatgagga 720
aaggtt 726

<210> 362
<211> 747
<212> DNA
<213> Homo Sapiens

<400> 362
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ccattatcag ggaaaagtat caagggttna taaaattttt aggaanggca nattcacaga 120
acatgctagt cagctngcag ttttacctcg taaagatanc aganaattat agncaaacca 180
gtaaacangg aattnacttt tcaaaagatt aaatccaaac tgancaaaat tntaccctaa 240
aacttactcc atccaaatat tggaataaaa gtcagcaggg atncattctn ttctgaactt 300
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gggactaacc ncaattttng gttaaag 747

<210> 363
<211> 1227
<212> DNA
<213> Homo Sapiens

<400> 363
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caaacgttga ctgggaagta gaaacagata attctgattt accagcaggt ggagacatag 120
gaccacaaa tgggtgccagc aaggaaatac cagaattgga agaagaaaaa acaattccta 180
ccaaagagcc tgagcagata aaatcagaat acaaggaaga aagatgcaca gagaagaatg 240

aagatcgtca	tgactacac	atggattaca	tacttgtaaa	ccgtgaagaa	aattcacact	300
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gaatggacat	cccctttgaa	gagggcgtgc	tgagtcccag	tgctgcagac	atgaggcctg	960
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tcttttgagt	accctggccc	atgaagaatc	ccacagccac	aaagattctg	gcccagaag	1200
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<210> 364

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 364

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tctgaggagt	ccgtctcccc	cctcccggag	gagatccgga	gactggagga	agagctccgc	180
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tccaagagcc	aggagcacga	gcagcgccctg	gccgccttgc	aggggcgcct	ggaaggcctc	420
gggtcctcag	aggcagacca	ggatggcctg	gccagcacgg	tgaggagcct	gggcgagacc	480
cagctgggtg	tctacggtga	cgtggaggag	ctgaagagga	gtgtgggaga	gtccccagc	540
acccgtggaa	tactctcaga	aggtgcagga	acaggtgcac	acgctgctca	gtcaggacca	600
agcccaggcc	cgccgtctgc	cttctcagga	ctttctggac	agactttctt	ctctagacaa	660
cctgaaagcc	tcagtcaggc	cagtgggaagc	cggacttgaa	aatgctcaag	aactgctgtg	720
gacaagttgg	gtgcataact	cggtcaaaat	tagaaaccaa	cgagnacaat	tttggaatca	780
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<210> 365

<211> 785

<212> DNA

<213> Homo Sapiens

<400> 365

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cccttggctg	attccagatt	gttctcgttg	gtttctattt	tgaccgagta	tgcaaccaa	480
ctgtccacag	cagtctcgag	catttttcaag	tccgcctcca	cttggctgac	tgaggctttc	540
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<210> 366
 <211> 816
 <212> DNA
 <213> Homo Sapiens

<400> 366						
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tcacagcccc	aaatatcaat	ctttctctgg	accaaagtga	aggatctatt	ctctctgatg	660
ataacttttg	acagtccaga	tgaaattgac	atcaatgtgg	atgaacttga	tacccccgat	720
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<210> 367
 <211> 803
 <212> DNA
 <213> Homo Sapiens

<400> 367						
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gattttctgg	tacagaaaaa	gatcaatcct	caagtgatga	aagctgggag	actctgccag	480
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<210> 368
 <211> 809
 <212> DNA
 <213> Homo Sapiens

<400> 368						
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tgcattccat	tttaacaatt	cgtatgtatc	taacaaatac	ataaatccag	atcacaaata	180
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tcagcattca	tattataaga	aataagaaaa	tgttaaaaaa	ataaaattag	gttaagtcac	300
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<210> 369

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 369

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aagatcgta	tgcactacac	atggattaca	tacttgtaaa	ccgtgaagaa	aattcacact	300
caaagccaga	gacctgtgaa	gaaagagaaa	gcatagctga	attagaattg	tatgtaggtt	360
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cctccttaaa	tgaagaaaaa	ggtctctctg	cagagaaaaat	gtcttctaaa	ggcgatacga	480
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ttggtgatcc	atcactggat	gccagggact	cagggcctgg	gtggtctggc	aagactgtgg	600
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<210> 370

<211> 783

<212> DNA

<213> Homo Sapiens

<400> 370

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cagacacttt	attctgagca	atccaatgca	tgatagaaaa	accttttagat	atataaaaga	180
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cgagagttgc	aaacatagta	ccataactga	atatttataa	ttacatctta	acaaaggcta	300
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<210> 371
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 371

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<210> 372
<211> 804
<212> DNA
<213> Homo Sapiens

<400> 372

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ggaaaagggc	cacattatta	aaattactaa	ctgtacagaa	attgatttaa	aaaagtcaca	420
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<210> 373
<211> 792
<212> DNA
<213> Homo Sapiens

<400> 373

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aactgaaaga	ggcaaagcac	attgctgaag	atgccgaccg	caaatatgaa	gaggtggccc	420

gtaagctggt	catcattgag	agcgacctgg	aacgtgcaga	ggagcgggct	gagctctcag	480
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<210> 374
 <211> 745
 <212> DNA
 <213> Homo Sapiens

<400> 374

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taaacagcgt	atgctagcca	gagaggagcg	ccatcgtaga	agaatggaag	aagaaagatt	660
gcgtncacca	tnttcacccc	cagtggctac	tatttagatc	atgaatgcag	cattggtgct	720
gaaaaataa	aaggaggatt	ccaaa				745

<210> 375
 <211> 734
 <212> DNA
 <213> Homo Sapiens

<400> 375

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<210> 376
 <211> 822
 <212> DNA
 <213> Homo Sapiens

<400> 376

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gaatggggaa	tatgtaggta	aatggattac	ccgaaaaaan	ttatctgntt	aacaaactta	780
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<210> 377

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 377

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gaatgataca	aattaggggtc	catatcattt	aatttccctt	gaacctgctc	tgctaggtta	660
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<210> 378

<211> 870

<212> DNA

<213> Homo Sapiens

<400> 378

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870

<210> 379

<211> 837

<212> DNA

<213> Homo Sapiens

<400> 379

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<210> 380

<211> 793

<212> DNA

<213> Homo Sapiens

<400> 380

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<210> 381

<211> 807

<212> DNA

<213> Homo Sapiens

<400> 381

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<210> 382

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 382

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atgccactc	cagagccaca	ggagttaggt	tgagctgtgc	aggctcctac	atcctccctt	420
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<210> 383

<211> 1203

<212> DNA

<213> Homo Sapiens

<400> 383

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<210> 384
 <211> 2651
 <212> DNA
 <213> Homo Sapiens

<400> 384

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<210> 385
<211> 804
<212> DNA
<213> Homo Sapiens

<400> 385

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<210> 386
<211> 782
<212> DNA
<213> Homo Sapiens

<400> 386

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<210> 387
<211> 865
<212> DNA
<213> Homo Sapiens

<400> 387

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<210> 388
 <211> 753
 <212> DNA
 <213> Homo Sapiens

<400> 388

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 gattcncaaa aanactggng aaatagaaca tgg 753

<210> 389
 <211> 737
 <212> DNA
 <213> Homo Sapiens

<400> 389

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<210> 390
 <211> 775
 <212> DNA
 <213> Homo Sapiens

<400> 390

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<210> 391

<211> 776

<212> DNA

<213> Homo Sapiens

<400> 391

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gcagaaggtc	tacacccctg	aggatttggc	gtatcagaac	cgactgcgtc	ttctttcact	720
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<210> 392

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 392

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tttttct	tgggaca	ttaaagt	tcttttgt	caaaaacag	aatgtaccta	180
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ctaatacat	tgaagtgt	ttgtataaaa	tatcacgt	agaagacttt	atcaatgtct	360
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cctcaaggtc	nccaggaatg	ggggatttcc	ctcntaaaaa	atttttaatt	ttgggggggt	840
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<210> 393

<211> 769

<212> DNA

<213> Homo Sapiens

<400> 393

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tttctgtttg	ggacaatttt	aaagtttttc	ttttgtcaca	aaaacaggaa	tgtacctata	180
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aatagaacat	gtaactagtt	gatacaaato	taataggatt	tgttaaaatc	agtcacatct	300
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aaaagtgggt	ttgttcatag	acaatctgac	aagttaccat	aaaaagtgtt	tcctgagaca	420
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atactttttt	tttttttttg	catcatcana	gggttttact	gaacttacaa	cgcacttgcc	600
cgctcagtat	gccagttcan	atgtgaaagg	cgctttnttg	tcagcagcct	gnactggctt	660
caatcctatg	cgtgcaggng	tttaccacaca	ggcaaacagg	ttttctnccc	catttttgga	720
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<210> 394

<211> 813

<212> DNA

<213> Homo Sapiens

<400> 394

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ctggatttct	tgactggcca	cagggcacat	tcgctccca	ggtgacgctg	gagggggaca	480
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cctccaagct	ctctgtgatc	agtgtggagg	acccgcccc	gcgcacggcc	ggcgtcaagg	720
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ccagagatgg	caataaaaact	gactctcaac	atc			813

<210> 395

<211> 762

<212> DNA

<213> Homo Sapiens

<400> 395

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tggccatggg	tgcagaccga	ggtatccacg	tggaggtgcc	cccagcagaa	gcagaacgct	300
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atgaaagcca	agaagaagaa	gatcgangtg	atcaacctgg	gganctgggt	gtggacctga	660
ctccagcttt	tttngatca	gtgtgganga	ccggccccacg	cacgggcgcg	tcaangtgga	720
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<210> 396

<211> 822

<212> DNA

<213> Homo Sapiens

<400> 396

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ccacactgat	cacagagagc	ttggaggtea	ggtccacacc	caggtcccca	ggettgatca	180
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tgcctctgtg	ccagtcaaga	aatccagctg	tcattctgcc	tgtctggtta	cagtcacatc	420
cgatggcctg	tttgcccagc	agcaccaggt	ccaccttctc	cttctctgcc	agcttggtcca	480
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ggatacctcg	gtctgcaccc	atggccaggg	cggtaccaat	cgtctcctgg	cactgtgcag	600
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gaaccaccg	gncttgtna	ggctttactt	cggatctttn	acnggggaat	cgatgaccn	780
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<210> 397

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 397

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ggtcctccac	actgatcaca	gagagcttgg	aggtcaggtc	cacacccagg	tccccaggct	180
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cgaatgtgcc	ctgtggccag	tcaagaaatc	cagctgtcat	ctgccctgtc	tggttacagt	420
catcatcgat	ggcctgtttg	cccagcagca	ccaggccac	cttctccttc	tctgccagct	480
tggccaggac	ccgagccacc	tgcaggggac	ccaagcgttc	tgcttctgct	gggggcacct	540
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cggngaccac	accgggccct	gtcaggcttt	aactcggant	ctttacgggg	taatcgnntg	780
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<210> 398

<211> 751

<212> DNA

<213> Homo Sapiens

<400> 398

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cgaatgtgcc	ctgtggccag	tcaagaaatc	cagctgtcat	ctgccctgtc	tggttacagt	420
catcatcgat	ggcctgtttg	cccagcagca	ccagggtccac	cttctccttc	tctgccagct	480
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<210> 399

<211> 800

<212> DNA

<213> Homo Sapiens

<400> 399

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gggtcctcca	cactgatcac	agagagcttg	gaggtcagg	ccacacccag	gtccccaggc	180
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ggacaagnct	tcttcaaccg	ggatctcaca	agaaggggtc	atggagtgtc	ttcacaccat	720
tcgggancac	aaccggnctt	gncaaggctt	naacttggtc	ntttacggng	taatccgatg	780
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<210> 400

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 400

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ttccagaaga	aaggggagaac	tttcttcagc	aattgtacaa	atztatggaa	gatagaggta	180
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tctaccaaga	tcttggaaac	cctgtcttaa	attcagctgc	aggatacaat	gttaaattgtg	360
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aggaaaaaga	agttacatta	aaaaaccnga	agacaatgaa	aatctgggcc	gaccaagatg	720
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<210> 401
<211> 860
<212> DNA
<213> Homo Sapiens

<400> 401

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cccagctaga	gctagcagat	ataaagtcca	agcttgagaa	ggtagggccag	cagaaacaag	180
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<210> 402
<211> 779
<212> DNA
<213> Homo Sapiens

<400> 402

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<210> 403
<211> 1443
<212> DNA
<213> Homo Sapiens

<400> 403

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gaatcagtta	aaagccagat	gaaacaaaag	gatgaagatc	ttgagcgaag	actggaacag	360
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<210> 404

<211> 819

<212> DNA

<213> Homo Sapiens

<400> 404

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gaacatgaca	agcagatttg	ggagtccaag	gccagacag	aggctcagct	tcagcagaag	180
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aatatgaaag	agcaaaagat	tataagcctg	ctttctggca	aggaagaggc	aatccaagta	540
gctattgctg	aactgcgtca	gcaacatgat	aaagaaatta	aagagctgga	aaacctgctg	600
tnccaggagg	aagaggagaa	tattggttta	gaagaggaga	acaanaangc	ttgtgggttaa	660
aacccaatca	gcttatggga	acacttgaaa	accatcaaaa	nggaaacatt	tagncaaaag	720
gencagttgg	attccttgg	naaatcctgn	cttctnttcc	aatggatcc	gagaaccgcn	780
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<210> 405

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 405

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ttaggganag	gctaggcagt	gaacacatca	tgtatgcaat	ganaaaataa	ccaactggta	180
ggatggggga	ggggaggggga	ggcagggaat	aggcncaa	ggaattctat	cctggctgtc	240
cttctcaggt	ctatctatat	ttaattttgt	cttctctata	ttctcttcc	attgccacag	300
agggcanaga	caatggggct	gaaaaactgt	aataactgnc	actaacagca	aagtanctta	360
gtnccttcaag	aggtcaggag	ttgcagtgtg	gtgttanacc	agtcnactc	ctggctgaaa	420

gtcaatgcct	aatattggct	cccagnggcc	cctgagcact	gtctcagggg	ccacattcca	480
ggaatnttca	natnttcctg	gaatgacaag	aattggaacc	ctgctgncca	tagacacttc	540
tccctgcctt	ttggtgaaag	gaaagacttt	gggccccttt	aataccttan	tatcccattg	600
gatcaagggc	caaaagccaa	aggggattct	tatcettata	gcctaagacc	ctgaaattct	660
tcccttccca	attatatctg	gaaattggcc	aggggaanaa	aaatgctgnc	cttcccattg	720
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<210> 406
 <211> 758
 <212> DNA
 <213> Homo Sapiens

<400> 406						
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attaggctca	acaaaccaaa	tgtgattctc	agattaagca	gaagcgttca	ggctcagggc	180
agtagaagaa	agcagactcg	ccagtcctcg	cagctccaac	ctgtcctcgt	atcacctctg	240
tttttgcagg	cactttccgt	gaagagttgg	agagaagacc	tgtaaattgg	aagactgttc	300
cactggaatt	gatgttctga	tgtagaggt	gagagaattc	caagttttga	ggggagtggg	360
ccaaagagta	acaactaagt	ctatagatgg	cccgtaaaac	acagaatgag	caggacatga	420
atcattagaa	agtagatggc	tgctagaagt	ggcactcggg	tccgtgaatg	acagagtga	480
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gtcccattca	ctgngctcta	accggtcgga	tctgctctc	ggccacagga	gagagcattt	660
ttcagcagcc	actctttggc	cncggtcttt	cttcagcag	cttcctttaa	atcattcctt	720
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<210> 407
 <211> 778
 <212> DNA
 <213> Homo Sapiens

<400> 407						
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cgcaaaaagg	cacaagcaga	attagctagc	ttcaaagtcc	tgctagatga	cactcaaagt	240
gaagcagcaa	gggtcctagc	agacaatctc	aagttgaaaa	aggaacttca	gtcaaataaa	300
gaatcagtta	aaagccagat	gaaacaaaag	gatgaagatc	ttgagcgaag	actggaacag	360
gcagaagaga	agcacctgaa	agagaagaag	aatatgcaag	agaaactgga	tgctttgcgc	420
agagaaaaag	tccacttgga	agagacaatt	ggagagattc	aggttacttt	gaacaagaaa	480
gacaaggaag	ttcagcaact	tcaggaaaac	ttggacagta	ctgtgaccca	gcttgacgcc	540
tttactaaga	gcattgtctc	ccttcaggat	gatcgtgaca	gggtgataga	tgaagctaag	600
aaatgggaga	ggaagtttag	tgatgctgatt	caaagcaaa	aagaagaaat	tagactcaaa	660
gaagataatt	gcagtgtcta	aaggacactt	agacagatgt	ccttcntatg	gaagaattaa	720
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<210> 408
 <211> 752
 <212> DNA
 <213> Homo Sapiens

<400> 408						
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nttttacngg	accncaaaan	atcagggnc	tgcaaaatct	cancaaatnt	taggctcanc	120

aaaccaaang ngattntnaa attaancaaa ancgttcagg ctcagggcag taaaaaaaag 180
 caaactegcc agnccntgca gctccaacct gncctcgtat cncctntggt tttgcaggcn 240
 ntttccngga anagttggan anaaaacctg taaanggnaa aactgttcca ntggatnga 300
 ngttctgatg ttanaggnga nanaattcca agttttgagg ggagnggncc aaagagtacc 360
 aactaagtnt ntananggcc cgtaaaaacnc anantganca ggacntgaat cnttaaaaag 420
 taaatggctg ntaaaagngg cncctcgggtc cgtgaatgac agagtganen caggactcgn 480
 ttccatccaa cgccantccg ggtccttcga caactgtngc ttgtaanatc tattaacagg 540
 gctgntcct gantgccaca ggagccaatg ntaggagtcc gggaagagtc ccatttcact 600
 ggggctttaa ccgtctgaat ctggtccttg gccncagaga gagcnttttt nagnaggccc 660
 ncnttttggg ccccgttntt ttttccagca ngcttccctt taattcattc ncttcccggg 720
 ctgggggttg caaaacntgc tggntgacct tt 752

<210> 409

<211> 736

<212> DNA

<213> Homo Sapiens

<400> 409

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 gctcagccaa gatcaagtta aagagcagtg agctgcaggc catcaagacg gagctgacac 120
 agatcaagtc caatctgat gccctgctga gccgcttggg gcagatcgct gcggagcaaa 180
 aggccaatcc agatggcaag aagaagggtg atggaggtgg cgccagcggc ggcggcggcg 240
 gtgggtgggg cagcgggtggc ggtggcagtg gtgggtggcg tggcgggtggc aacagccggc 300
 caccagcccc ccaagagaac acaacttctg aggcaggcct gccccagggg gaagcacgga 360
 cccgagacga cggcgatgag gaagggtcc tgacacacag cgaggaagag ctggaacaca 420
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 caccagcagg tgaaggcat cgctgccag gcccaagcc gggcacccaa ccttgatgc 540
 cccccccag cgggtaccag aggaaagctg cagcaggccg cctcctcccc caacgcacnc 600
 cagccagtgc catgtcctct gcagggtggg ttactggcct actccttccc atgaaccctt 660
 ccttgtctgc acttgccagg ccagagggtg gagcacangg gtttccccat acttaccttc 720
 ccttcccagg acactt 736

<210> 410

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 410

gggatccaat ctctttattg tcagggtccc ctccctgngg ccccccgcca aacctataga 60
 aaaaacccaa gcttgggagt gtccctgggga ggggaggtag tatggggaaa cccctgngct 120
 ctaccctctg gcttgggcag tgcanacagg gagggctcat ggggaaggag taggccagta 180
 actccacctg cagaggacat ggcactggct gggatgcgtt gggggaggag gcgctgctg 240
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 cctggggcag cgatgccctt cacctgctgg nggccattgc tctgtcagg ctgcttactg 360
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 caggagccct tctcatcgc cgtcgtctcg ggtccgtgct tccccctggg gcaggcctgc 480
 ctcanaagtt gngttctctt ggggggctgg tggcccggct gttgccaccg gcaccggcac 540
 caccactgnc accgncaccg ctgcaccacc accgncggcg cccgncgntt ggcgccaact 600
 tcatnaccct tcttcttgca tctggaatgg ncttttgcct ncgcancgaa ctgntccaaa 660
 cgggttaanc agggcatcna tatttggact tgaactgggn caancttccg ncttgaangg 720
 ccttgcaagc tttaatgggc tttaacttga actttggctt gaacct 766

<210> 411

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 411

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agatcaagtc caatatcgat gccctgctga gccgcttgga	gcagatcgct gccggagcaaa	180
aggccaatcc agatggcaag aagaaggggtg atggagggtg	cgccagcggc gccggcggcg	240
gtggtggtgg cagcgggtggc ggtggcagtg gtggtggcgg	tggcgggtggc aacagccggc	300
caccagcccc ccaagagAAC acaacttctg aggcaggcct	gccccagggg gaagcacgga	360
cccgagacga cggcgatgag gaaggggtcc tgacacacag	cgaggaagag ctggaacaca	420
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caccagcagg tgaagggcat cgctgccccA ggcctcaagc	cgggcaccca accctggatg	540
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ccagccagtg ccatgtcttc tgcagggtga gttactggcc	tactccttcc ccatgagccc	660
tcctgtctg cactgcccag gccagagggg agagcacagg	ggtttcccca tactacctcc	720
cctccccagg aactcccag gcttgggttt tttctatagg	tttggcgggg ggcncaggg	780
aggggaccct gacaataaag agattggatc cc		812

<210> 412

<211> 857

<212> DNA

<213> Homo Sapiens

<400> 412

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tctgacatgc ttctcgaagg tggctctact acagcttctg	taagagaggc caaagaggat	120
gaagaagatg aggagaagat tcagaatgaa gattatcatc	acgagctttc agatggagat	180
ctggatctgg atcttgttta tgaggatgaa gttaaatacgc	tcgatggcag cagttcctct	240
gctagtctca cagcaacaag taatacagaa gaaaatgata	ttgatgaaga aactatgtct	300
ggagaaaatg atgtggaata taacaacatg gaattagaag	agggagaact catggaagat	360
gcagctgctg caggacccgc aggtagtagc catggttatg	tgggttccag tagtagaata	420
tcaagaagaa cacatttatg ctccgctgct accagtagtt	tactagacat tgatccatta	480
attttaatac atttgttggA ccttaaggac cggagcagta	tagaaaattt gtggggctta	540
cagcctcgcc cacctgcttc acttctgcag cccacagcat	catattctcg aaaagataaa	600
gaccaaagga agcaacaggc aatgtggcga agtgccctct	gatttaaaga tgctaaaaag	660
actcaaaact caaatggccc gaagttcgat gtatgaaaac	tgatgtaaag gaatacactt	720
tcagaaataa aaagcacagt gctgcttctg gagacatgcn	gacaagnctt tttttgctga	780
nccagcagnt ntggctgatg tggactgaaa cttttggcag	aatgcaggat ttggatggac	840
tcctggcnaa agtctta		857

<210> 413

<211> 790

<212> DNA

<213> Homo Sapiens

<400> 413

ctcaagtnga ttttattanc aaaaagngca aactattttg	ancaaaaagta aactatgagt	60
cacagcnttc agcaagacat canacncgga anagnanca	atattcacta agtaaaatnc	120
agcanatgan atgtctntca catgtatatt naattattca	tgctttttca atagtctntt	180
agtcaacttt cagnhtaatt tccacaaata tatagcagnt	caaacncaaA tgcaggannc	240
caanggcaaa gttnggcaac tgtttngggc taattatgag	tntgaaagaa anccttatat	300
cacagtttca cgttcatgta anccactgng caacatgaat	gaatntttaa angngttgac	360
nctgaaatca angtncaact aangaaanta aagaanaaaa	gggggcttta aaatatnngt	420
ngcnctacag tcgtatagta agaggcagaa aaaaatgaan	gaatttttaa taatcttaca	480
cgtgtntaca gggccaggaa cgtaatgaat ccatgttaac	ttaatttcat ttaaaattnc	540

attttagtaa	gtcnncnaac	agaaagatcc	atgcgggtga	acagtgtgcc	tgtnccttgac	600
aagttagaga	agatccttct	ccaaaaggga	gattcagctc	agggntactt	cagttnttcc	660
catagnngct	acagggcana	atctttttca	aaagcaattt	tctgggtccct	aaatctacag	720
gcnc tantgg	gacctgtaat	taaaancccc	caattttaag	gangattttt	aaacccact	780
taagctttta						790

<210> 414
 <211> 1063
 <212> DNA
 <213> Homo Sapiens

<400> 414						
gnnnnntnch	gccanncnan	agnntgntca	cctccnagat	nngggatggn	ntgggtgaccc	60
nggcnttgac	tctgnnnngc	gaentnttgc	tagtcttcag	gnctcctact	acaggctttg	120
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gcangctggn	ctatngcaan	ntgggnctna	nnctgnanaa	tcannngcng	ccatgnnaga	240
tnaatagaag	ctcatnntgt	cataaatggn	ccatgactta	taaatnaagt	ggactggata	300
tcttatgaca	gnagcnatnt	angcttngtg	ngnagttaan	gcttccacct	nnggangata	360
agaggncnac	cttgtntnan	ctnntgcngc	tgnaagancc	agaganannt	gcctngggag	420
attcatggcc	natgatagta	tatnatctct	tacaccanat	atgccttgct	gnatcncaaa	480
tctggacata	caegntttcc	ccatctcaga	cttcnttgca	gcagctgctt	nccnacnnta	540
cccatgaacg	acanntgctt	acgntanagc	ntgaacnatin	tgatgagctt	cntcagccca	600
gacctcatca	tttcogagaag	cacatgtccc	tgcgtttcaa	cctatggatg	aggaaaagnc	660
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ctctgagntg	cccacatngn	gtntctggaag	gcttccggnt	annatggttc	cgggacctnc	780
aacctttccg	tttgaatnct	nacntgaccg	ganagggtnt	gcctgggttc	cttnggcenc	840
gaacttaacc	ntcacaattn	ggntgngant	tcttggtaac	ggcntaatct	ccccaggaa	900
ttggccgctg	cttcnacggg	aattaanggg	aatctttccc	atcccncctta	nnaccagtta	960
ggngcccntt	tttcaatttt	cngactcccg	gagcttttaa	aaaccggggg	ccttaggttn	1020
cttgatggc	nttgggggtn	gcccccttta	gggaattaaa	ggg		1063

<210> 415
 <211> 824
 <212> DNA
 <213> Homo Sapiens

<400> 415						
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anatnaaaat	ancagttata	attacacaca	taatataggt	acottataca	atgattccaa	120
taaatatcac	aggaaataca	ntgcattttc	aagntgnana	gacnaatact	tnctcattca	180
cagnngttga	catanganag	cctattttaca	tancnatctg	tataaagtca	tgctctnant	240
ancaggntat	ncagnctgn	gccancacaa	tgnttttnaga	angtgaagaa	ccggncaaaac	300
cactnntggn	gctggggatc	tgganaagcc	acctgnanaa	gcttcaactct	gagcangact	360
cannaatgnc	ttnggccctt	taggtggcac	tggctgtgga	agtgggttaag	ctgctgctga	420
actcaattcg	tggactgnag	aattaggaat	ggganccagg	cggtnnggat	gaccattgcc	480
cactcnanca	natnccaaag	nnctnagaan	gggaacnctc	caancctgct	tnatggngat	540
taancatnct	tcttcttttg	cttaacccat	ggattananc	acancagcna	gtacngactt	600
ggntttaccc	ncttngttg	gaaataagga	ttcttgatng	actaaannnc	agctggtnaa	660
aaentaactn	tcctcaatt	tagcnttatt	ntatgaancc	ggggcctant	ntcntgttca	720
aaaangngnt	tttaagttcc	ggtaatccta	cggnaatta	nttgggggct	ntgaattcan	780
cnccttana	anatttnggn	ttaccatttn	aatccaaagg	ccac		824

<210> 416
 <211> 838
 <212> DNA

<213> Homo Sapiens

<400> 416

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tgcacttcga	aaaagaacat	aaagctgaga	aagtcacagc	agtagccaac	tacattatga	120
aaatacacaa	ttttactagc	aatgcctct	actgtaatcg	ctatttaccc	acagatactc	180
tgctcaacca	tatgttaatt	catggtctgt	cttgctcata	ttgccgttca	actttcaatg	240
atgtggaaaa	gatggcgcga	cacatgcgga	tggttcacat	tgatgaagag	atgggaccta	300
aaacagattc	tactttgagt	tttgatttga	cattgcagca	gggtagtcac	actaacatcc	360
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cccaaaataa	tctccaggtt	cctccaaagc	cacagccaaa	ggttcaggaa	aaggcagata	480
tccttgtaaa	aagttcacct	caagctgcag	tgccctataa	aaaagatggt	gggaaaaccc	540
tttgtcctct	ttgcttttca	atcctaaaag	gacccatata	tgatgcactt	gcacatcact	600
tacgagagag	gcaccaagtt	attcagacgg	tcattccagtt	tgagaaaaag	ctnacctaca	660
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gnatctagnt	cactggangg	gccgtttggn	aagganccca	aatggggccag	gataagacaa	780
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<210> 417

<211> 880

<212> DNA

<213> Homo Sapiens

<400> 417

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tgatggtggt	gaactaaaga	taaaactaaa	tatccaaaat	gcagcactca	ttggtttgct	180
gcttcaacac	aacacacttt	tatacagatc	taaaaggtgt	caaaattagt	agctgcaaag	240
tcaattcttg	catgtgattt	tagcttaaaa	gatttcagaa	aacagatctg	aaataccagt	300
ttttgttttt	gacagctgta	atgtcaagga	tattcagaac	aagaaaaatc	ctataatata	360
agagagtcca	gatataatc	ttacgtggct	ggcctctggt	gcaagattgt	acaagggtat	420
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taaactagat	agagcgttta	ttacacagca	agggcaacac	taaaaaaaga	aatctatgat	540
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tacncattan	actgggagct	tgatgtttgg	ggcctacact	accatgggga	attangttta	720
acacttntta	aaaacatttg	gccaatcatt	tcncagangg	gaaagaaatg	ttgaaaaggc	780
cgataaaata	aacccttggg	ttttcctcgg	gggattcatg	gagtcacccg	ccttaatggg	840
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<210> 418

<211> 763

<212> DNA

<213> Homo Sapiens

<400> 418

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cggaacatc	ttctgtgtca	acaacaacca	gcagtaccac	caccaccacc	atcaccactt	120
cctcctctcg	aatgcagcag	ccacagatct	ctgtctacag	tggttcagac	cgacatgctg	180
tacaggtaat	tcaacaggca	ttgcatcggc	ccccagctc	agctgctcag	taccttcagc	240
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atttaagcag	ctcccagctt	cagagccttg	ctgctgttca	ggcaagtttg	tccagtggaa	360
gaccatctac	atctcccaca	ggaagtgtca	cacagcagtc	aagtatgtcc	caaacgtctg	420
tagaaattct	tatggactgg	aatcttcttc	aaggcttact	ttgttctctg	gatgcagtgg	480
tgcatagaag	atagggcatt	gactcactca	gacctggctt	gccagcatg	cattgcaaca	540

ataatgtgca agttattaaa gacatgagtg aattcgtgac agattgtcag aaaagaaaca 600
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gttggggctg agtgaagaa aatgcaagct gcaaatctgg cttacatgtg gaaccaaagc 720
tggaaatgng tgctttaaan gcaacttgta aaattggatt tcc 763

<210> 419

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 419

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tggattcact acttttttta nagngtogtt ttaccactac tattggccta ttacctgtat 180
ctetttttttt taatggcatt tctctaggat ttacaatatg catcttttagc ttatagtatc 240
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<210> 420

<211> 799

<212> DNA

<213> Homo Sapiens

<400> 420

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acttgatgat atctaccct tcttacaaca aattccatcc aaggaaacctg cggctctcat 180
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tgaacataag actaaactgg agcaacttca tataatgcaa gaacagcaga aatctttgga 420
tataggaaat caaatgaatg tttctgagga gatgaaagt acaaattattg ggaatcagca 480
aattgacaaa gtttttaaca acattggagc agaccttctg actggcagtg agtccgaaaa 540
taaagaggac gggttacaga ataaacataa aagagcatca cttacacttg aagaaaaaca 600
aaaattagca aaagaacaag agcaggcaca gaagctgaaa agccagcagc ctcttaaacc 660
ccaagtgcac acacctgttg ctactgttaa acagactaag gacttgacag acacactgat 720
ggataatatg tcctccttga ccagccttcc tggtagtacc cctaaatctt ctgcttcaag 780
tctttcactt ctggtcctt 799

<210> 421

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 421

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aggaaaaacca ttgtgtaaaa cagtaggcgg atctttcaga gactccaaat cattgacaat 180

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gttggaaaag	tttctagctt	taatatctaa	agccagcaac	acgccaaagc	ttttaacaat	600
atataaggag	aatgggacan	agtaacaaag	aaatcttgca	gcagcttcac	cagcagctgg	660
ntgaagcttg	aaccgtaggt	caatgacata	cctcaaacgg	naccataaga	tccaggcccg	720
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<210> 422

<211> 733

<212> DNA

<213> Homo Sapiens

<400> 422

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ctgtggccgc	cgggggtgac	ggnccctttg	aggggctcat	ccccgctcca	ctgcacatta	180
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agaacaccat	ctggtagctc	ttcggaattt	agctgcttga	tgatgaattc	tatctggcgg	420
atcatttcag	cattgccttc	tttgatgaag	cagcgtagga	tgtcttccat	tcccattgct	480
cttgccttct	cacgaatgga	tggancagaa	aggatgctgt	acagagctcc	attcacatac	540
ggctgtatct	catggttttc	atggccaaga	agatccgaaa	ggactttgag	caccgaggcc	600
tgccaccttg	gcacacatgg	tcttccctgn	gctgcggagg	gcagagggtc	atggagcaaa	660
agccaccgag	tactccaacg	gggnagccag	acagggcgagn	cagggtcctt	tcanaacatc	720
aaccagcccc	gaa					733

<210> 423

<211> 862

<212> DNA

<213> Homo Sapiens

<400> 423

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atcgagaaac	tgcacctgtt	tcccagcctg	aaaacaaacc	agaaagtaag	ccaggcccag	180
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ctgctccagt	tccttgtcct	cctcccagcc	ctggcccttc	tgtgttcccc	tcttccccca	360
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caaaaccagg	agaagccgag	gctcccccaa	aacatccagg	agtgtctgaa	gtggaagcca	480
tcttgagaaa	ggtgcagggg	ctggagcagg	ctgtagacaa	ccttgaaggc	agaagactgt	540
acaaaaagta	cctgatgatc	gaagagtatt	tgaccaaaaga	gctgtctggc	ctggattcag	600
tggaccccga	gggacgaagc	cgatgtgctg	caggccagga	gagacgggtg	caggaagggt	660
cagaccatct	tggaaaaact	tgaacagaaa	gccattgatg	tccangtcaa	gtccagggtc	720
atgaacttca	agccaagcaa	cnnttgaagc	agatcaagcc	cctggaggga	atcatggaaa	780
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acacnggaaa	ccagcaggcc	cg				862

<210> 424

<211> 859

<212> DNA
<213> Homo Sapiens

<400> 424

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gagatgaaga	aaatcatctc	attaaaatgg	caacatttct	gataaatggt	tcataattat	180
gtgatgggta	attgactccc	catctacccc	tccagtcag	agetacaaaa	gacagtgcac	240
aaccacagct	aacaggtggt	gggggtgccc	aagtagacag	ggctgcagaa	caagcaacgg	300
ggttaaactt	ctcaaacaac	aagcaacttc	tttatttgta	cagagtaaga	atatagaaga	360
aaagcatcat	tttctttttt	agccctttta	ttagtggttt	gctccacccc	aagttactgc	420
ataccaagca	gctaataaaa	accaactgac	ttaaagtctc	tgaaatgcat	gcaacttaaa	480
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gctgggttac	caggggtgtc	tggcatgctg	ctgggggttg	aagtcgctgc	tgctgnngct	600
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<210> 425
<211> 837
<212> DNA
<213> Homo Sapiens

<400> 425

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tgatactttg	aaaaggtcac	agctttttac	agcagaaagc	ctacaggcca	gcaaagaaaa	180
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aaaattaaag	acagagttac	agatggtaga	ggatgaagct	ggaagtcttc	ttgacaaatg	300
ccaaaagctt	cagacggcac	ttgccatagc	agagaacaat	gttcagggtc	ttcaaaaaca	360
gcttgatgat	gccaaggagg	gagaaatggc	cctattaagc	aagcacaag	aagtggaaag	420
tgagctagca	gctgccagag	aacgtttaca	acagcaagct	tcagatcttg	tcctcaaagc	480
tagtcatatt	ggaatgcttc	aagcaactca	aatgaccag	gaagttacaa	ttaaagattt	540
agaatcagaa	aaatcgagag	tcaatgagag	attatctcaa	cttgaagagg	aaagagcttt	600
tttgcgagc	caaaacccaa	agtctggatg	aagagcagaa	gcacagatt	ctaagaactg	660
ggagaagaaa	gtaaatgaac	caagagactc	agcaggaata	ttatgaaagg	gaacttaaaa	720
anctgcaagt	agaatggaag	aagaggggct	taattaacga	nggccattct	aagacttttg	780
gaagaattag	cttggaaacnc	cttttggaac	ttgaacttgt	cncaggtaat	gccattt	837

<210> 426
<211> 724
<212> DNA
<213> Homo Sapiens

<400> 426

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atcacaggaa	atacagtgc	ttttcaagtt	ggagagacaa	atactttctc	attcacagtg	180
tttgacatag	gaaagcctat	ttacataaca	atctgtataa	agtcatgctc	ttagtaacag	240
tctatacaga	gctgtgccaa	cacaattctt	tcagaatgtg	aagtaccggg	caaaccactc	300
ctggcgctgg	ggatctggag	aagccactgg	agaagcttca	ctctgagcag	gactcaaaaa	360
tgtcttgggc	ccttttaggtg	gactgggctg	tggaaagtgg	ttgctgctgt	tgaactcaat	420
atcgtggact	ggagaattag	gaatgggatc	caggcggtta	ggatgtccat	tgcccactcc	480

accagattcc	agagcactta	nattgggaac	actcacaac	ctgtttgttg	gtgatttatt	540
attctttcttc	ttttgcttag	ccaatggatt	aataacacca	acagtaggac	ttgagttaaa	600
cacttttggtg	aaagttagtt	tctcgaattg	actaattcca	gctgataaaa	cttattatcc	660
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catc						724

<210> 427

<211> 981

<212> DNA

<213> Homo Sapiens

<400> 427

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tagatgatga	tagntncaat	gaanctgnga	ncatanatta	angaaacana	naacantncn	180
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aaggcacacn	taancnatat	cagcaataaa	angggnnact	ttantacana	ttctgcaanc	360
attannnnna	taatganagg	atattatgaa	cagttgtatg	gcnatatgtt	tgaaaactta	420
gatgccgata	tgtttgaaaa	cttaaatgaa	acggaaaaat	tccttgaaga	accacaantt	480
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ggttncagaa	ccactcccc	antaccnaaa	tttataattg	ctcaagttcc	tgatataaaa	600
tggcaaaagta	tttgcatata	ncctatccct	acccttttac	atactttaaa	taacctntga	660
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catangattt	tgggaanggn	ccaacttggg	gccttngtaa	ctttttaaag	aaatngggaa	900
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aaatggggaaa tttncccaaa c

<210> 428

<211> 655

<212> DNA

<213> Homo Sapiens

<400> 428

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aaacccaatt	tggtcatgat	ttaatatatt	ttggatcgct	ctggatttgg	tttgctaata	120
ttttattcat	ccaagaaata	ttcattagag	aaattggcat	gggatttttt	tttcattgta	180
atgtccttgt	caggtatcaa	ggctttttca	gcctgataaa	gcatattaag	aaatgcttcc	240
tcttttccta	ttctctggaa	aagatttgtt	aatattgctg	ttactacttc	ctgtaatgtt	300
tggtgaaatt	cacaattgaa	gacatctggg	cctagcgtgt	tcctttagtg	aagaatatta	360
agaaagaatt	ccatttcttt	aaaagttacg	agcacagttg	gccttccaga	tcctatggatc	420
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cacagaatgt	nccattatgt	taggnattat	aagtaactca	gaggnatttt	aaagnatgtg	600
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<210> 429

<211> 788

<212> DNA

<213> Homo Sapiens

<400> 429

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aaacagtagg	cggatctttc	agagactcca	aatcattgac	aattcagaag	gatcttgtcg	240
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tcccagca						788

<210> 430
 <211> 655
 <212> DNA
 <213> Homo Sapiens

<400> 430						
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gcccttgga	caaagtntnt	tcctggcttc	cgaaggccaa	ggttcattga	ccaaa	655

<210> 431
 <211> 844
 <212> DNA
 <213> Homo Sapiens

<400> 431						
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cctgtcacta	gagaatttga	tgttggtcga	cacattgcc	gtgggtggca	tgggctagct	180
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gaataaaagt	ggagcctgga	aaataatggg	ttttgatttt	tgngtatcat	caaccaatcc	660
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<210> 432

<211> 807
<212> DNA
<213> Homo Sapiens

<400> 432

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aaactacttc	cttattcagt	gtaaaggagg	cttataagca	ttccaaaata	aaaacaaaca	180
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catactggat	ttttttcaaa	tgacttattt	tcataatttag	tagttcaagg	totataagct	660
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<210> 433
<211> 866
<212> DNA
<213> Homo Sapiens

<400> 433

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<210> 434
<211> 764
<212> DNA
<213> Homo Sapiens

<400> 434

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gaaaatgaaa	gtggagaaca	tggaacagca	atatttgncc	tcttctcata	ggatgcagtt	180
acacacacat	atgactggaa	tcacttcaga	gtaaaaaaa	agtgggctgg	gtgcagtggc	240
tcacacctgt	aatcccagca	ctttgggagg	ccaaggacag	gagcatcact	taaggccaga	300
agtttgagac	cagcctgggc	cacatagtga	gaccctgtct	ctatgggagg	ggtgggggtg	360
gggggcattg	taaaaaagca	gttggttctt	tanaaggcat	cagagagccc	tntagtgaac	420

acgaagggga	gttaatgcag	agatgactcg	agacagagaa	gcagtcacga	gtgtttacaa	480
aggaaaaagt	gagggagggg	aagctctttt	ggttaacagc	atattttacaa	ttagttaact	540
gnattcttaa	atacttttaa	cctgagtaac	atattataat	atgttatagg	aaacctcaca	600
gtcacaagtc	acactagaat	ccatctgtcc	agtatctggg	ctttccccac	accagaatcc	660
atctgtccag	tatctgggct	ttcccgagtc	ttcctcttct	cataagttcc	caanggcagc	720
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<210> 435
 <211> 834
 <212> DNA
 <213> Homo Sapiens

<400> 435						
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tccaggagct	ctgtctaaac	atcattccaa	cctttgcaaa	tcttatagac	tacccatcca	180
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ttcgtgtaaa	ttcatttagt	tgcttaggaa	agattttgga	atacttggt	aagtggtttg	300
tacttgatga	tatcctaccc	ttcttacaac	aaattccatc	caaggaacct	gcggtcctca	360
tgggaatttt	aggtattttac	aaatgtactt	ttactcataa	gaagtggga	atcaccaaag	420
agcagctggc	cggaaaaagt	ttgctctatc	ttattcccc	gagtattgaa	aacaatctta	480
atcttaataca	gttcaattct	ttcattttcc	tcataaaaaga	aatgcttaat	agattggagt	540
ctgaacataa	gactaaactg	gagcaacttc	atataatgca	agaacagcag	aaatctttgg	600
atataggaaa	tcaaatgaat	gtttctgagg	agatgaaagt	tcaaatattg	ggaatcagca	660
aattggcaaa	gtttttaaca	acattggagc	agaccttntg	actggcagtg	agtcggaaaa	720
taaagangac	gggttacaga	ataaccttaa	aagagcatcc	ttaccacttg	gaggaaaaac	780
caaaatttgc	caaaagaacc	aggaccggcn	ccgaagctgg	aaaagccgca	ggct	834

<210> 436
 <211> 812
 <212> DNA
 <213> Homo Sapiens

<400> 436						
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tcagaagttt	gaatttgaaa	tgaaatatga	aggtagtagt	caggggaagt	acatcagagt	180
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gtgattctaa	atatatccaa	gtgaatgcag	aaaaatacat	tactatttga	ggcagaccat	300
gctaaaatat	aattttacaat	gattagtttg	cacttaagat	ggttaataac	gcatttaaac	360
caatgaaatg	aagggttaagt	tgaattttgt	agtattttgt	cagtctctgt	actaaacaat	420
agttcatctg	aaaagtgttg	aaaaagcaaa	taacctgata	cttctcttta	tgcttatcat	480
tttctcactg	tcactcttaa	tgcaaacaaa	tcaatacagc	atcaagattt	tttacatatt	540
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aatgaccatc	acctcaattt	tttaataaac	accaagatcc	acaagccaaa	ataaacattt	660
gattaaaaag	ttatgggtatt	caagataact	cagtttcctt	tttctctttg	agattgggna	720
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<210> 437
 <211> 842
 <212> DNA
 <213> Homo Sapiens

<400> 437

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ctctagggtt	gttgaatgtt	gggtcacgaa	gatctcaacc	tggccaaaga	agagaaccca	180
gaaagatcat	cacagtttct	gtaaaagaag	atgtacacct	gaaaaaggca	gaaaatgcct	240
ggaagccaag	ccaaaaacga	gacagccaag	ccgatgatcc	cgaaaaacatt	aaaaccagg	300
agcttttttag	aaaagtttga	agtatcttaa	ataaattgac	accacagatg	ttcaatcaac	360
tgatgaagca	agtgtcagga	cttactgttg	acacagagga	gcggctgaaa	ggagtatttg	420
acctgggtctt	tgagaaggct	attgatgaac	ccagtttctc	tgtggcttac	gcaaaccatgt	480
gtcgatgtct	agtaacgctg	aaagtaccca	tggcagacaa	gcctggtaac	acagtgaatt	540
tccggaagct	gctactgaac	cgttggccaga	aggagtgtga	aaaagataaa	gcagatgatg	600
atgtctttga	gaagaagcag	aaagaacttg	aggctgccag	tgctccagag	gagaggacaa	660
ggcttcatga	tgaactggaa	gaagccaagg	acaaaagccc	ggcggagatc	cattggcaac	720
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cg

842

<210> 438

<211> 678

<212> DNA

<213> Homo Sapiens

<400> 438

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nngctctaaa	gatntcaaga	gnattaanag	nactttnttc	agggnagcac	tntttttttt	180
ttaaacantt	nttggngttc	tgtggncac	annatttct	tntgtntcaa	ngtnatgtat	240
gtnttgatna	cnatngngat	nttttaaan	ttntgaanca	agctgagagg	cnngcanaaa	300
gatntgangc	cnnaaaaaaa	aaaatctttt	ttaccttgtn	caccccaaac	tttttcaa	360
ctggncataa	tgctntacct	taaaacanac	atgaggggca	tcttgaagg	gagggaaant	420
tattttctctg	cntttctatn	atacangtng	tttacanaaa	ctngngaatta	naaaattaca	480
ctggnatattg	cngaccttaa	aataaattaa	aagtntctcaa	ctnttttttt	ttttgntaaa	540
cnttttttta	agnatgannc	cntgggttaa	aagaaaagnt	ttaaaccgaa	aatattttct	600
ataaataata	cctggatttt	ggnttttaggg	cccccgccct	aaggnttgna	ggttactttt	660
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<210> 439

<211> 826

<212> DNA

<213> Homo Sapiens

<400> 439

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gaaaaattat	cagccacgga	gagcattgtg	gaaatagtaa	aacaggaagt	attgccattg	180
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gtccccatca	ccccttcac	agttccttcc	tttccctcaa	ctcctccaac	tcctccagct	300
tctcctcctc	acactccagt	cattgttctc	gctgctgcca	ctactgttag	ttctccagat	360
gctgccatca	cagtccagag	agtccagag	gaggacgaga	gcataagaac	ttgccttagt	420
gaagatgcaa	aagagattca	gaacaaaata	gaggtagaag	cagatgggca	aacagaagag	480
attttggatt	ctcaaaactt	aaattcaaga	aggagccctg	tcccagctca	aatagctata	540
actgtacca	agacatggaa	gaaacaaaa	gatcggaccc	gaaccactga	agagatgtta	600
gaggcagaat	tggagcttaa	agctgaagag	gagctttcca	ttggcaaagt	acttgaatct	660
gaccaggata	aaatgagcca	ggggtttcat	cctgaaagag	acccctntgg	cctaaaaaaa	720
gtgaaaagct	gtggaagaaa	atggagaaga	actgagccag	accgtaatgg	ggcctgaaag	780
ggttctgang	gtgaaggaat	agatgcttaa	ttcangcttc	cccaga		826

<210> 440
 <211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 440
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 ccacagcatt tccttctgtt tcaatgttat gtatgttttg attactattg tgatttttta 180
 aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaaatc 240
 tttcttacct tggtcacccc aaactttctc aaatctggac taaatgctat accttaaac 300
 aaacatgagg tgcactctga aggggaggga aattttatttc tctgcttttc tattatacaa 360
 gttgtttaca gaaactgcaa attaaaaaat tacactggca tttgcagtc ttaaaataaa 420
 ttaaaagttc tcaacttttt ttttttgcta aacatttttt taagtatgag tccttgttta 480
 aaaagaaaag attaaaaacag aaaatatatt ctataaataa tacatgtatt ttgggttttag 540
 tgctcccgcc ctaaggtttg aagtttactt ttatccagta cttttttcct ccatgatcac 600
 ctttttttct ctttccctn ttccactcgg gcacacgtgg ggggtttctg cnanaattgg 660
 ccttgctgca ctgngaattg gcnaaaacc 689

<210> 441
 <211> 883
 <212> DNA
 <213> Homo Sapiens

<400> 441
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 cagccaagag agagaaaaaa actataagaa ttcgggatcc aaaccaggga ggtaaagaca 180
 taacagagga gattatgtct ggaggtggca gcagaaatcc tactccacc ataggaagac 240
 ccacgtccac acctactcct cctcagcagc tgcccagcca ggtccccgag cacagccctg 300
 tggtttatgg gactgtggag agcgtcatc ttgctgccag caccctgtc actgcagcta 360
 gcgaccagaa gcaagctcaa atagctataa ctgtaccaa gacatggaag aaaccaaag 420
 atcggaccog aaccttgaa gagatgttag aggcagaatt ggagcttaaa gctgaagagg 480
 agctttccat tgacaaagta cttgaatctg aacaagataa aatgagccag gggtttcatc 540
 ctgaaagaga cccctctgac ctaaaaaaag tgaaagctgt ggaagaaaat ggagaagaag 600
 ctgagccagt acgtaatggg gcttgagagt gtttcttgag ggtgaaggaa tagatgctaa 660
 ttcaggcttc acagatagtt ctgggtgatg ggttacattt ccatttaaac cagaatnctg 720
 gaagcctact ggtacttgaa ggtaagaaca gtatgaccag ggagtttctg gtggactttc 780
 cagttcatgc ctggctgnat tccaaaancc naagggcctg gcttctatta anggatgngg 840
 ttnttgacag gatcaaccaa ncccaaatgg ccaatgggga act 883

<210> 442
 <211> 777
 <212> DNA
 <213> Homo Sapiens

<400> 442
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 ttttctataa ataatacatg tattttgggt ttagtgctcc cgcctaagg tttgaagttt 120
 acttttatcc agtacctttt tctccatga tcacctttt ttctctttcc cctctccac 180
 tctgtcacac gtgggggttt ctgcgagaat tggccttgct gcaactgtgat tggcgaagac 240
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 tagaaggcat cctcggagat cacctcctcg tcatatagac aatcaaaaaa catccgcagc 480

aaattggcag	gttgatcaag	ttttactatc	gatgcttgta	gtgcataaag	tgcttgagct	540
tcctttctctg	natctgagtc	taggtacttg	agtaagatcg	gcactctctg	cttgaaacag	600
cagtgtccac	ttcttgaang	tagaagaagt	cggctattaa	tagctgggtt	acaaacagca	660
gtcattttaa	gctctaagga	atggtaggtg	aactctctcg	ggatttcggc	taagaataag	720
cccttttance	aggccaaaga	acctgggtcan	tcaattcgct	tttgccctc	caataaa	777

<210> 443
 <211> 875
 <212> DNA
 <213> Homo Sapiens

<400> 443

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agaggagagg	acaaggcttc	atgatgaact	ggaagaagcc	aaggacaaag	cccggcggag	180
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catcatgcat	gactgtgtgg	tgaagctgct	aaagaacct	gatgaagaat	ccctggagtg	300
cctgtgtcgc	ctgtccacca	ccattggcaa	agacttggac	tttgaaaaag	caaagccacg	360
tatggaccag	tactttaatc	agatggagaa	aattgtgaaa	gaaagaaaaa	cctcatctag	420
gattcgggtc	atgcttcaag	atgttataga	cctaaggctg	tgcaattggg	tatctcgaag	480
agcagatcaa	gggcctaaaa	ctatcgaaca	gattcacaaa	gaggctaaaa	tagaagaaca	540
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gagagtggac	gaaggtgggt	ggaacactgt	acaaggggcc	caagaacagt	cgggtactgg	660
acccctcaaa	antcctaaaa	atcactaagc	ctacaattga	tgaaaaaant	cactggacct	720
aaagccagct	aggcagctgg	ggaaaaggca	gcagtgggtg	accaangcaa	gtgaaactga	780
gccntacggc	aagtgtctnc	agttaaacag	atctntgncc	tgaaccttca	gaaccttang	840
gtcccgccat	cacgcctgta	aagttggatt	cccgga			875

<210> 444
 <211> 756
 <212> DNA
 <213> Homo Sapiens

<400> 444

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taaagttgct	ctaaagattt	caagagtatt	aagagtactt	ttctcagggt	agcacttttt	180
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gccaacattt	tttttaagta	tgagnccttg	nttaaaaaga	aaagattnaa	nccgaaaata	600
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ttcccacttn	gggccccccc	tngggggggt	tttgcg			756

<210> 445
 <211> 783
 <212> DNA
 <213> Homo Sapiens

<400> 445

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gttcaaacca	ttgtacatag	attaaaagat	gaagagacca	atgaagactc	aggaagagat	300
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gaaacctcta	ttaaccagcc	aaaagtcgta	gcacttagta	ataacaaaaa	agatgatata	660
aaggaaacag	attcttttatc	agatgaagtt	acacacaata	gcaatcagaa	taccagcaat	720
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cct						783

<210> 446
 <211> 866
 <212> DNA
 <213> Homo Sapiens

<400> 446

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tttacaaga	gttggttaaag	ggtttcaatc	aaaattatta	aaactataca	gtacaataac	180
caattgataa	catcttgaaa	gaagtgcaat	atttgagttc	acatattttt	aaaagtgtctg	240
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gttggttggt	gttttaagct	agtcttataa	aagtcttaat	taaaatcaag	gttgataaac	360
aaagcataac	agattaaaaa	ttcccaaatt	gcatttctta	gtaaataaaa	atgaagtgc	420
ataaccaa	attgctctaa	tgaagggttc	cagactagcc	tcaactaaac	agttattgggt	480
cttctatggc	acttttttct	ggtccaaata	accatgcatt	aatccttacc	attacatggt	540
actcaaat	tatttgatta	catagaacaa	aaacaaataa	aattaatggg	ctggataaac	600
aaaattaata	aacctctatc	atcaaatt	tgttacagta	actaggaaca	aagaaaggca	660
gtttgggtggg	taaaacacta	ttacactgat	ccccatagga	aaccctttta	aagactctgg	720
aagtgttgag	ttcacattta	atggtacctg	tagaaacagn	cctttatttg	gacaccttta	780
cccactggca	ngccctaang	gacccatccc	tttgccttat	aacttttcac	aagcaattct	840
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<210> 447
 <211> 789
 <212> DNA
 <213> Homo Sapiens

<400> 447

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aatcggctgc	acttcccatc	ttttcctcgt	ttgtcagcaa	ttgggatgaa	gccacaaaaa	180
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ctaataaaaa	agtagagatt	caaaaacatg	ccacaggaaa	gaagtctcca	gcaaagagtc	540
ctaatacccag	cacacctcgt	gggaagaaaa	gaaaggcttt	gccagcatct	gagaccccaa	600
aagctgcaga	gtctgagacc	ccagggaataa	gcccagagaa	gaagccaaaa	atcaaagaag	660
agcagtgaag	gaaaaaagtc	cttcgctggg	gaaaaaagat	gccgaagaca	gacttcaaaa	720
aagccagang	ccagggttttc	ccactcctag	taaatctgtg	agaaagcttt	ccacaccccc	780

<210> 448
 <211> 820
 <212> DNA
 <213> Homo Sapiens

<400> 448

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cctgcctcag	cctccctagt	agctgggatt	acagggtgtc	accaccatgc	ccaattaatt	180
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gcccctggac	tacttatgga	ggttttaaaa	aatcttttaa	gtccaggcct	gacgtttaga	360
gaaggttaca	aaggcggcca	ggatctgagt	atttccaaaa	agctctggag	gcagcattga	420
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ccattttttg	ggggtgtggg	aagcttttct	cacagattta	ctaggagtgg	tgaaaaactt	540
ggcctctggc	ttttttggag	tctgtctcgc	atcttttttc	cccagcgaag	gacttttttc	600
cttactgcc	tcttctttga	tttttggcct	cttctcttgg	gcttttccct	ggggtctcag	660
actctgcagc	tttttggggg	tcttcaanat	gctggcaaaa	gccttttctt	ttcttcccac	720
gaggggngc	ctggggatta	ggactctttt	gcctgggana	cttcttttct	tgngggngang	780
tttttgaaac	nntacttttt	ccaattttagc	ctggaggcct			820

<210> 449
 <211> 936
 <212> DNA
 <213> Homo Sapiens

<400> 449

aaaaagaagga	aacagttact	caactccaaa	atatcattga	ggctaattct	cagcattacc	60
aaaaaaatat	taatagtttg	caggaagagc	ttttacagtt	gaaagctata	caccaagaag	120
aggtgaaaga	gttgatgtgc	cagattgaag	catcagctaa	ggaacatgaa	gcagagataa	180
tataagttgaa	cgagctaaaa	gagaacttag	taaaacaatg	tgaggcaagt	gaaaagaaca	240
tccagaagaa	atatgaatgt	gagttagaaa	atttaaggaa	agccacctca	aatgcaaacc	300
aagacaatca	gatatgttct	attctcttgc	aagaaaatac	atttgtagaa	caagtagtaa	360
atgaaaaagt	caaacactta	gaagatacct	taaaagaact	tgaatctcaa	cacagtatct	420
taaaagatga	ggtaacttat	atgaataatc	ttaagttaaa	acttgaaatg	gatgctcaac	480
atataaagga	tgagtttttt	catgaacggg	aagacttaga	gtttaaaatt	aatgaattat	540
tactagctaa	agaagaacag	ggctgtgtta	ttgaaaaatt	aaaatctgag	ctagcagggtt	600
taaataaaca	gttttgctat	actgtagaac	agcataacag	agaagtacag	agtcttaagg	660
aacaccatca	aaaagaaata	tcagaactaa	atgagacatt	tttgtcagat	tcagaaaaag	720
gaaaaattaa	cattaatggt	tgaaattcaa	ggtcttaang	gacagtgtga	aaacctaccg	780
ccaggaaaag	caagaagcca	ttttaaantt	ntgagagntt	acctcagagga	ttttggaaat	840
ttcccaancn	gaactggggg	gaatctgctg	ggaaaaatag	gtcaggaggt	cgaatcatgg	900
aaccaccagc	aggcctttga	ngtcatgacc	tgagca			936

<210> 450
 <211> 806
 <212> DNA
 <213> Homo Sapiens

<400> 450

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aacagtgaga	tctctgagca	catggctgtg	acctcaacca	cttttctatc	accagggtct	120
agaatagttg	ggcattttaa	taaaatttgc	taaatgaatg	aaaaatccaa	aataaatcat	180

gaagccattt.ataaatcaca ccaatcttgc ttgggttaaa caatagaaag taacactttt	240
gaaagagaag gcaaacaggt gtagagggg caagaatgtg agctcgagga aaagacagct	300
acgaactgtg tttttaacaa ctcatattt ggctactata tttccaatc tattctaaca	360
ctaacaagaa tctgtctaata taattgtgac aacatctgca aaaccatagt tacctatttt	420
ttcttccaac tcttttactg aagacagagg atcatttttt acagaagggtg attttgctaa	480
ggaatccttt aatagtatca actctgctct cctatctcgt aattcttttt gntctagtag	540
tggcttttagg ttttcatgtt cttttataaa acattttttt ttttcattat ggatttcaact	600
tttgctacat gtttgagata cttctttcaa cttgaattaa aagaatctga ttttcaagcc	660
ttggtttttc attagcattc ttcattttcta gaagatccag actgcanggn ctctttttct	720
ggactggaat tcttctaact cttttccttt aagaagaacc tttttcttgg ntcataggcc	780
tcttcaatta aggacttaag gtcttt	806

<210> 451

<211> 909

<212> DNA

<213> Homo Sapiens

<400> 451

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tcattttata cacactagtc agtggctcac ttccctttga tgggcaaaac ctaaagggaac	120
tgagagagag agtattaaga gggaaataca gaattccctt ctacatgtct acagactgtg	180
aaaaccttct caaacgtttc ctggtgctaa atccaattaa acgcggcact ctagagcaaa	240
tcataagga caggtggatc aatgcagggc atgaagaaga tgaactcaaa ccattttgtt	300
aaccagagct agacatctca gacaaaaaa gaatagatat tatggtggga atgggatatt	360
cacaagaaga aattcaagaa tctcttagta agatgaaata cgatgaaatc acagctacat	420
atttgttatt ggggagaaaa tcttcagagc tggatgctag tgattccagt tctagcagca	480
atctttcaact tgctaagggt aggcccgagc agtgatctca acaacagtac tggccagtct	540
cctcaccaca aagtgcagag aagtgtttct tcaagccaaa agcaaagacg ctacagtgcac	600
catgctggac cagctattcc ttctgttgtg gctatcccg aaaaggagtc agaccagcac	660
tgcagatagg tgaccctcaa agaagatggg aaatttctt ccnggaaatc aaagtggcag	720
tgctggttgg aaggaaangg gaattgcttc cagccaggtc ccattgctttg ggnaatgcc	780
ggtaatnct aataaggcgg atattcctgg aagccaggga aaagctccac tggnccttag	840
tagtanenca gcatctggtg ggaatgaacn gacccgaaatt ncttaagggt tgcagtggag	900
agaacttcc	909

<210> 452

<211> 672

<212> DNA

<213> Homo Sapiens

<400> 452

actgaaaaaa agtgaanttt naattatntt gtnaatnnac tnaaaaaacc ncacncaagc	60
aatgttcaca antntaaatt naaacctttt gactaaaaaa ancacaaaan ancaaacaca	120
aaaccacagg cntgaactgn aaacctgtct taactatgaa ctggncctta gggttaattct	180
tannngccat tcantatttc nntccttggg aactgtaatg ttntagcacc ggatgatctc	240
ccgnanaggt nctagaanng acngnctgcc agngnangga gatncttccn tatacaccac	300
ttnanacnca taccgtcnan tttnanacen acccagacgg nangcacatg gngatggggc	360
cncacnccna ctntnanggn aacggaagta gggcagnggg cgcattnggt gcacatcttt	420
aatgtattgc attcgnaaaa aaaaggccag ntttcnatcc caggcgtgct ctngacctna	480
gactttaatn ncatgattta naanatncag nacgntattg cctaaatntt attctataca	540
tttccatcag tggtnagga aaacacttta aatgcaactn anttccacat cananncact	600
gnggttacag ntttagctca ttgggcaatt tttngaagca attttttnng aaangctntt	660
ggaatgnccc cc	672

<210> 453

<211> 834
 <212> DNA
 <213> Homo Sapiens

<400> 453

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ggaagaagaa	gcttcgttgt	gagagggagg	agcttcccac	catctacaag	tgtccttacc	120
agggctgcac	ggccgtgtac	cgaggcgctg	acggcatgaa	gaagcacatc	aaggagcacc	180
acgaggaggt	ccgggagcgg	ccctgcccc	accctggctg	caacaagggt	ttcatgatcg	240
accgctacct	gcagcgccac	gtgaagctca	tccacacaga	ggtgcggaac	tatatctgtg	300
acgaatgtgg	acaaaccttc	aagcagcgga	agcaccttct	cgccaccaaa	atgcgacatt	360
cgggagccaa	gcctttgcag	tgtgaggtct	gtgggttcca	gtgcaggcag	cgggcatccc	420
tcaagtacca	catgaccaa	cacaaggctg	agactgagct	ggactttgcc	tgtgaccagt	480
gtggccggcg	gtttgagaag	gccacaacc	tcaatgtaca	catgtccatg	gtgcaccgcg	540
tgacacagac	ccaggacaag	gccctgccct	ggaggcgga	ccaccacctg	ggccaccgag	600
cccctctgtg	accacagacg	gccaggcggt	gaagcccgaa	cccacctgag	gacggcagtg	660
aggatgagca	cctctagcag	cctggacttc	gcagtggctg	tgtcaagcct	cacccttcgt	720
gtgcaccgcg	atgggagggg	cggagggttg	cttgccgncc	ttggtgctgg	angcgggctt	780
ggtgtccggc	tcaagtagcc	ttctttgntc	ttgggaccag	tgggttattt	tccc	834

<210> 454
 <211> 703
 <212> DNA
 <213> Homo Sapiens

<400> 454

cccgtgtaaa	taatttatta	caagcataac	atggagctct	tgttgacta	aaaagtggat	60
tacaaatctc	ctcgactgct	ttagtgggga	aaggaatcaa	ttatttatga	actgtccggc	120
cccaagtcac	tcagcgtttg	cgggaaaata	aaccactggg	cccagagcag	aggaaggcta	180
cttgagccgg	acaccaagcc	cgctccagc	accaagggcg	ggcagcacc	tcgaccctc	240
ccatgcgggt	gcacacgaag	ggtgaggctg	acacagccac	tgcggagtcc	aggetgctan	300
aggtgctcat	cctcactgcc	gtcctcaggt	gggttcgggc	ttcaccgcct	ggcgtctgt	360
ggtcacagag	gggtcgggtg	gccaggtgg	tgggtccggc	tccaggggca	gggccttgte	420
ctgggtctgt	gtcagcgggt	gcaccatgga	catgtgtaca	ttgaggttgt	gggccttctc	480
aaaccgcgg	ccacactggg	cacaggcaaa	gtccagctca	gtctcagcct	tngtgggt	540
catgtggtac	ttgagggatg	cccgtgcct	gcactggaac	ccacagacct	cacactgcaa	600
aggcttggt	nccgaatgtc	gcatttgggg	gacgaaaaag	gtgcttccgc	tgcttgaaag	660
gnttgccca	attnggtaca	agatatagtt	ccccaccttt	ggg		703

<210> 455
 <211> 825
 <212> DNA
 <213> Homo Sapiens

<400> 455

atggcaatca	ggaaaagggtg	ccagaacccg	aggctttgga	ccttccagat	gacttgaacc	60
ttgacagtga	agacaagaat	ggtggtgagg	acaccgacaa	tgaagaagga	gaagaagaga	120
atccttttga	gataaaagaa	aaaccagaag	aagcaggtca	tgaagctgag	gaaagaggag	180
agaccgagac	cgaccagaac	gaaagtcaga	gtccacagga	gcctgaggaa	ggccccagtg	240
aagatgacaa	ggcagaaggg	gaagaggaaa	tggacacagg	agctgatgac	caagatggag	300
atgctgctca	gcctcctgaa	gaacactctg	aggagcagca	gcagtctgtg	gaggaaaaag	360
acaagggaagc	cgatgaagaa	ggtggagaga	atggccctgc	tgaccaagggt	ttccagcccc	420
aggaggaaga	agaacgggag	gactctgata	cagaggagca	ggtgccagag	gctttggaga	480
ggaaggagca	tgctcctgt	gggcagactg	gtgtggagaa	catgcagaac	acacaggcca	540
tggagctggc	tggggccgca	cctgagaagg	agcaggggaa	agaggaacac	ggaagtggag	600

ctgcagatgc aaaccaggca gaaggccatg aatcgaattt cattgcccag ttggccttcc	660
agaacacacc aggaaaaaca cacagagttt taagaggaaa cctgggcagg cttgacaatt	720
gaacgttnca tgggtgatca caattgaacg tgtgcacaag aagctganga cttgtggaat	780
ccggacaggc attgccaacc agggggccagc ttaacaagcc ccagg	825

<210> 456

<211> 740

<212> DNA

<213> Homo Sapiens

<400> 456

acatcaacaa cagtgggtata tgttttaata gttttcagaa tataagctgc atagcttttt	60
agaataaaaa atgatataac ttcagggtaca tgctttggga cacttggtta aacaaggaat	120
ctgtgtcttt gatgaccacc tcaaaagggt cgcagacttc acagtgtaac ttggaaacag	180
acaaggagat agatgattac atcatgacat actgcctaca aaagaacatt ctgacagaac	240
attaagtaga acagagcaca cagtttcaag tattcagcac tgctttctgg ccaagtaaaa	300
actgcctaaa gatcagtttc ttteogactgg aaaaaataga tggagctgct gaggttctgga	360
cacagcgttt ctttcccaga atgagactgg ctcagtcacag cttgaaagca gtgtgaggaa	420
tcactcttcc ccttgactgt taagaaaaaa aaaaatgaac taaacaaata aattactaca	480
acaacaggga ccattggcact gaatgaaata aaggggcaat caccttccca tcattgcata	540
gtctcccgaa gcagcaagtg tgaaagagga tactgaaaag ccacttcatt ttacacagc	600
ccaagggatc gtttttatng atgacctggg cacctataat gnccagttgc tttatgagaa	660
ccacacacac accacattct tcctaccctn taagagaagg taggttccct tcacaataag	720
gaaaaccccc ccttatactt	740

<210> 457

<211> 726

<212> DNA

<213> Homo Sapiens

<400> 457

aaaatgtagt caacttttatt ctcccttaaac caaaaaatag agtctttggt tgtacaaaca	60
tcactagtta cagctctcgcc gaggtctcgg ctgggggtgg gcagttagtt agtcacaggc	120
cagaactcct gtgggggtctc tttaaaatgc taacaccacag gttaaaagac ttggggcaag	180
ggtggtgctg gagctggcag ggccccacc ccaagtctgg gggaggtgcc tgctcctcta	240
ggagggcaca gggcccaggc cacggcgccc aggccttacg gggcggcggc tgctgcacag	300
tgccacatct tcagggccca cagcgccggg tgagggcctg ccagaaagca ccagagccac	360
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agcaaagtcc ggtgacaggc gtcccgggga ggtgctgggc tggggggcga ggtcttccac	480
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ccgcgtgccc cggcctttct gggacctgct gaggaccatc tgtgctcgga gacgctcctg	600
ttccaatgac ttcatcctgg ctggccttca caagcgcacg cttctcggnr ttcaggggccc	660
cggacttcgg caaggggaca nggcacgctt cgggtgcccg tggcttccgg actttggacg	720
ccgcaa	726

<210> 458

<211> 870

<212> DNA

<213> Homo Sapiens

<400> 458

cgcgccctct ccgcggggtg taccacctgt cgcggcgca gacctctggt gaaagaaaag	60
atgttgctcc ggttaagagt agtttccacc acttgtaact tggcatgtcg acatttgcac	120
ataaaagaaa aaggcaagcc acttatgctg aaccaagaa caaacaaggg aatggcattt	180
actttacaag aacgacaaat gcttggtctt caaggacttc tacctccaa aatagagaca	240

caagatat	ttc	aagccttacg	atttcataga	aacttgaaga	aaatgactag	ccctttggaa	300
aaatata	tct	acataatggg	aatacaagaa	agaaatgaga	aattgtttta	tagaatactg	360
caagatg	aca	ttgagagttt	aatgccaatt	gtatatacac	cgacgggttg	tcttgccctgc	420
tcccagt	atg	gacacatctt	tagaagacct	aagggattat	ttatttcgat	ctcagacaga	480
ggatcat	gtta	gatcaattgt	ggataactgg	ccagaaaatc	atgttaaggc	tgttgtagtg	540
actgatg	ggag	agagaattct	gggtcttggg	gatctgggtg	tctatggaat	gggaattcca	600
gtaggaaa	ac	tttgttgnat	cagcttgtgc	aggaatacgg	cctgatagat	gcctgccagt	660
gtgtatt	gat	gtgggaactg	ataatatcgc	actcttaaaa	ganccatttt	acatgggctt	720
gaccagaa	ac	gagatcgcac	ccacagttga	tganctgatg	gatgagttta	tgaaagcttt	780
actgacag	at	atggccggaa	cacctttatt	cagttcgaag	acnttggaaa	tcataangcc	840
ttcaggtc	ctt	tgagaaagtc	cggggaaaaa				870

<210> 459

<211> 761

<212> DNA

<213> Homo Sapiens

<400> 459

aaatgtaaga	tatttattaa	ataaaaaggt	tacactatga	tttttataca	ctgttgaaaa	60
caatgacttt	tatttactta	aagccagcag	tagttcccat	tactctcata	atgttatagt	120
taaggcttga	tttagttcca	gaaaataaat	agggtaaatt	tttaatat	ttccctagctct	180
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aagagtatta	cccataatag	taaatagcaa	atactttggc	aagtctgaat	tagagtacaa	420
gtgaagacat	tcacaaacac	actttttaca	tctcctggat	gtgggtacggg	ctgtatgtta	480
gaattaaagc	atcacaaacta	tctgattgta	gggtgctggg	gggcaatgca	atcaatcaac	540
acgtctaccc	caacagatgt	ggagacccat	ggaaaaaata	catcaaccaa	agtgggtcagg	600
gagaacaaaa	cccagaaaaa	caccottaaa	actgaagaca	ttatctcttc	ttgggtgaaa	660
aaaggggttc	cctgggagc	angaaaggtt	ttatcaaggg	aggcttctat	tcngtaatca	720
caggaaggct	tgatgcanat	tcttggccat	tcatacccca	t		761

<210> 460

<211> 876

<212> DNA

<213> Homo Sapiens

<400> 460

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cactcagccc	tccagtgtcg	ggctctgcag	gtgtgacatt	cggctaccag	ggacagaaac	120
cactctttta	gaacttggat	tttggcatcg	acatggattc	aaggatttgc	attgtgggccc	180
ctaattggtgt	ggggaagagt	acgctactcc	tgctgtctgac	tggcaagctg	acaccgaccc	240
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agcagctgcg	catggaggag	acgcccactg	agtacctgca	gcggggcttc	aacctgccct	360
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agatctgcaa	actctctggg	ggtcagaagg	cgcgagttgt	gtttgctgag	ctggcctgtc	480
gggaacctga	tgtcctcctc	ttggacgagc	caaccaataa	cctggacata	gagtctattg	540
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cccgaactcat	cacagaaacc	aattgccagc	ttgtgggttg	tggaggaaca	gagtggtagc	660
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aattgggggg	gcctaaaann	cctctggggg	cttcccttct	tttgaanaat	gctntggnc	840
gcaantgact	tggcaaccat	ttaggccctt	taaagg			876

<210> 461

<211> 689
 <212> DNA
 <213> Homo Sapiens

<400> 461

gcaaacaaga	tccatttagt	ggggaagagg	ggactattaa	aagctgctag	aaaactgaat	60
aaagcaaata	aagactgaga	acagttccaa	ctcccatcaa	tctccaaaca	gtgacaggtc	120
ggcagcaact	ccttttcctt	atttcttccc	cttgtaaagg	gaaattcaag	ttcagcagca	180
ttcctttcct	gccccaaagt	ctcaaccaga	caagaggctg	caggcaccaa	atcttgggct	240
ggataatggc	aaaggcctca	gaagctcacc	tccagctctg	agcttcaaca	gctgtttgta	300
ccagtgaagc	agcattaaat	ccaccagaaa	agaacagcac	cacccaaaga	ctggggggca	360
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acaataggcc	acataaactt	ggctggatgg	aacctcacia	taagggtggt	acctcttggt	480
tgtttagggg	gatgccaagg	ataaggccag	ctcagttata	tgaagagaag	cagaacaaac	540
aaagtctttc	agagaaatgg	atgcaatcag	aagtgggagc	cccggncaca	tcaagggtcac	600
actccacctt	catgtgcctg	aaatgggtgc	caggtcagct	gcaggcccan	aggcagtcct	660
canaaggaag	gggagaccac	agaggactt				689

<210> 462
 <211> 840
 <212> DNA
 <213> Homo Sapiens

<400> 462

aggagccttt	ggagttccat	gccaagcggc	cttggcgccc	cgaggaggca	gtagaagatc	60
cggacgagga	ggatgaggat	aatactagt	aagccagaga	tgggttctcc	ctggaggaag	120
tgttacggct	cggaggcacc	aagcaagatt	accttatgct	ggctactttg	gatgagaatg	180
aggaagtgat	agatggaggc	aaaaaaggag	caatcgatga	ccttcagcaa	ggtgaattgg	240
aagcatttat	tcaaaatctt	aatttggcga	agtatacaaa	agcttcotta	attgaagaag	300
atgaaccagc	tgaaaaagaa	aattccagca	aaaaagaagt	aaaaatacct	aaaataaata	360
ataaaaaatac	agcagaaagt	caaaggacat	cagttataaa	ggtgaaaaat	aagaataggc	420
cagaaccaca	ttctgatgag	aatggcagta	ccacaccgaa	agtaaaagaa	gataaacaga	480
acatctttga	atTTTTTgag	agacagactt	tgttacttag	gcttggaggc	aaatgggatg	540
atctggagta	cagcaatgaa	tattctttga	aaccccagcc	tcaggatgtt	gnatctaagt	600
acaaaaccct	tgctcagaag	ctgtatcagc	atgaaatcaa	cttattcaaa	agtaagacga	660
atagtcaaaa	gggagcctct	tctacctgga	tgaaaggcaa	ttgtgtcatc	ggggaccact	720
agggtgacagg	atggcagcca	ttgattcttc	ttattcagga	tgatgcccg	tcacaccact	780
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<210> 463
 <211> 784
 <212> DNA
 <213> Homo Sapiens

<400> 463

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tttgcattct	tggtgtgtag	ccagtcattc	cggttcagct	cccatctaag	ctgtttgaga	180
cttgcaattat	ctttgttagc	catggcattc	atgccaatgt	tatcaaaact	ggatcccata	240
ttttcatcca	atagatggcc	aaactcttca	gcagatacaa	ataggctgga	atcatttaag	300
tttcttttct	ttttcttgg	cccttgaaat	gagccagcaa	agtcaaaatc	atctgtacct	360
tttctcttgc	ttttcttagt	actgactttg	gagtggaact	caagttctgg	aacactctca	420
ctttcatcat	ctaacacatc	catgaatgtt	cctccatctt	catcaacttc	agcaaattct	480
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<210> 464

<211> 850

<212> DNA

<213> Homo Sapiens

<400> 464

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ccacagaagc	cgcaggtcgg	ggtctgcagc	ccctgaagct	ggactaccgc	gccctggccg	180
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<210> 465

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 465

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cagaactcct	gtggggtctc	tttaaaatgc	taacaccag	gttaaaagac	ttggggcaag	180
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ccgcgtgccc	cggcctttct	gggacctgct	gaggaccatc	tgggctcngg	aaagcgtcct	600
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ggagcttttg	canggggaca	aggcaacgct	tgggtgccc	ggtgggttcc	ggacttttga	720
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<210> 466

<211> 1240

<212> DNA

<213> Homo Sapiens

<400> 466

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ggattactttt	ccatcctgga	actactaaat	ctaagtctgg	gatgaagcat	ggaaccatgg	180
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<210> 467

<211> 885

<212> DNA

<213> Homo Sapiens

<400> 467

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tccatccttg	aactactaaa	tctaatgctg	ggatgaagca	tggaaccatg	gacactgaat	180
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tttgaccta	gcttgcccaa	agaaggacat	gataaagttc	tcaagtatct	tacttaagcn	780
caaaaanggc	agcactactt	tnttgaccac	ccccaacggg	ggacggctct	gaatgccatt	840
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<210> 468

<211> 748

<212> DNA

<213> Homo Sapiens

<400> 468

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atactatctg	taagtgaacc	aaactaaaat	tcatttatga	accaagaaag	gaagccaagt	360
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catggggcat	tttgttgaga	gttagcagtg	aggcaccact	ggtcagagac	tcggtaaagc	600
tgagtttgcg	gaaggatgtc	tccacgccgc	ttgtcgcaga	cactgtcact	ggcttcggag	660
ctcgnctatt	tgtctccttg	tggaggcagg	cgaaanaagc	agcgagtggg	ccctgaaaag	720
gngggcnttc	actgggctgg	aaggcttg				748

<210> 469

<211> 770

<212> DNA

<213> Homo Sapiens

<400> 469

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atgctgtgg	cagaaggaat	gccaggtggc	gaccgtgata	cctttaatga	caataggaac	180
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ggatgcactt	cagcttctgt	cttgtggaca	acgcagtggg	attttagggc	tttggtttac	480
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agctgagttt	gcgggaaagg	atgtnttcca	cgccgcttnt	cgcanacact	ggcactgnct	660
tgggagctcn	gctattttgc	ttgcccttgt	ggangcaggc	caaaanaagc	caacgaatgg	720
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<210> 470

<211> 892

<212> DNA

<213> Homo Sapiens

<400> 470

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ccttctatga	cctggatgac	tcttgggaaa	atgcaggaaa	aggattgaag	gagttggntc	840
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<210> 471

<211> 759

<212> DNA

<213> Homo Sapiens

<400> 471

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atcaagtac	tctcatttta	aaatatctct	tttcttaacc	cttaatttga	atgcaaaatg	120
atgctgtggt	cagaaggaat	gccaggtggc	gaccgtgata	cctttaatga	caataggaac	180
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acgggtgtggg	aaattgtcag	caggctaaat	tttgcttct	agaggctcct	cctgcccata	540
atcatggggc	attttgttga	gagtttagcag	tgaggcacca	ctggtcagag	actcggtaaa	600
gctgagtttg	cggaaggatg	tctccacgcc	gctgtccgca	gacactgtca	ctgnctcgga	660
gctcgtctat	ttgctgcctt	gtggaggcag	gogananagg	caacgagtgg	gccctgaaaa	720
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<210> 472

<211> 852

<212> DNA

<213> Homo Sapiens

<400> 472

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ggattacttt	ccatcctgga	actactaaat	ctaattgctg	gatgaagcat	ggaaccatgg	180
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tatcttactt	cagcccaaaa	anggcagcac	tacttntttg	accaccccaa	cgggggacgg	840
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<210> 473

<211> 804

<212> DNA

<213> Homo Sapiens

<400> 473

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804

<210> 474
<211> 819
<212> DNA
<213> Homo Sapiens

<400> 474

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<210> 475
<211> 721
<212> DNA
<213> Homo Sapiens

<400> 475

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<210> 476
<211> 442
<212> DNA
<213> Homo Sapiens

<400> 476

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nacaaaaanc tcanttaaan gtnttccanc anangnggan gnccttngaa ngcaaaaanc 420
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<210> 477
<211> 878
<212> DNA
<213> Homo Sapiens

<400> 477
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agtaccgggg atgtgatgga tgtctttatt ccccaagccc ntccaggggc ttttggcttt 780
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<210> 478
<211> 768
<212> DNA
<213> Homo Sapiens

<400> 478
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ttcaaaatct tcttagggta aaataaatac ccgtatctat gcagtaccat aaacatgtta 180
ataaaaggcc actcaacatt gaaagccttc tatgaccagt aactgaaatt tacacaagtg 240
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gctgagtaat agtgcaagtg cattttaggt ggggtcacc agacttattc aaaactagat 420
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aaataagttt atttgaagca aaataaacta ctgccagaa actttatgaa agttccatct 600
caaaagggtc aaaaagggg aattaactgc tatgaattct ttgcattcag ggcgtcaaaa 660
gacgccggcc tnggatgcc gtgatgacca attcttgaat gagaaagcat gtagaccgna 720
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<210> 479
<211> 815
<212> DNA
<213> Homo Sapiens

<400> 479
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tgagaacgat gagccattg aaataccatc ggaagacgat gggacgggtg tgctctccac 180
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tcttatgggtg	cagggtcaaga	aagatcttaa	gactgggtcat	tcaaaggggt	ttggcctttgt	540
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acgatgggtgt	gactgcaaac	ttcctaattc	taagcaaagc	ccagatgaac	ctttgagaag	660
cagaaaagtgt	tttgtggggg	cgctgtacag	angacatgac	tgangataa	cttcnggagt	720
tcttttttta	ataccgggat	gtgatggatg	cttcatttcc	caacccttc	agggcctttg	780
nctttggtac	catttgcaga	tgatcanatt	gcccc			815

<210> 480

<211> 812

<212> DNA

<213> Homo Sapiens

<400> 480

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gtaaagaagg	gattaaacca	tgccgttgac	aagttaactt	acccctgggc	tccttgaagg	300
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caaataagtt	tatttgaagc	aaaataaact	actgccaaaga	aactttatga	aaagttccat	600
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aaaacaaaga	ccccatatta	tttaaaatcc	agtttattta	agaatttncc	accntggaca	720
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<210> 481

<211> 1127

<212> DNA

<213> Homo Sapiens

<400> 481

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ttaaacggaa	cttgccctgtg	aatttcgagg	tggcccggga	gagtggccca	ccccacatga	240
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agaagatttc	aaagaaaaat	gcccgcctag	ctgttcttga	ggagctgaag	aagttaccgc	360
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tcaaagtccc	gcaggcgagc	cccaccaaac	ccgcaactca	gtcagaggag	aagacaccca	720
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aataacatct cttcaggcca cgtaccccat ggacctctca cgagaccctn tgagcaactg 1080
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<210> 482
<211> 773
<212> DNA
<213> Homo Sapiens

<400> 482
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cccagatcca gcaggcaaaa aaggagaagg agccagagta cacgctcctc acagagcgag 180
gcctccccgcg ccgcaggagg tttgtgatgc aggtgaagg tggaaaccac actgcagaag 240
gaacggggcac caacaagaag gtggccaagc gcaatgcagc cgagaacatg ctggagatcc 300
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atgaaaatgg gactagtaat aaagaggatg agttcaggat gccttatcta agtcatcagc 480
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ctgccatgat agcccgagag ttgttgatg ggggcacctc gccacagcc cgagaccatt 660
ttaagaata acatctcttc aggccacgta ccccatggac ctctcagag accctntgag 720
caactggact atctttncag agtccaggga ttncagggtg aataccaaga ctt 773

<210> 483
<211> 794
<212> DNA
<213> Homo Sapiens

<400> 483
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ggcaagttgg gaggggacca acctagcagt agnggcattt ganaataaat tancaaaaaa 180
atttagtatt accattnatt gatgacaaac acttaagttt tacttacatt ccatggggag 240
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caaaagcaac acagntgtat acagaaacgt aggtcattct tttcagccct aanggagatg 420
taattaacag tatcgagcac tntggaaaat cactctgcag gtttatatgg actacatgga 480
gatcatatcc tgtagtgtag tgaaagctaa gtccctcaaga gccatatgta tagatncaca 540
atgtttttta ataattctta aaacagagat caaagttcat ttaagncttg tttgcattac 600
caaaaataaaa aatgaaataa aaatggaacc aaatgaacat ctaangttta aaattcctaa 660
atnggccaat ttatncaact ggnggggaga cttattcaag ggttttgaaa gtccaggaac 720
tggtttcaag ctggaaccca ggggggcccc acaatttggc attccttgga aactggccct 780
ggggttaagc caaa 794

<210> 484
<211> 788
<212> DNA
<213> Homo Sapiens

<400> 484
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tcagtgccgt tgaaacacga ggtataaatg accaaggatt gtacagagtt gtgggggtga 120
gttcaaaggt ccagagactt ctgagtatgt tgatggatgt aaaaacatgc aatgaggtgg 180
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tgaggccaca	ggaagaaact	gtcgtgcct	catggacttg	aagtttcaga	atattgttgt	540
ggaaatctta	attgaaaacc	atgaaaagat	ttttcggacg	ccgnccgata	ctacattccc	600
tgagcccacc	tgcctgtcag	catcaccccc	aaatgcgcga	ccaangcagt	cnaagagaca	660
aggncagaga	accaagaagg	cccggtgggc	gtctacaata	tttggctgga	gctggaaaga	720
tggtgacaat	ccttaccctt	tccanggagg	acacccctta	ccacagtctg	gactcacttt	780
tcttccccg						788

<210> 485

<211> 430

<212> DNA

<213> Homo Sapiens

<400> 485

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agtgcagtga	gtgtggggtc	ctgcagggtg	ccgtctagga	agggcaggct	tgagacgcgc	180
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tttanaatcg	nagcagcang	tgctcagggg	ggagagggag	ccnnngtggc	tctgggtggc	360
tgactgccag	tgnaggcgga	cacangtggc	ataaggctgc	ccgtcccctc	tcattcttat	420
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<210> 486

<211> 831

<212> DNA

<213> Homo Sapiens

<400> 486

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ttatggtgac	aaaaccagtg	caggaatata	aaaaggaata	cacagtgcag	caggccttgt	120
tttgacttcc	tggaattgtt	acttctatac	cgggtgccctt	ggcaggaagt	gcccttctcc	180
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tgctgttttc	tggaagaaga	tcacagttga	caccagaaa	agtcttncca	aatttnctga	780
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<210> 487

<211> 728

<212> DNA

<213> Homo Sapiens

<400> 487

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cagggtgcctg	ccaccacgcc	tggtcaattt	ttgtattttt	ggtagagacg	gggtttcacc	180

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ctttatctcc	taccttgatc	tctgtagcag	aaaagaacag	tatagatata	aattgtcatc	360
aacagatgca	acatatcttg	taaatcaata	tattttcaag	tgagggtctct	gaatcacctg	420
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caatcctgga	tgagccccgc	tttttctctg	tgccagaacc	ttaatgccac	gcagcattac	600
attaagtcac	attacaactt	tggtcaatgg	aaacacaggg	tctttttctg	acaaaatgcc	660
atcaagccag	gtttggctcc	ccacttaagt	tcaaatnttt	aatcattaat	tttctgagcc	720
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<210> 488

<211> 788

<212> DNA

<213> Homo Sapiens

<400> 488

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atgtatcaga	agtatcccac	tgcacacatg	atctcttaca	tgctacatta	gaagactcct	420
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agaataatat	tcttgcaaaa	aagaaaccct	tttagtgnga	taatgtagaa	aagnctttan	720
tcatagatca	tcgnttacta	aaccttgaga	aaacccttta	angggaaagg	gagctttcct	780
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<210> 489

<211> 875

<212> DNA

<213> Homo Sapiens

<400> 489

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gttaattttt	ttaatggtga	aatcttttct	ttgcacataa	aatgagccag	tgcatgttgc	180
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aaaaagtcac	tagtagttca	accatctaca	gtttctgtta	aattgtgggt	tgtaagcctc	480
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<210> 490

<211> 844
<212> DNA
<213> Homo Sapiens

<400> 490

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aaggtgaagg	gaaaagcaag	aagatttcaa	agaaaaatgc	cgccatagct	gttcttgagg	180
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aaacaaaacc	catagtcaag	ccacagacaa	gcccagaata	tggccagggg	atcaatccga	300
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tcacagagcg	aggcctcccg	cgccgcaggg	agttttgtgat	gcaggtgaag	gttggaaacc	420
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ctgctcttgg	ggatgaaaat	gggactagta	ataaagagga	tgagtccagg	atgccttata	660
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<210> 491
<211> 825
<212> DNA
<213> Homo Sapiens

<400> 491

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ggcaagttag	gaggggacca	acctagcagt	agtggcattt	gagaataaat	taacaaaaaa	180
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aaaaattcca	gcgtaaacaa	tgaatggaag	cagtacttaa	ctcgcagggc	taccaggctt	300
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caaaagcaac	acagctgtat	acagaaaagt	aggtcattct	tttcagccct	aatggagatg	420
taattaacag	tatcgagcac	tctggaaaat	cactctgcag	gtttatatgg	actacatgga	480
gatcatatcc	tgtagtgtag	tgaaagctaa	gtcctcaaga	gccatatgta	tagatacaca	540
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<210> 492
<211> 946
<212> DNA
<213> Homo Sapiens

<400> 492

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<210> 493

<211> 804

<212> DNA

<213> Homo Sapiens

<400> 493

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aagcttccga	ccatggatca	actgggagct	atncatctgg	ctttctgaag	cagntcaatt	660
gtaagagaaa	gcccataccn	ggaatggagt	tcntccattt	tcagaactaac	cctgggcnctn	720
aagcaaggca	tgggatcccc	tgggaattgcc	anaaanttgg	gttgcagggg	ccatacnccg	780
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<210> 494

<211> 856

<212> DNA

<213> Homo Sapiens

<400> 494

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<210> 495

<211> 757

<212> DNA
<213> Homo Sapiens

<400> 495

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tgctaagtca	gngttaaatc	cacagactaa	tttttcgata	tagnattcct	ggntctggnc	540
cttaaagaga	aataaaggca	ttaaaccact	tttttatatg	tcaaggaaat	ataatttngc	600
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<210> 496
<211> 1759
<212> DNA
<213> Homo Sapiens

<400> 496

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<210> 497
<211> 842
<212> DNA
<213> Homo Sapiens

<400> 497
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tgagagaggg aatcattgtc actggaaagc ggctggggac tctggtggtg acttatgtag 180
atgccatcaa cagtggagca gtaccttgtc tggagaatgc agtgacagca ctggcccagc 240
ttgagaaccc agcggctgtg cagagggcag ccgaccacta tagccagcag atggcccagc 300
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tactgtctgg agagaaggcc atacaaccgg aaccgggcca tgaaggaagc acttgagaag 780
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<210> 498
<211> 707
<212> DNA
<213> Homo Sapiens

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<210> 499
<211> 772
<212> DNA
<213> Homo Sapiens

<400> 499
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aatacatggn	ccaaatggag	aagaagttgg	aggangaaa	ggaaaaccnt	ntcagagagc	720
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<210> 500

<211> 787

<212> DNA

<213> Homo Sapiens

<400> 500

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<210> 501

<211> 886

<212> DNA

<213> Homo Sapiens

<400> 501

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<210> 502

<211> 626

<212> DNA

<213> Homo Sapiens

<400> 502

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<210> 503

<211> 884

<212> DNA

<213> Homo Sapiens

<400> 503

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<210> 504

<211> 612

<212> DNA

<213> Homo Sapiens

<400> 504

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<210> 505

<211> 2215

<212> DNA

<213> Homo Sapiens

<400> 505

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<211> 742

<212> DNA

<213> Homo Sapiens

<400> 506

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 <212> DNA
 <213> Homo Sapiens

<400> 508
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 <211> 818
 <212> DNA
 <213> Homo Sapiens

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<211> 651

<212> DNA

<213> Homo Sapiens

<400> 510

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<211> 712

<212> DNA

<213> Homo Sapiens

<400> 511

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<210> 512

<211> 850

<212> DNA

<213> Homo Sapiens

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 <212> DNA
 <213> Homo Sapiens

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 <211> 790
 <212> DNA
 <213> Homo Sapiens

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 <211> 747
 <212> DNA
 <213> Homo Sapiens

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 <212> DNA
 <213> Homo Sapiens

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<400> 520

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<211> 710

<212> DNA

<213> Homo Sapiens

<400> 521

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<211> 638

<212> DNA

<213> Homo Sapiens

<400> 522

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<210> 523

<211> 833

<212> DNA

<213> Homo Sapiens

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<210> 524

<211> 766

<212> DNA

<213> Homo Sapiens

<400> 524

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<211> 847

<212> DNA

<213> Homo Sapiens

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<211> 842

<212> DNA

<213> Homo Sapiens

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<211> 815

<212> DNA

<213> Homo Sapiens

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901

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<211> 761

<212> DNA

<213> Homo Sapiens

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<211> 869

<212> DNA

<213> Homo Sapiens

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<212> DNA
<213> Homo Sapiens

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Tyr	Gln	Arg	Thr	Cys	Glu	Asp	Leu	Lys	Glu	Gln	Leu	Lys	His	Lys	Glu
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His	Met	Gln	Thr	Ile	Glu	Arg	Leu	Val	Lys	Glu	Arg	Asp	Asp	Leu	Met
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Ser	Ala	Leu	Val	Ser	Val	Arg	Ser	Ser	Leu	Ala	Asp	Thr	Gln	Gln	Arg
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 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Ser
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 Glu Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu
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 Gly Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln
 340 345 350
 His Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp
 355 360 365

Lys His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys
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agccatcacc	gcaaaactcc	tacagcagaa	gttgaacgtg	ggcaaggtcc	tcacgtgga	2040
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ctacatctct	ctgcatcgct	atgacaacgg	gaacttcttt	ccaggctctg	gggctcctga	2160
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tgcccacgag	ttctcacctg	atgtggctct	agtctccgcc	gggtttgatg	ctgttggaagg	2340
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gcagctgatg	accctggcag	ggggccgggt	ggtgctggcc	ctggagggag	gccatgactt	2460
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gaaagtcac	gagatccaga	gcaaactctg	gagctgtgtg	cagaagttcg	ccgctggtct	2640
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atggccttgc	tgttggtggg	ggccgaacag	gcccagctg	cggcagccc	ggaacacagc	2760
cccaggccgg	cagaggagcc	catggagcag	gagcctgccc	tgtgacgccc	cggcccccat	2820
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aattt						2885

<210> 547
 <211> 897
 <212> PRT
 <213> Homo Sapiens

<400> 547
 Glu Phe Leu Leu Ser Lys Ser Lys Glu Pro Thr Pro Gly Gly Leu Asn
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 His Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser
 20 25 30
 Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Pro Pro Gly Thr Pro Pro
 35 40 45
 Ser Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe
 50 55 60
 Pro Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Val Arg Ser Arg
 65 70 75 80
 Leu Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg
 85 90 95
 Lys Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile
 100 105 110
 Thr Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly
 115 120 125
 Ser Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn
 130 135 140
 Gly Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln
 145 150 155 160
 His Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr
 165 170 175
 Thr Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val
 180 185 190
 Thr Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln
 195 200 205
 Gln Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr

210 215 220
 Leu Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu
 225 230 235 240
 Gly Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu
 245 250 255
 Leu Gln His Val Leu Leu Leu Glu Gln Ala Arg Gln Gln Ser Thr Leu
 260 265 270
 Ile Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg
 275 280 285
 Val Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro
 290 295 300
 Leu Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu
 305 310 315 320
 Gln Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln
 325 330 335
 Lys Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu
 340 345 350
 Leu Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Glu Leu
 355 360 365
 Thr Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro
 370 375 380
 Arg Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu
 385 390 395 400
 Glu Asp Glu Glu Glu Asp Gly Glu Glu Glu Glu Asp Cys Ile Gln Val
 405 410 415
 Lys Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu
 420 425 430
 Glu Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu
 435 440 445
 Gln Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro
 450 455 460
 His Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly
 465 470 475 480
 Met Lys Asn Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Ser
 485 490 495
 Val Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn
 500 505 510
 Thr His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser
 515 520 525
 Arg Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly
 530 535 540
 Arg Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His
 545 550 555 560
 Thr Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser
 565 570 575
 Lys Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro
 580 585 590
 Cys Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His
 595 600 605
 Ser Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala
 610 615 620
 Phe Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg
 625 630 635 640
 Pro Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe
 645 650 655

Phe Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn
 660 665 670
 Val Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly
 675 680 685
 Thr Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu
 690 695 700
 His Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu
 705 710 715 720
 Glu Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp
 725 730 735
 Thr Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala
 740 745 750
 Phe Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val
 755 760 765
 Val Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro
 770 775 780
 Leu Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg
 785 790 795 800
 Gln Leu Met Thr Leu Ala Gly Gly Arg Val Leu Ala Leu Glu Gly
 805 810 815
 Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser
 820 825 830
 Ala Leu Leu Ser Val Lys Leu Gln Pro Leu Asp Glu Ala Val Leu Gln
 835 840 845
 Gln Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu
 850 855 860
 Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu
 865 870 875 880
 Gly Arg Ser Leu Arg Gly Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu
 885 890 895

Met

Met

Met

Met

<210> 548

<211> 1298

<212> DNA

<213> Homo Sapiens

<400> 548

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tgatggagag agaaagcatc naaagcttct ggaagcaatc agttcccttg atggaaagaa	180
taggcggaaa ttggctgana ggtctgaggc tagtctgaag gtgtcagagt tcaatgtcag	240
ttctgaagga tcaggagaaa agctggtcct tgcagatctg cttgagcctg ttaaaacttc	300
atcttctttg gccactgtga aaaagcaact gagtagagtc anatcaaaga anacagtgga	360
gttacctctg aacaaagaag agattgaacg gatccacaga gaatagcatt caataaaacg	420
cacaagtcct ctccaaatgg gaccctgtcg tcctgaagaa ccggcaggca gaggagctgg	480
tttttcccct ggagaaagag gagccagcca ttgctcccat tgaacatgtg ctgagtggt	540
ggaaggcaag aactcccctg gagcaggaaa ttttcaacct cctccataag aacaagcagc	600
cagtgcagaga ccttttactg acccctgtgg aaaaggcctc tctccgagcc atgagcctag	660
aagaggcaaa gatgcgacga gcagagcttc agagggctcg ggctctgcag tctactatg	720
angccaaggc tcgaagagag aagaaaatcn aaagttaaaa gtatcacaaa gtcgtgaaga	780
aaggaaaggc caagaaagcc ctaaaagagt ttgagcagct gcggaagggt aatccagctg	840
ccgcactaga agaacgaaga aaagaggaaa gaaggaggag gagaaagaag aagaacaagg	900
agaagaagaa agaagaaggg agaaggagaa gaaaagaagg agaagaggaa aaggaagaag	960

gagaaagaaa aggagaagga aaaggaaaag aaggagaaga aagaagaact aagaagaagg 1020
agaggaagaa taagaaggaa agaagaaaga aaaaagtnaa agaagaagaa agaaggaaga 1080
aggaaagaag aggaagaact nagaagaaga aagaggagga aagaagaaaag aagaataagg 1140
aacnagaaag aaggagaaga aagaataaga agaggaagaa gaaaaagaag aaaagaagaa 1200
ggaaagaagg agaaaaagga agaaaaaagg aagaagaaag tagaaagcgg aagaaagaaa 1260
agaaagtata agaaggaaga agaagaaaga aggaaaaa 1298

<210> 549
<211> 236
<212> PRT
<213> Homo Sapiens

<400> 549
Ala Ala Glu Met Thr Ala Asn Arg Leu Ala Glu Ser Leu Leu Ala Leu
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Ser Gln Glu Glu Leu Ala Asp Leu Pro Lys Asp Tyr Leu Leu Ser Glu
20 25 30
Ser Glu Asp Glu Gly Asp Asn Asp Gly Glu Arg Lys His Lys Leu Leu
35 40 45
Glu Ala Ile Ser Ser Leu Asp Gly Lys Asn Arg Arg Lys Leu Ala Arg
50 55 60
Ser Glu Ala Ser Leu Lys Val Ser Glu Phe Asn Val Ser Ser Glu Gly
65 70 75 80
Ser Gly Glu Lys Leu Val Leu Ala Asp Leu Leu Glu Pro Val Lys Thr
85 90 95
Ser Ser Ser Leu Ala Thr Val Lys Lys Gln Leu Ser Arg Val Ser Lys
100 105 110
Thr Val Glu Leu Pro Leu Asn Lys Glu Glu Ile Glu Arg Ile His Arg
115 120 125
Glu Ile Ala Phe Asn Lys Thr His Lys Ser Ser Pro Asn Gly Thr Leu
130 135 140
Ser Ser Val Leu Lys Asn Arg Gln Ala Glu Gln Leu Val Phe Pro Leu
145 150 155 160
Glu Lys Glu Glu Pro Ala Ile Ala Pro Ile Glu His Val Leu Ser Gly
165 170 175
Trp Lys Ala Arg Thr Pro Leu Glu Gln Glu Ile Phe Asn Leu Leu His
180 185 190
Lys Asn Lys Gln Pro Val Thr Asp Pro Leu Leu Thr Pro Val Glu Lys
195 200 205
Ala Ser Leu Arg Ala Met Ser Leu Glu Glu Ala Lys Met Arg Arg Ala
210 215 220
Glu Leu Gln Arg Ala Arg Ala Leu Gln Ser Tyr Tyr
225 230 235

<210> 550
<211> 2236
<212> DNA
<213> Homo Sapiens

<400> 550
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gggtcgtgca acgacgcagc tggacctggc ccagccatgg accgaaaagt ggcccagaaa 120
ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
gtgctgcgaa tgtaccacca gaccatggac gtggcctgct tctgaggaga cctgaagctg 240
gtcatcaatg aaccagccg tctgcctctg tttgatgccca ttcggccgct gatccactg 300

aagcaccagg tggaatatga tcagctgacc ccccggcgct ccaggaagct gaaggaggtg 360
cgtctggacc gtctgcaccc cgaaggcctc ggcctgagtg tgcgtggtgg cctggagttt 420
ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
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ctgatccccg tgaagagctc tctgatgag cccctcactt ggcagtatgt ggatcagttt 660
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gccctgaacc agggccagat aaggaacagc tcgggccact ttttgaagg ccaatgtgga 1980
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taagacccca ctggagtctc tctctctcca tccctctctc ctgcctctg ctctaattgc 2160
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ttccagctta aaaaaa 2236

<210> 551
<211> 652
<212> PRT
<213> Homo Sapiens

<400> 551
Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
1 5 10 15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
20 25 30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35 40 45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50 55 60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65 70 75 80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85 90 95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100 105 110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu

115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
 420 425 430
 Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
 435 440 445
 Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
 450 455 460
 Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
 465 470 475 480
 Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
 485 490 495
 Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
 500 505 510
 Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
 515 520 525
 Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu
 530 535 540
 Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
 545 550 555 560

Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
 565 570 575
 Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
 580 585 590
 His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
 595 600 605
 Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
 610 615 620
 Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
 625 630 635 640
 Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
 645 650

<210> 552
 <211> 2162
 <212> DNA
 <213> Homo Sapiens

<400> 552

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ttccggcata	aggtggattt	tctgattgaa	aatgatgcag	agaaggacta	tctctatgat	180
gtgctgcgaa	tgtaccacca	gacctgggac	gtggccgtgc	tcgtgggaga	cctgaagctg	240
gtcatcaatg	aaccagccg	tctgcctctg	ttgatgccca	ttcggccgct	gatccactg	300
aagcaccagg	tggaatatga	tcagctgacc	ccccggcgct	ccaggaagct	gaaggaggtg	360
cgtctggacc	gtctgcaccc	cgaaggcctc	ggcctgagtg	tgctggtgg	cctggagttt	420
ggctgtgggc	tcttcacctc	ccacctcatc	aaaggcggtc	aggcagacag	cgctggggctc	480
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gaggtcatca	acctcattcg	aaccaagaaa	actgtgtcca	tcaaagttag	acacatcggc	600
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aagatcctcc	aggagcagca	ggagatggag	cggcaaagga	gaaaagaaat	tgcccagaag	1140
gcagcagagg	aaaatgagag	ataccggaag	gagatggaac	agattgtaga	ggaggaagag	1200
aagtttaaga	agcaatggga	agaagactgg	ggctcaaagg	aacagctact	cttgccctaaa	1260
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caccctggct	gaggtgacg	ctgccctgca	gaaggcctgg	aatcagggcg	gggactggat	1620
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ccagataagg	aacagctcgg	gccacttttt	tgaaggccaa	tgtggaggaa	agggagcagc	1920
cagccgtttg	ggagaagatc	tcaaggatcc	agactctcat	tcctttctct	tggcccagtg	1980
aatttggtct	ctcccagctt	tgggggaact	cttcttgtaa	ccctaataag	acccacttgg	2040
agtctctctc	tctccatccc	tctcctctgc	cctctgctct	aattgctgcc	aggattgtca	2100
ctccaaacct	tactctgagc	tcattaataa	aataaacaga	tttattttcc	agcttaaaaa	2160

<210> 553
 <211> 403
 <212> PRT
 <213> Homo Sapiens

<400> 553
 Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
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 Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
 20 25 30
 Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
 35 40 45
 Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
 50 55 60
 Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
 65 70 75 80
 Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
 85 90 95
 Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
 100 105 110
 Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
 115 120 125
 Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
 130 135 140
 Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
 145 150 155 160
 Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
 165 170 175
 Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
 180 185 190
 Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
 195 200 205
 Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu

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 Lys Pro Lys

<210> 554
 <211> 1789
 <212> DNA
 <213> Homo Sapiens

<400> 554

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<210> 555
 <211> 493
 <212> PRT
 <213> Homo Sapiens

<400> 555

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				20				25					30		
Tyr	Gln	Arg	Thr	Cys	Glu	Asp	Leu	Lys	Glu	Gln	Leu	Lys	His	Lys	Glu
				35				40					45		

Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
 50 55 60
 Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
 65 70 75 80
 His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
 85 90 95
 Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
 100 105 110
 Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
 115 120 125
 Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
 130 135 140
 Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
 145 150 155 160
 Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
 165 170 175
 Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
 180 185 190
 Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
 195 200 205
 Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
 210 215 220
 Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
 225 230 235 240
 Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
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 Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
 260 265 270
 Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
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 Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
 290 295 300
 Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln
 305 310 315 320
 Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala Gln
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 Ala Leu Gln Ala Gln Gln Arg Glu Gln Glu Leu Thr Gln Lys Ile Gln
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 Gln Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln Tyr Leu Leu
 355 360 365
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 370 375 380
 Thr Leu Ala Lys Lys Leu Glu Gln Ile Ser Gln Lys Thr Arg Ser Glu
 385 390 395 400
 Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly
 405 410 415
 Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His
 420 425 430
 Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys
 435 440 445
 His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln
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 Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys

485

490

<210> 556
<211> 1306
<212> DNA
<213> Homo Sapiens

<400> 556

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cggcaaagga gaaaagaaat tgcccagaag gcagcagagg aaaatgagag ataccggaag     240
gagatggaac agattgtaga ggaggaagag aagtttaaga agcaatggga agaagactgg     300
ggeteaaagg aacagetaet cttgcetaaa accateactg ctgaggtaca cccagtaccc     360
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<210> 557
<211> 328
<212> PRT
<213> Homo Sapiens

<400> 557

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Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu Lys Phe Lys Lys
 35            40            45
Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu Leu Pro Lys
 50            55            60
Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg Lys Pro Lys Tyr
 65            70            75            80
Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp Asp Leu Asp Gly
 85            90            95
Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys Tyr Glu Glu Gly
100          105          110
Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile Met Gly Lys Asp
115          120          125
Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu Asp Leu Ala Leu
130          135          140

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Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val Val Ser Ala Val	
145	150 155 160
Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile Val Lys Gly Asp	
	165 170 175
Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp Tyr Thr Leu Ala	
	180 185 190
Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln Gly Gly Asp Trp	
	195 200 205
Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu Tyr Asp Asp Glu	
	210 215 220
Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln Ile His Ala Leu	
225	230 235 240
Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr Lys Pro Arg Thr	
	245 250 255
Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp His Pro Trp Asp	
	260 265 270
Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu Ala Leu Asn Gln	
	275 280 285
Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu Gly Gln Cys Gly	
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Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu Lys Asp Pro Asp	
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<210> 558

<211> 2289

<212> DNA

<213> Homo Sapiens

<400> 558

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<210> 559
 <211> 481
 <212> PRT
 <213> Homo Sapiens

<400> 559

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20          25          30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35          40          45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50          55          60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65          70          75          80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85          90          95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100         105         110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
115         120         125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
130         135         140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145         150         155         160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
165         170         175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
180         185         190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
195         200         205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210         215         220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225         230         235         240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245         250         255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys

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290	295	300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln		
305	310	315
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu		
325	330	335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu		
340	345	350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu		
355	360	365
Lys Phe Lys Lys Gln Trp Glu Asp Trp Gly Ser Lys Glu Gln Leu		
370	375	380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg		
385	390	395
Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp		
405	410	415
Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Pro Gln Glu Met		
420	425	430
Leu Lys Arg Met Val Val Tyr Gln Asp Ser Ile Gln Asp Lys Ile Ser		
435	440	445
Gly Asn Met Arg Lys Ala Leu Thr Pro Thr Leu Cys Ser Pro Gln Ser		
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Pro		480

<210> 560

<211> 2409

<212> DNA

<213> Homo Sapiens

<400> 560

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<210> 561
 <211> 521
 <212> PRT
 <213> Homo Sapiens

<400> 561

Met	Asp	Arg	Lys	Val	Ala	Arg	Glu	Phe	Arg	His	Lys	Val	Asp	Phe	Leu
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Ile	Glu	Asn	Asp	Ala	Glu	Lys	Asp	Tyr	Leu	Tyr	Asp	Val	Leu	Arg	Met
			20						25					30	
Tyr	His	Gln	Thr	Met	Asp	Val	Ala	Val	Leu	Val	Gly	Asp	Leu	Lys	Leu
			35						40					45	
Val	Ile	Asn	Glu	Pro	Ser	Arg	Leu	Pro	Leu	Phe	Asp	Ala	Ile	Arg	Pro
			50						55					60	
Leu	Ile	Pro	Leu	Lys	His	Gln	Val	Glu	Tyr	Asp	Gln	Leu	Thr	Pro	Arg
			65						70					75	
Arg	Ser	Arg	Lys	Leu	Lys	Glu	Val	Arg	Leu	Asp	Arg	Leu	His	Pro	Glu
				85					90					95	
Gly	Leu	Gly	Leu	Ser	Val	Arg	Gly	Gly	Leu	Glu	Phe	Gly	Cys	Gly	Leu
			100						105					110	
Phe	Ile	Ser	His	Leu	Ile	Lys	Gly	Gly	Gln	Ala	Asp	Ser	Val	Gly	Leu
			115						120					125	
Gln	Val	Gly	Asp	Glu	Ile	Val	Arg	Ile	Asn	Gly	Tyr	Ser	Ile	Ser	Ser
			130						135					140	
Cys	Thr	His	Glu	Glu	Val	Ile	Asn	Leu	Ile	Arg	Thr	Lys	Lys	Thr	Val
			145						150					155	
Ser	Ile	Lys	Val	Arg	His	Ile	Gly	Leu	Ile	Pro	Val	Lys	Ser	Ser	Pro
				165					170					175	
Asp	Glu	Pro	Leu	Thr	Trp	Gln	Tyr	Val	Asp	Gln	Phe	Val	Ser	Glu	Ser
			180						185					190	
Gly	Gly	Val	Arg	Gly	Ser	Leu	Gly	Ser	Pro	Gly	Asn	Arg	Glu	Asn	Lys
			195						200					205	

Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
 210 215 220
 Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
 225 230 235 240
 Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
 245 250 255
 Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
 260 265 270
 Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
 275 280 285
 Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
 290 295 300
 Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
 305 310 315 320
 Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
 325 330 335
 Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
 340 345 350
 Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
 355 360 365
 Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
 370 375 380
 Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
 385 390 395 400
 Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
 405 410 415
 Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Thr Phe Cys Pro
 420 425 430
 Ser Pro Gln Pro Pro Arg Gly Pro Gly Val Ser Thr Ile Ser Lys Pro
 435 440 445
 Val Met Val His Gln Glu Pro Asn Phe Ile Tyr Arg Pro Ala Val Lys
 450 455 460
 Ser Glu Val Leu Pro Gln Glu Met Leu Lys Arg Met Val Val Tyr Gln
 465 470 475 480
 Asp Ser Ile Gln Asp Lys Ile Ser Gly Asn Met Arg Lys Ala Leu Thr
 485 490 495
 Pro Thr Leu Cys Ser Pro Gln Ser Arg Ser Trp Gly Arg Met Ser Gly
 500 505 510
 Ser Tyr Ala Ser Arg Arg Arg Asp Pro
 515 520

<210> 562

<211> 1445

<212> DNA

<213> Homo Sapiens

<400> 562

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 acctgcggac gctgcagata agttacgacg cactgaaaga tgaaaattct aagctgagaa 120
 gaaagctgaa tgagggttcag agcttctctg aagctcaaac agaaatggtg aggacgcttg 180
 agcggaaagt agaagcaaaa atgatcaagg aggaaagcga ctaccacgac ctggagtcgg 240
 tggttcagca ggtggagcag aacctggagc tgatgaccaa acgggctgta aaggcagaaa 300
 accacgtcgt gaaactaaaa caggaaatca gtttgctcca ggcgcaggtc tccaacttcc 360
 agcgagagaa tgaagccctg cggcgccggc aggggtgccag cctgaccgtg gtgaagcaga 420
 acgccgacgt ggccctgcag aacctccggg tggatcatgaa cagtgcacag gcttccatca 480

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agcaactggt ttccggagct gagacactga atcttgttgc cgaaatcctt aaatctatag      540
acagaatttc tgaagttaaa gacgaggagg aagactcttg aggacccttg ggtgttctca      600
gcatgaagct ccgtgtatac cctgagggtca ccaccgctcg atctaaatgt gcagttgtgt      660
ccttaaatat gcagtcttca cccagagtaa agtgttgatc gcaagagtcc agtgtcgtgc      720
cctcagccag ttcttggcca ccacaatggg agcagccctg gccgagttgt ctctgtggtt      780
tctatgcagc ccttcttggc gaaattcctg cgatcttata gattctaata agctcttgga      840
agacattgtc ataaaagcca gtgattttta gaaaaagagt ggttctggaa tcaatgtttt      900
ccagtcccat cccagaacat cagttgtaag ataagtacaa ttggttggtc ttgatttcat      960
aagtagaaca aacactaaat gtgcctctga gatggccacc ccgggcaggg acctgtgcct     1020
tccgccgatg ctcaggggtc cctctgggtc ccgggtcact cttgtggccc cagtgggtgg     1080
tccctgcagt catggcctga gtgcgcaggg gccaccgctg ggctgctgct gtcctcctcc     1140
gggggaccacg ggggaacaag gtcacacctt ccgtgctgtg aagctgtcca gatgtgcctc     1200
tttggtctggg ggttttgggt gacgtttcaa gtggcatttt gtacaatgca ggtagaatt      1260
caggaatttc aagtatgtgc ccgggtntgt caggtcccag ttgcctttnt gacggccccc     1320
ctcagaggga cggcgatgag cactaaatgc ttttttgant attttctat agattttttt     1380
taaaactttt ttttctcct gttccaattg atagctttct tatttaataa attctgtagt     1440
tcacc                                             1445

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<210> 563
 <211> 192
 <212> PRT
 <213> Homo Sapiens

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<400> 563
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Gly Asp Arg His Leu Arg Thr Leu Gln Ile Ser Tyr Asp Ala Leu Lys
  20             25             30
Asp Glu Asn Ser Lys Leu Arg Arg Lys Leu Asn Glu Val Gln Ser Phe
  35             40             45
Ser Glu Ala Gln Thr Glu Met Val Arg Thr Leu Glu Arg Lys Leu Glu
  50             55             60
Ala Lys Met Ile Lys Glu Glu Ser Asp Tyr His Asp Leu Glu Ser Val
  65             70             75             80
Val Gln Gln Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val
  85             90             95
Lys Ala Glu Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu
  100            105            110
Gln Ala Gln Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys
  115            120            125
Gly Gln Gly Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala
  130            135            140
Leu Gln Asn Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys
  145            150            155            160
Gln Leu Val Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu
  165            170            175
Lys Ser Ile Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
  180            185            190

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<210> 564
 <211> 1226
 <212> DNA
 <213> Homo Sapiens

<400> 564

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 agggcaagga ggagaaggag ggcgggcgac ggctggggcg tggcgggcga agccccgaga 120
 agagccccgag cgcgcaggag ctcaaggagc agggcaatcg tctgttcgtg ggccgaaagt 180
 acccgagggc ggcggcctgc tacggccgcg cgatcacccg gaaccgcgtg gtggccgtgt 240
 attacaccaa ccgggccttg tgctacctga agatgcagca gcacgagcag gccctggccg 300
 actgccggcg cgccttggag ctggacgggc agtctgtgaa ggcgcacttc ttcttggggc 360
 agtgccagct ggagatggag agctatgatg aggccatcgc caatctgcag cgagcttaca 420
 gcctggccaa ggagcagcgg ctgaacttcg gggacgacat cccagcgct cttcgaatcg 480
 cgaagaagaa gcgctggaac agcattgagg agcggcgcat ccaccaggag agcgagctgc 540
 actcctacct ctccaggctc attgccgcgg agcgtgagag ggagctggaa gaggccagc 600
 gaaaccacga ggggtgatgag gacgacagcc acgtccgggc ccagcaggcc tgcattgagg 660
 ccaagcacga caagtacatg gcggacatgg acgagctttt ttctcagggt gatgagaaga 720
 ggaagaagcg agacatcccc gactacctgt gtggcaagat cagctttgag ctgatgcggg 780
 agccgtgcat cagccccagt ggcacacact acgaccgcaa ggacatcgag gaggacctgc 840
 agcgtgtggg tcattttgac ccggtgaccg ggagccccct gaccaggaa cagttcatcc 900
 ccaacttggc tatgaaggag gttattgacg cattcatctc tgagaatggc tgggtggagg 960
 actactgagg ttccctgccc tacctggcgt cctgggtccag gggagccctg ggcagaagcc 1020
 cccggccctt aaacatagtt tatgtttttg gccaccccca ccgcttcccc caagttctgc 1080
 tgttggaactc tggactgttt cccctctcag catcgctttt gctgggcccgt gattgtcccc 1140
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 gtgtaataaa atccgtgagc acgaaa 1226

<210> 565
 <211> 303
 <212> PRT
 <213> Homo Sapiens

<400> 565
 Met Lys Gly Lys Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly
 1 5 10 15
 Gly Gly Ser Pro Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln
 20 25 30
 Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Ala Cys
 35 40 45
 Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr
 50 55 60
 Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu
 65 70 75 80
 Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala
 85 90 95
 His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu
 100 105 110
 Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg
 115 120 125
 Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Lys
 130 135 140
 Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu
 145 150 155 160
 Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala Glu Arg Glu Arg Glu
 165 170 175
 Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp Glu Asp Asp Ser His
 180 185 190
 Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys His Asp Lys Tyr Met
 195 200 205
 Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp Glu Lys Arg Lys Lys

210	215	220
Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile Ser Phe Glu Leu Met		
225	230	235
Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp		240
	245	250
Ile Glu Glu His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Gly		255
	260	265
Ser Pro Leu Thr Gln Glu Gln Phe Ile Pro Asn Leu Ala Met Lys Glu		270
	275	280
Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr		285
	290	300

<210> 566
 <211> 1857
 <212> DNA
 <213> Homo Sapiens

<400> 566

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tagtggccgg	cggccgctc	tcatcccccg	taaggagcag	agtcctttgt	actgaccaag	180
atgagcaaca	tctacatcca	ggagcctccc	acgaatggga	aggttttatt	gaaaactaca	240
gctggagata	ttgacataga	gttgtgggtcc	aaagaagctc	ctaaagcttg	cagaaatfff	300
atcccaactt	tgtttggaag	cttattatga	caataccatt	tttcatagag	ttgtgcctgg	360
tttcatagtc	caaggcggag	atcctactgg	cacagggagt	ggtggagagt	ctatctatgg	420
agcgccattc	aaagatgaat	ttcattcacg	gttgcgtttt	aatcggagag	gactgggtgc	480
catggcaaat	gctggttctc	atgataatgg	caccactttt	ttcttcacac	tgggtcgagc	540
agatgaactt	aacaataagc	ataccatctt	tggaaagggt	acaggggata	cagtatataa	600
catgttgcca	ctgtcagaag	tagacattga	tgatgacgaa	agaccacata	atccacacaa	660
aataaaaagc	tgtgaggttt	tgtttaaatcc	ttttgatgac	atcattccaa	gggaaattaa	720
aaggctgaaa	aaagagaaac	cagaggagga	agtaaagaaa	ttgaaaccca	aaggcacaaa	780
aaattttagt	ttactttcat	ttggagagga	agctgaggaa	gaagaagagg	aagtaaactg	840
agtttagtcag	agcatgaagg	gcaaaaagcaa	aagtagtcat	gacttgctta	aggatgatcc	900
acatctcagt	tctgttccag	ttgtagaaag	tgaaaaaggt	gatgcaccag	atttagttga	960
tgatggagaa	gatgaaagtg	cagagcatga	tgaatatatt	gatggtgatg	aaaagaacct	1020
gatgagagaa	agaattgccca	aaaaattaaa	aaaggacaca	agtgcgaatg	ttaaatcagc	1080
tggagaagga	gaagtggaga	agaaatcagt	cagccgcagt	gaagagctca	gaaaagaagc	1140
aagacaatta	aaacgggaac	tcttagcagc	aaaacaaaaa	aaagtagaaa	atgcagcaaa	1200
acaagcagaa	aaaagaagtg	aagaggaaga	agccccctcca	gatggtgctg	ttgccgaata	1260
cagaagagaa	aagcaaaagt	atgaagcttt	gaggaagcaa	cagtcaaaga	agggaaacttc	1320
ccgggaagat	cagacccttg	cactgctgaa	ccagtttaaa	tctaaactca	ctcaagcaat	1380
tgctgaaaca	cctgaaaatg	acattcctga	aacagaagta	gaagatgatg	aaggatggat	1440
gtcacatgta	cttcagtttg	aggataaaaag	cagaaaagtg	aaagatgcaa	gcatgcaaga	1500
ctcagatata	tttgaaatct	atgatcctcg	gaatccagtg	aataaaaagaa	ggaggggaaga	1560
aagcaaaaag	ctgatgagag	agaaaaaaga	aagaagataa	aatgagaata	atgataacca	1620
gaacttgctg	gaaatgtgcc	tacaatggcc	ttgtaacagc	cattgttccc	aacagcatca	1680
cttaggggtg	tgaagaagaag	tattttttgaa	cctgtttgtct	ggttttgaaa	aacaattatc	1740
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tttcttagct	gaccttttat	attgctaaat	ctgaaataaa	ataactttcc	ttccaaa	1857

<210> 567
 <211> 372
 <212> PRT
 <213> Homo Sapiens

<400> 567

Met Ala Asn Ala Gly Ser His Asp Asn Gly Thr His Phe Phe Phe Thr
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 20 25 30
 Val Thr Gly Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp
 35 40 45
 Ile Asp Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys
 50 55 60
 Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys
 65 70 75 80
 Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys Pro
 85 90 95
 Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu Ala Glu
 100 105 110
 Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met Lys Gly Lys
 115 120 125
 Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro His Leu Ser Ser
 130 135 140
 Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala Pro Asp Leu Val Asp
 145 150 155 160
 Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu Tyr Ile Asp Gly Asp
 165 170 175
 Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys Lys Leu Lys Lys Asp
 180 185 190
 Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly Glu Val Glu Lys Lys
 195 200 205
 Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu Ala Arg Gln Leu Lys
 210 215 220
 Arg Glu Leu Leu Ala Ala Lys Gln Lys Lys Val Glu Asn Ala Ala Lys
 225 230 235 240
 Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala
 245 250 255
 Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys
 260 265 270
 Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu
 275 280 285
 Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro
 290 295 300
 Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met
 305 310 315 320
 Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp Ala
 325 330 335
 Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg Asn Pro
 340 345 350
 Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met Arg Glu Lys
 355 360 365
 Lys Glu Arg Arg
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<210> 568

<211> 1537

<212> DNA

<213> Homo Sapiens

<400> 568

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caccaaccag atccgcctaa ccaatgtggc cgtggtacgg atgaagcgtg ccgggaagcg      180
cttcgaaatc gcctgtaca aaaacaaggc cgtcggctgg cggagcggcg tggaaaaaga      240
cctcgatgaa gttctgcaga ccactcagt gtttgtaaag gtttctaaag gtcagggttc      300
caaaaaggaa gatctcatca gtgcgttttg aacagatgac caaactgaaa tctgtaagca      360
gattttgact aaaggagaag ttcaagtatc agataaagaa agacacacac aactggagca      420
gatgttttag gacattgcaa ctattgtggc agacaaatgt gtgaatcctg aaacaaagag      480
accatacacc gtgatcctta ttgagagagc catgaaggac atccactatt cggtgaaaac      540
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aagatgcaaa gtccagagtg gcattttgct actctgtctc atgccttgat agctttccaa     1140
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ttattagggg tatgtctata caacaaaagg gggggtcttt cctaaaaaag aaaacatatg     1260
atgcttcatt tctacttaat ggaacttggt ttctgagggt cattatggta tcgtaatgta     1320
aagcttggtg gatgttcctg attatttgag gaacagatat aggaaaattg tgccggaatt     1380
acctttcatt gaacatgctg ccataaatta gggtattttt gggttaaaaa taaaagtcaa     1440
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<210> 569

<211> 210

<212> PRT

<213> Homo Sapiens

<400> 569

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Ala Ala Arg Arg Ser Val Val Thr Ala Arg Arg Trp Trp Pro Ser Gly
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Trp Thr Ala Arg Val Ser Pro Gly Ser Pro Ala Ser Gly Ser Leu Asn
              20              25              30
Ser Arg Asp Val Asp Leu His Pro His Gln Pro Asp Pro Pro Asn Gln
              35              40              45
Cys Gly Arg Gly Thr Asp Glu Ala Cys Arg Glu Ala Leu Arg Asn Arg
              50              55              60
Leu Leu Gln Lys Gln Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp
65              70              75              80
Leu Asp Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys
              85              90              95
Gly Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp
              100              105              110
Asp Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln
              115              120              125
Val Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp
              130              135              140
Ile Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg
145              150              155              160
Pro Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr

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165 170 175
 Ser Val Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile
 180 185 190
 Lys Gln Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Lys Leu
 195 200 205
 Arg Phe
 210

<210> 570
 <211> 1211
 <212> DNA
 <213> Homo Sapiens

<400> 570

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gtttaatcct	tttgatgaca	tcattccaag	ggaaattaaa	aggctgaaaa	aagagaaacc	180
agaggaggaa	gtaaagaaat	tgaaacccaa	aggcacaaaa	aatttttagtt	tactttcatt	240
tggagaggaa	gctgaggaag	aagaggagga	agtaaatacga	gtagtcaga	gcataagggg	300
caaaagcaaa	agtagtcatg	acttgcttaa	ggatgatcca	catctcagtt	ctgttccagt	360
tgtagaaagt	gaaaaagggtg	atgcagcaga	tttagttgat	gatggagaag	atgaaagtgc	420
agagcatgat	gaatatattg	atggtgatga	aaagaacctg	atgagagaaa	gaattgccaa	480
aaaattaaaa	aaggacacaa	gtgcgaatgt	taaatcagct	ggagaaggag	aagtggagaa	540
gaaatcagtc	agccgcagtg	aagagctcag	aaaagaagca	agacaattaa	aacgggaact	600
cttagcagca	gaacaaaaaa	aagtagaaaa	tgcagcaaaa	caagcagaaa	aaagaagtga	660
agaggaagaa	gccccctccag	atggtgctgt	tgccgaatac	agaagagaaa	agcaaaagta	720
tgaagctctg	aggaagcaac	agtcaaagaa	gggaacttcc	cgggaagatc	agacccttgc	780
actgctgaac	cagtttaaat	ctaaactcac	tcaagcaatt	gctgaaacgc	ctgaaaatga	840
cattcctgaa	acagaagtag	aagatgatga	aggatggatg	tcacatgtac	ttcagtttga	900
ggataaaaagc	agaaaagtga	aagatgcaag	catgcaagac	tcagatacat	ttgaaatcta	960
tgatcctcgg	aatccagtga	ataaaagaag	gagggaagaa	agcaaaaagc	tgatgagaga	1020
gaaaaaagaa	agaagataaa	atgagaataa	tgataaccag	aacttgctgg	aaatgtgcct	1080
acaatggcct	tgtaacagcc	attgttccca	acagcatcac	ttaggggtgt	gaaaagaagt	1140
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gatgtaagca	a					1211

<210> 571
 <211> 354
 <212> PRT
 <213> Homo Sapiens

<400> 571

Pro	Ser	Leu	Glu	Arg	Leu	Gln	Gly	Tyr	Thr	Val	Tyr	Asn	Met	Leu	Arg
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Leu	Ser	Glu	Val	Asp	Ile	Asp	Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His
			20				25						30		
Lys	Ile	Lys	Ser	Cys	Glu	Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile
		35					40					45			
Pro	Arg	Glu	Ile	Lys	Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val
	50					55					60				
Lys	Lys	Leu	Lys	Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe
65					70					75				80	
Gly	Glu	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln
				85					90					95	
Ser	Met	Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp

100	105	110
Pro His Leu Ser Ser Val	Pro Val Val Glu Ser Glu Lys Gly Asp Ala	
115	120	125
Ala Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu		
130	135	140
Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys		
145	150	155
Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly		
165	170	175
Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu		
180	185	190
Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala Glu Gln Lys Lys Val		
195	200	205
Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg Ser Glu Glu Glu Ala		
210	215	220
Pro Pro Asp Gly Ala Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr		
225	230	235
Glu Ala Leu Arg Lys Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp		
245	250	255
Gln Thr Leu Ala Leu Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala		
260	265	270
Ile Ala Glu Thr Pro Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp		
275	280	285
Asp Glu Gly Trp Met Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg		
290	295	300
Lys Val Lys Asp Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr		
305	310	315
Asp Pro Arg Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys		
325	330	335
Leu Met Arg Glu Lys Lys Glu Arg Arg Ile Leu Pro Val Asn Glu Gly		
340	345	350
Lys Asn		

<210> 572
 <211> 604
 <212> DNA
 <213> Homo Sapiens

<400> 572	
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tccttttagc aacagggcc ccaagaagct cccgttcatt cacccttacc ttggccccc	120
ggttggacc ccaaaggct ccttacccca aagtgggttg ttgaataaat cttctcagtt	180
ccctggctcc caaggcccat tgaagaagat tgtacaaggc gtgcctcaag taccctgagt	240
ggaaacagaa gcacctgcct cacttcaagc cgtggctgca cccggagcag agcccggttg	300
cgagcctggc gctgtcggag ctgtcgggtg agcatgcgga ctactggag aacatcgacg	360
agagcgcggt ggccgagagc agagaggagc ggatgggcgg cgcgggcggc gagggcagcg	420
acgacgacac cttcacctga gccgcacccg cttcagggac ggagacagga ccgggcgagc	480
cctggggcgg cgccgcgtcc tgcactttct cccctcccc acccggcacc tgggtggcacc	540
gggccaggcc caggcgggtg ctgcagcctg gctggacaga gcccaataaa cggatcccac	600
agcc	604

<210> 573
 <211> 195
 <212> PRT

<213> Homo Sapiens

<400> 573

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Leu Arg Gln Lys Ile Leu Val Pro Thr Phe Cys Ser Ile Pro Lys Gly
 1          5          10          15
Leu Thr Phe Ile Pro Phe Ser Asn Arg Ala Pro Lys Lys Leu Pro Phe
 20          25          30
Ile His Pro Tyr Leu Gly Pro Gln Val Gly Pro Pro Lys Ala Pro Leu
 35          40          45
Pro Gln Ser Gly Trp Leu Asn Lys Ser Ser Gln Phe Pro Gly Ser Gln
 50          55          60
Gly Pro Leu Lys Lys Ile Val Gln Gly Val Pro Gln Val Pro Arg Val
 65          70          75          80
Glu Thr Glu Ala Pro Ala Ser Leu Gln Ala Val Ala Ala Pro Gly Ala
 85          90          95
Glu Pro Val Ala Glu Pro Gly Ala Val Gly Ala Val Gly Ala Ala Cys
100          105          110
Gly Leu Thr Gly Glu His Arg Arg Glu Arg Gly Gly Arg Glu Gln Arg
115          120          125
Gly Ala Asp Gly Arg Arg Gly Arg Arg Gly Gln Arg Arg Arg His Leu
130          135          140
His Leu Ser Pro His Arg Phe Arg Asp Gly Asp Arg Thr Gly Arg Ala
145          150          155          160
Leu Gly Arg Arg Pro Leu Leu His Phe Leu Pro Ser Pro Thr Arg His
165          170          175
Leu Val Ala Pro Gly Gln Ala Gln Ala Gly Ala Ala Ala Trp Leu Asp
180          185          190
Arg Ala Gln
195

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<210> 574

<211> 742

<212> DNA

<213> Homo Sapiens

<400> 574

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ggctgccggc aatggggggg cctggccccg gcccctgtga ggaccccgcg ggtgctgggg      180
gagcaggtgc agggggctcc gagccctgg tgactgtcac cgtgcagtgc gccttcacag      240
tggccctgag ggcaggaaga ggagccgacc tgtccagcct gcgggcactg ctgggccaag      300
ccttcttca ccaggcccag cttgggcaat tcagttacct agccccaggt gaggacgggc      360
actgggtccc catccccgag gaggagtcgc tgcagagggc ctggcaggac gcagctgcct      420
gccccagggg gctgcagctg cagtgcaggg gagccggggg tcggccggtc ctttaccagg      480
tggtggccca gcacagatac tccgcccagg ggccagagga cctgggcttc cgacaggggg      540
acacggtgga cgtcctgtgt gaagtggacc aggcattggt ggagggccac tgtgacggcc      600
gcatcggcac cttccccaaag tgcttcgtgg tccccgcgg cctcggatg tcaggagccc      660
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742

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<210> 575

<211> 232

<212> PRT

<213> Homo Sapiens

<400> 575
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 Thr Ser Thr Ala Tyr Gln Glu Gln Arg Pro Gln Val Glu Gln Val Gly
 20 25 30
 Lys Val Ala Pro Leu Ser Pro Gly Leu Pro Ala Met Gly Gly Pro Gly
 35 40 45
 Pro Gly Pro Cys Glu Asp Pro Ala Gly Ala Gly Gly Ala Gly Ala Gly
 50 55 60
 Gly Ser Glu Pro Leu Val Thr Val Thr Val Gln Cys Ala Phe Thr Val
 65 70 75 80
 Ala Leu Arg Ala Gly Arg Gly Ala Asp Leu Ser Ser Leu Arg Ala Leu
 85 90 95
 Leu Gly Gln Ala Phe Leu His Gln Ala Gln Leu Gly Gln Phe Ser Tyr
 100 105 110
 Leu Ala Pro Gly Glu Asp Gly His Trp Val Pro Ile Pro Glu Glu Glu
 115 120 125
 Ser Leu Gln Arg Ala Trp Gln Asp Ala Ala Ala Cys Pro Arg Gly Leu
 130 135 140
 Gln Leu Gln Cys Arg Gly Ala Gly Gly Arg Pro Val Leu Tyr Gln Val
 145 150 155 160
 Val Ala Gln His Arg Tyr Ser Ala Gln Gly Pro Glu Asp Leu Gly Phe
 165 170 175
 Arg Gln Gly Asp Thr Val Asp Val Leu Cys Glu Val Asp Gln Ala Trp
 180 185 190
 Leu Glu Gly His Cys Asp Gly Arg Ile Gly Ile Phe Pro Lys Cys Phe
 195 200 205
 Val Val Pro Ala Gly Pro Arg Met Ser Gly Ala Pro Gly Arg Leu Pro
 210 215 220
 Arg Ser Gln Gln Gly Asp Gln Pro
 225 230

<210> 576
 <211> 1087
 <212> DNA
 <213> Homo Sapiens

<400> 576
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 ttcaaaacaac cggtaaccac agtcacaaat catcctagta ataaagtga atcagaccca 180
 caacgaatga atgaacagcc acgtcagctt ttctgggaga agaggctaca aggacttagt 240
 gcatcagatg taacagaaca aattataaaa accatggaac taccocaaagg tcttcaagga 300
 gttggtccag gtagcaatga tgagaccctt ttatctgctg ttgccagtgc tttgcacaca 360
 agctctgctg caatcacagg gcaagtctcc gctgctgtgg aaaagaaccc tgctgtttgg 420
 cttaacacat ctcaaccct ctgcaaagct tttattgtca cagatgaaga catcaggaaa 480
 caggaagagc gagtacagca agtacgcaag aaattggaag aagcactgat ggcagacatc 540
 ttgtcgcgag ctgctgatac agaagagatg gatattgaaa tggacagtgg agatgaagcc 600
 taagaatatg atcaggtaac tttcgaccga ctttcccca gagaaaattc ctagaatttg 660
 aacaaaaatg tttccactgg cttttgctg taagaaaaaa aatgtacccg agcacataga 720
 gctttttaat agcactaacc aatgcctttt tagatgtatt tttgatgtat atatctatta 780
 ttcaaaaaat catgttttatt ttgagtctta ggacttaaaa ttagtctttt gtaatatcaa 840
 gcaggaccct aagatgaagc tgagcttttg atgccagggt caatttactg gaaatgtagc 900
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 taaatttccc agttaagat tattgtgact tcaactgtata taaacatatt tttatacttt 1020

attgaaaggg gacacctgta cattcttcca tcgtcactgt aaagacaaat aaatgattat 1080
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<210> 577

<211> 200

<212> PRT

<213> Homo Sapiens

<400> 577

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20 25 30
Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val
35 40 45
Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn
50 55 60
Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser
65 70 75 80
Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys
85 90 95
Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser
100 105 110
Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln
115 120 125
Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser
130 135 140
Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys
145 150 155 160
Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu
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Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile
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Glu Met Asp Ser Gly Asp Glu Ala
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<210> 578

<211> 2569

<212> DNA

<213> Homo Sapiens

<400> 578

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tgtttctcat ataaatgacc tttcagactt ttatgttcaa ctaatagaag atgaagctga 180
aattagtcac ctttcagaga gattaaacag tgttaaaaca aggcccgaaat attatgtagg 240
tccacctttg caaagaggag atatatgatg tgctgttttc ccagaagata atttatggta 300
tcgtgctgtg atcaaggagc aacaacccaa tgaccttctc tctgtgcagt ttatagatta 360
tggcaatgtt tctgtggttc atactaacia aataggtagg cttgaccttg ttaatgcaat 420
attgcccggg ttgtgcattc attgctcctt gcagggattt gaggttcctg acaataaaaa 480
ttctaagaaa atgatgcatt acttttccca acggaccagc gaggctgcaa taagatgtga 540
atttggttaa tttcaagaca gatgggaagt tattcttgct gatgaacatg ggatcatagc 600
agatgatatg attagcagggt atgctctcag tgaaaaatct caagtagaac tttctaccca 660
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tcttaactgg tataatccag aaaaaaaaaat gataagagct tatgccactg tgatagatgg 780

acctgagtag	ttttggtgtc	agtttgcgtga	tacggagaaa	cttcagtgtt	tagaagtaga	840
agtagacact	gctggagaac	aggttagcaga	caggagaaat	tgtatcccat	gtccttatat	900
tggagatcct	tgtatagtaa	gatacagaga	agatggacat	tattataggg	cacttatcac	960
taatatttgt	gaagattatc	ttgtatctgt	caggcttgtg	gaatttggaa	acattgaaga	1020
ctgtgtggac	ccaaaagcac	tctgggccat	tccttctgaa	cttctgtcgg	ttcccatgca	1080
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tattaatgag	aaaatggaga	aatattctaa	gactggtatt	aaaagtgtc	ttccctatga	1320
aaatattgac	tcagagataa	agcagactct	tgggtcctac	aatcttgatg	taggacttaa	1380
gaaattaagt	aataaagctg	tacaaaataa	aatatatatg	gaacaacaga	cagatgagct	1440
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agaactgaat	tcacttgagg	tgccgctttc	tcctgatgat	gaatcaaaag	aattcttaga	1740
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cctgagaatg	tctggaatgn	nanacccaaa	ttggataaga	gtccacctga	gaaaaggggt	2460
ttggaggtga	tggagattta	accgtggatn	tatagctgtg	gccaatcagt	cagaagctgc	2520
ccntgaacaa	gtggcatctt	acgcagacca	acagagtatt	tgagaaaat		2569

<210> 579

<211> 752

<212> PRT

<213> Homo Sapiens

<400> 579

Arg	Val	Lys	Ala	Thr	Leu	Ser	Glu	Arg	Lys	Ile	Gly	Asp	Ser	Cys	Asp
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Lys	Asp	Leu	Pro	Leu	Lys	Phe	Cys	Glu	Phe	Pro	Gln	Lys	Thr	Ile	Met
		20						25					30		
Pro	Gly	Phe	Lys	Thr	Thr	Val	Tyr	Val	Ser	His	Ile	Asn	Asp	Leu	Ser
		35					40					45			
Asp	Phe	Tyr	Val	Gln	Leu	Ile	Glu	Asp	Glu	Ala	Glu	Ile	Ser	His	Leu
	50				55					60					
Ser	Glu	Arg	Leu	Asn	Ser	Val	Lys	Thr	Arg	Pro	Glu	Tyr	Tyr	Val	Gly
65			70						75					80	
Pro	Pro	Leu	Gln	Arg	Gly	Asp	Met	Ile	Cys	Ala	Val	Phe	Pro	Glu	Asp
			85					90						95	
Asn	Leu	Trp	Tyr	Arg	Ala	Val	Ile	Lys	Glu	Gln	Gln	Pro	Asn	Asp	Leu
	100						105					110			
Leu	Ser	Val	Gln	Phe	Ile	Asp	Tyr	Gly	Asn	Val	Ser	Val	Val	His	Thr
	115					120						125			
Asn	Lys	Ile	Gly	Arg	Leu	Asp	Leu	Val	Asn	Ala	Ile	Leu	Pro	Gly	Leu
	130					135					140				

Cys Ile His Cys Ser Leu Gln Gly Phe Glu Val Pro Asp Asn Lys Asn
 145 150 155 160
 Ser Lys Lys Met Met His Tyr Phe Ser Gln Arg Thr Ser Glu Ala Ala
 165 170 175
 Ile Arg Cys Glu Phe Val Lys Phe Gln Asp Arg Trp Glu Val Ile Leu
 180 185 190
 Ala Asp Glu His Gly Ile Ile Ala Asp Asp Met Ile Ser Arg Tyr Ala
 195 200 205
 Leu Ser Glu Lys Ser Gln Val Glu Leu Ser Thr Gln Val Ile Lys Ser
 210 215 220
 Ala Ser Ser Lys Ser Val Asn Lys Ser Asp Ile Asp Thr Ser Val Phe
 225 230 235 240
 Leu Asn Trp Tyr Asn Pro Glu Lys Lys Met Ile Arg Ala Tyr Ala Thr
 245 250 255
 Val Ile Asp Gly Pro Glu Tyr Phe Trp Cys Gln Phe Ala Asp Thr Glu
 260 265 270
 Lys Leu Gln Cys Leu Glu Val Glu Val Gln Thr Ala Gly Glu Gln Val
 275 280 285
 Ala Asp Arg Arg Asn Cys Ile Pro Cys Pro Tyr Ile Gly Asp Pro Cys
 290 295 300
 Ile Val Arg Tyr Arg Glu Asp Gly His Tyr Tyr Arg Ala Leu Ile Thr
 305 310 315 320
 Asn Ile Cys Glu Asp Tyr Leu Val Ser Val Arg Leu Val Asp Phe Gly
 325 330 335
 Asn Ile Glu Asp Cys Val Asp Pro Lys Ala Leu Trp Ala Ile Pro Ser
 340 345 350
 Glu Leu Leu Ser Val Pro Met Gln Ala Phe Pro Cys Cys Leu Ser Gly
 355 360 365
 Phe Asn Ile Ser Glu Gly Leu Cys Ser Gln Glu Gly Asn Asp Tyr Phe
 370 375 380
 Tyr Glu Ile Ile Thr Glu Asp Val Leu Glu Ile Thr Ile Leu Glu Ile
 385 390 395 400
 Arg Arg Asp Val Cys Asp Ile Pro Leu Ala Ile Val Asp Leu Lys Ser
 405 410 415
 Lys Gly Lys Ser Ile Asn Glu Lys Met Glu Lys Tyr Ser Lys Thr Gly
 420 425 430
 Ile Lys Ser Ala Leu Pro Tyr Glu Asn Ile Asp Ser Glu Ile Lys Gln
 435 440 445
 Thr Leu Gly Ser Tyr Asn Leu Asp Val Gly Leu Lys Lys Leu Ser Asn
 450 455 460
 Lys Ala Val Gln Asn Lys Ile Tyr Met Glu Gln Gln Thr Asp Glu Leu
 465 470 475 480
 Ala Glu Ile Thr Glu Lys Asp Val Asn Ile Ile Gly Thr Lys Pro Ser
 485 490 495
 Asn Phe Arg Asp Pro Lys Thr Asp Asn Ile Cys Glu Gly Phe Glu Asn
 500 505 510
 Pro Cys Lys Asp Lys Ile Asp Thr Glu Glu Leu Glu Gly Glu Leu Glu
 515 520 525
 Cys His Leu Val Asp Lys Ala Glu Phe Asp Asp Lys Tyr Leu Ile Thr
 530 535 540
 Gly Phe Asn Thr Leu Leu Pro His Ala Asn Glu Thr Lys Glu Ile Leu
 545 550 555 560
 Glu Leu Asn Ser Leu Glu Val Pro Leu Ser Pro Asp Asp Glu Ser Lys
 565 570 575
 Glu Phe Leu Glu Leu Glu Ser Ile Glu Leu Gln Asn Ser Leu Val Val

580	585	590
Asp Glu Glu Lys Gly Glu Leu Ser Pro Val Pro Pro Asn Val Pro Leu		
595	600	605
Ser Gln Glu Cys Val Thr Lys Gly Ala Met Glu Leu Phe Thr Leu Gln		
610	615	620
Leu Pro Leu Ser Cys Glu Ala Glu Lys Gln Pro Glu Leu Glu Leu Pro		
625	630	635
Thr Ala Gln Leu Pro Leu Asp Asp Lys Met Asp Pro Leu Ser Leu Gly		
645	650	655
Val Ser Gln Lys Ala Gln Glu Ser Met Cys Thr Glu Asp Met Arg Lys		
660	665	670
Ser Ser Cys Val Glu Ser Phe Asp Asp Gln Arg Arg Met Ser Leu His		
675	680	685
Leu His Gly Ala Asp Cys Asp Pro Lys Thr Gln Asn Glu Met Asn Ile		
690	695	700
Cys Glu Glu Glu Phe Val Glu Tyr Lys Asn Arg Asp Ala Ile Ser Ala		
705	710	715
Leu Met Pro Phe Ser Leu Arg Lys Lys Ala Val Met Glu Ala Ser Thr		
725	730	735
Ile Met Val Tyr Gln Ile Ile Phe Gln Asn Tyr Arg Thr Pro Thr Leu		
740	745	750

<210> 580
 <211> 2077
 <212> DNA
 <213> Homo Sapiens

<400> 580	
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gaaagaaact ccgttccttg aggttataac tcatgagtta caagactttg ctgtagatga	9000
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gaaattctaa aatatttgag aagagccaat tttatagcct tttggaagtt caaagatgaa	13200
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ttctacattt tcttgaaatt tgggaggtta ataccaagta ttcatttcat gatgtaaaga	15600
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aacatctaata atatatatta caggccaaat gaactaaaca ttgccttgct atattcacca 1680
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tatatatata ttataggcca gctacaagggt gtttaaatat ttaggattgt gtcttgaaaa 1980
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acccaaatgt aaaatataag taataattct catgaaa 2077

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<210> 581
 <211> 312
 <212> PRT
 <213> Homo Sapiens

<400> 581

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20          25          30
Ser Asn Ser Ser Asp Ser Lys Ser Gln Ser Arg Arg His Leu Ser Ala
35          40          45
Lys Glu Arg Arg Glu Met Lys Lys Lys Lys Leu Pro Ser Asp Ser Gly
50          55          60
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His Ile Glu Thr His Gln Asn Thr Ser Lys Asn Val Ala Ala Val Gln
85          90          95
Pro Met Lys Arg Gly Gln Lys Ser Lys Met Lys Lys Met Lys Glu Lys
100          105          110
Tyr Lys Asp Gln Asp Glu Glu Asp Arg Glu Leu Ile Met Lys Leu Leu
115          120          125
Gly Ser Ala Gly Ser Asn Lys Glu Glu Lys Gly Lys Lys Gly Lys Lys
130          135          140
Gly Lys Thr Lys Asp Glu Pro Val Lys Lys Gln Pro Gln Lys Pro Arg
145          150          155          160
Gly Gly Gln Arg Val Ser Asp Asn Ile Lys Lys Glu Thr Pro Phe Leu
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Glu Val Ile Thr His Glu Leu Gln Asp Phe Ala Val Asp Asp Pro His
180          185          190
Asp Asp Lys Glu Glu Gln Asp Leu Asp Gln Gln Gly Asn Glu Glu Asn
195          200          205
Leu Phe Asp Ser Leu Thr Gly Gln Pro His Pro Glu Asp Val Leu Leu
210          215          220
Phe Ala Ile Pro Ile Cys Ala Pro Tyr Thr Thr Met Thr Asn Tyr Lys
225          230          235          240
Tyr Lys Val Lys Leu Thr Pro Gly Val Gln Lys Lys Gly Lys Ala Ala
245          250          255
Lys Thr Ala Leu Asn Ser Phe Met His Ser Lys Glu Ala Thr Ala Arg
260          265          270
Glu Lys Asp Leu Phe Arg Ser Val Lys Asp Thr Asp Leu Ser Arg Asn
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<210> 582
 <211> 3309
 <212> DNA
 <213> Homo Sapiens

<400> 582

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<210> 583
<211> 872
<212> PRT
<213> Homo Sapiens

<400> 583

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35 40 45
Thr Pro Ser Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val
50 55 60
Ala Ala Lys Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn
65 70 75 80
Phe Lys Arg Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys
85 90 95
Glu Lys Glu Asn Leu Ser Tyr Asp Leu Val Pro Leu Lys Asn Gly Gly
100 105 110
Val Gly Ile Lys Val Met Tyr Met Gly Glu Glu His Leu Phe Ser Val
115 120 125
Glu Gln Ile Thr Ala Met Leu Leu Thr Lys Leu Lys Glu Thr Ala Glu
130 135 140
Asn Ser Leu Lys Lys Pro Val Thr Asp Cys Val Ile Ser Val Pro Ser
145 150 155 160
Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Leu Asp Ala Ala Gln Ile
165 170 175
Val Gly Leu Asn Cys Leu Arg Leu Met Asn Asp Met Thr Ala Val Ala
180 185 190
Leu Asn Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu Asp Glu Lys
195 200 205
Pro Arg Ile Val Val Phe Val Asp Met Gly His Ser Ala Phe Gln Val
210 215 220
Ser Ala Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Gly Thr Ala
225 230 235 240
Phe Asp Pro Phe Leu Gly Gly Lys Asn Phe Asp Glu Lys Leu Val Glu
245 250 255
His Phe Cys Ala Glu Phe Lys Thr Lys Tyr Lys Leu Asp Ala Lys Ser
260 265 270
Lys Ile Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys Leu Lys
275 280 285
Lys Leu Met Ser Ser Asn Ser Thr Asp Leu Pro Leu Asn Ile Glu Cys
290 295 300
Phe Met Asn Asp Lys Asp Val Ser Gly Lys Met Asn Arg Ser Gln Phe
305 310 315 320
Glu Glu Leu Cys Ala Glu Leu Leu Gln Lys Ile Glu Val Pro Leu Tyr

Ser	Leu	Leu	Glu	Gln	Thr	His	Leu	Lys	Val	Glu	Asp	Val	Ser	Ala	Val	
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			340						345						350	
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Ala	Lys	Phe	Phe	Gly	Lys	Asp	Ile	Ser	Thr	Thr	Leu	Asn	Ala	Asp	Glu	
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Ala	Val	Ala	Arg	Gly	Cys	Ala	Leu	Gln	Cys	Ala	Ile	Leu	Ser	Pro	Ala	
			385						390						395	
Phe	Lys	Val	Arg	Glu	Phe	Ser	Val	Thr	Asp	Ala	Val	Pro	Phe	Pro	Ile	
			405						410						415	
Ser	Leu	Ile	Trp	Asn	His	Asp	Ser	Glu	Asp	Thr	Glu	Gly	Val	His	Glu	
			420						425						430	
Val	Phe	Ser	Arg	Asn	His	Ala	Ala	Pro	Phe	Ser	Lys	Val	Leu	Thr	Phe	
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Leu	Arg	Arg	Gly	Pro	Phe	Glu	Leu	Glu	Ala	Phe	Tyr	Ser	Asp	Pro	Gln	
			450						455						460	
Gly	Val	Pro	Tyr	Pro	Glu	Ala	Lys	Ile	Gly	Arg	Phe	Val	Val	Gln	Asn	
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Val	Ser	Ala	Gln	Lys	Asp	Gly	Glu	Lys	Ser	Arg	Val	Lys	Val	Lys	Val	
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Arg	Val	Asn	Thr	His	Gly	Ile	Phe	Thr	Ile	Ser	Thr	Ala	Ser	Met	Val	
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Glu	Lys	Val	Pro	Thr	Glu	Glu	Asn	Glu	Met	Ser	Ser	Glu	Ala	Asp	Met	
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Glu	Cys	Leu	Asn	Gln	Arg	Pro	Pro	Glu	Asn	Pro	Asp	Thr	Asp	Lys	Asn	
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Val	Gln	Gln	Asp	Asn	Ser	Glu	Ala	Gly	Thr	Gln	Pro	Gln	Val	Gln	Thr	
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Asp	Ala	Gln	Gln	Thr	Ser	Gln	Ser	Pro	Pro	Ser	Pro	Glu	Leu	Thr	Ser	
			565						570						575	
Glu	Glu	Asn	Lys	Ile	Pro	Asp	Ala	Asp	Lys	Ala	Asn	Glu	Lys	Lys	Val	
			580						585						590	
Asp	Gln	Pro	Pro	Glu	Ala	Lys	Lys	Pro	Lys	Ile	Lys	Val	Val	Asn	Val	
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Glu	Leu	Pro	Ile	Glu	Ala	Asn	Leu	Val	Trp	Gln	Leu	Gly	Lys	Asp	Leu	
			610						615						620	
Leu	Asn	Met	Tyr	Ile	Glu	Thr	Glu	Gly	Lys	Met	Ile	Met	Gln	Asp	Lys	
			625						630						635	
Leu	Glu	Lys	Glu	Arg	Asn	Asp	Ala	Lys	Asn	Ala	Val	Glu	Glu	Tyr	Val	
			645						650						655	
Tyr	Glu	Phe	Arg	Asp	Lys	Leu	Cys	Gly	Pro	Tyr	Glu	Lys	Phe	Ile	Cys	
			660						665						670	
Glu	Gln	Asp	His	Gln	Asn	Phe	Leu	Arg	Leu	Leu	Thr	Glu	Thr	Glu	Asp	
			675						680						685	
Trp	Leu	Tyr	Glu	Glu	Gly	Glu	Asp	Gln	Ala	Lys	Gln	Ala	Tyr	Val	Asp	
			690						695						700	
Lys	Leu	Glu	Glu	Leu	Met	Lys	Ile	Gly	Thr	Pro	Val	Lys	Val	Arg	Phe	
</																

Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala Gln Ala
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 Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu Ile Lys
 785 790 795 800
 Thr Lys Ile Lys Glu Leu Asn Asn Thr Cys Glu Pro Val Val Thr Gln
 805 810 815
 Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly
 820 825 830
 Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe
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 Asn Ser Val Asn Met Asp Leu Asp
 865 870

<210> 584
 <211> 2918
 <212> DNA
 <213> Homo Sapiens

<400> 584

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<210> 585
 <211> 687
 <212> PRT
 <213> Homo Sapiens

<400> 585

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Ala Ser Tyr Thr Trp Gln Phe Glu Ala Arg Lys Ala Gln Ile Leu Lys
 35          40          45
Cys Met Glu Cys Gly Ser Ser His Asp Thr Leu Gln Gln Leu Thr Ala
 50          55          60
His Met Met Val Thr Gly His Phe Leu Lys Val Thr Thr Ser Ala Ser
 65          70          75          80
Lys Lys Gly Lys Gln Leu Val Leu Asp Pro Val Val Glu Glu Lys Ile
 85          90          95
Gln Ser Ile Pro Leu Pro Pro Thr Thr His Thr Arg Leu Pro Ala Ser
100          105          110
Ser Ile Lys Lys Gln Pro Asp Ser Pro Ala Gly Ser Thr Thr Ser Glu
115          120          125
Glu Lys Lys Glu Pro Glu Lys Glu Lys Pro Pro Val Ala Gly Asp Ala
130          135          140
Glu Lys Ile Lys Glu Glu Ser Glu Asp Ser Leu Glu Lys Phe Glu Pro
145          150          155          160
Ser Thr Leu Tyr Pro Tyr Leu Arg Glu Glu Asp Leu Asp Asp Ser Pro
165          170          175
Lys Gly Gly Leu Asp Ile Leu Lys Ser Leu Glu Asn Thr Val Ser Thr
180          185          190
Ala Ile Ser Lys Ala Gln Asn Gly Ala Pro Ser Trp Gly Gly Tyr Pro
195          200          205
Ser Ile His Ala Ala Tyr Gln Leu Pro Gly Thr Val Lys Pro Leu Pro
210          215          220
Ala Ala Val Gln Ser Val Gln Val Gln Pro Ser Tyr Ala Gly Gly Val
225          230          235          240
Lys Ser Leu Ser Ser Ala Glu His Asn Ala Leu Leu His Ser Pro Gly
245          250          255
Ser Leu Thr Pro Pro Pro His Lys Ser Asn Val Ser Ala Met Glu Glu

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260	265	270
Leu Val Glu Lys Val Thr Gly Lys Val Asn Ile Lys Lys Glu Glu Arg		
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Pro Pro Glu Lys Glu Lys Ser Ser Leu Ala Lys Ala Ala Ser Pro Ile		
290	295	300
Ala Lys Glu Asn Lys Asp Phe Pro Lys Thr Glu Glu Val Ser Gly Lys		
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Pro Gln Lys Lys Gly Pro Glu Ala Glu Thr Trp Glu Ala Lys Lys Glu		
325	330	335
Gly Pro Leu Asp Val His Thr Pro Asn Gly Thr Glu Pro Leu Lys Ala		
340	345	350
Lys Val Thr Asn Gly Cys Asn Asn Leu Gly Ile Ile Met Asp His Ser		
355	360	365
Pro Glu Pro Ser Phe Ile Asn Pro Leu Ser Ala Leu Gln Ser Ile Met		
370	375	380
Asn Thr His Leu Gly Lys Val Ser Lys Pro Val Ser Pro Ser Leu Asp		
385	390	395
Pro Leu Ala Met Leu Tyr Lys Ile Ser Asn Ser Met Leu Asp Lys Pro		
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Val Tyr Pro Ala Thr Pro Val Lys Gln Ala Asp Ala Ile Asp Arg Tyr		
420	425	430
Tyr Tyr Glu Asn Ser Asp Gln Pro Ile Asp Leu Thr Lys Ser Lys Asn		
435	440	445
Lys Pro Leu Val Ser Ser Val Ala Asp Ser Val Ala Ser Pro Leu Arg		
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Glu Ser Ala Leu Met Asp Ile Ser Asp Met Val Lys Asn Leu Thr Gly		
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Arg Leu Thr Pro Lys Ser Ser Thr Pro Ser Thr Val Ser Glu Lys Ser		
485	490	495
Asp Ala Asp Gly Ser Ser Phe Glu Glu Ala Leu Asp Glu Leu Ser Pro		
500	505	510
Val His Lys Arg Lys Gly Arg Gln Ser Asn Trp Asn Pro Gln His Leu		
515	520	525
Leu Ile Leu Gln Ala Gln Phe Ala Ser Ser Leu Arg Glu Thr Thr Glu		
530	535	540
Gly Lys Tyr Ile Met Ser Asp Leu Gly Pro Gln Glu Arg Val His Ile		
545	550	555
Ser Lys Phe Thr Gly Leu Ser Met Thr Thr Ile Ser His Trp Leu Ala		
565	570	575
Asn Val Lys Tyr Gln Leu Arg Arg Thr Gly Gly Thr Lys Phe Leu Lys		
580	585	590
Asn Leu Asp Thr Gly His Pro Val Phe Phe Cys Asn Asp Cys Ala Ser		
595	600	605
Gln Phe Arg Thr Ala Ser Thr Tyr Ile Ser His Leu Glu Thr His Leu		
610	615	620
Gly Phe Ser Leu Lys Asp Leu Ser Lys Leu Pro Leu Asn Gln Ile Gln		
625	630	635
Glu Gln Gln Asn Val Ser Lys Val Leu Thr Asn Lys Thr Leu Gly Pro		
645	650	655
Leu Gly Ala Thr Glu Glu Asp Leu Gly Ser Thr Phe Gln Cys Lys Leu		
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Cys Asn Arg Thr Phe Ala Lys Gln Ala Arg Ser Gln Thr Ala Pro		
675	680	685

<210> 586

<211> 1898
<212> DNA
<213> Homo Sapiens

<400> 586

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<210> 587
<211> 399
<212> PRT
<213> Homo Sapiens

<400> 587

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Pro	Pro	Gln	Pro	Pro	Ser	Ala	Leu	Glu	Ser	Asp	Gly	Glu	Gly	Pro	Pro
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	50				55					60					
Arg	Thr	Leu	Leu	Tyr	Gln	Glu	His	Val	Pro	Thr	Ser	Ser	Ala	Ser	Ala
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 <211> 541
 <212> DNA
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<400> 592

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 <212> DNA
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<400> 593

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<210> 594
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 <213> Homo Sapiens

<400> 594

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<211> 600
 <212> DNA
 <213> Homo Sapiens

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 <211> 835
 <212> DNA
 <213> Homo Sapiens

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<210> 597
 <211> 443
 <212> DNA
 <213> Homo Sapiens

<400> 597
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 aaattcangc tatngctgtt tgt 443

<210> 598
 <211> 491
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<213> Homo Sapiens

<400> 598

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<210> 599

<211> 802

<212> DNA

<213> Homo Sapiens

<400> 599

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<211> 523

<212> DNA

<213> Homo Sapiens

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<210> 601

<211> 530

<212> DNA

<213> Homo Sapiens

<400> 601

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<210> 602

<211> 311

<212> DNA

<213> Homo Sapiens

<400> 602

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<211> 289

<212> DNA

<213> Homo Sapiens

<400> 603

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<210> 604

<211> 356

<212> DNA

<213> Homo Sapiens

<400> 604

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<211> 290

<212> DNA

<213> Homo Sapiens

<400> 605

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<210> 606

<211> 714

<212> DNA

<213> Homo Sapiens

<400> 606

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attactggcc	agctgttggc	attgtgtttc	ttacttagtt	ctcccaaggg	aaaactctta	540
aattgaatct	tcagcagaat	aatccttaaa	tatactttgt	aagcaaaaca	aaagcttttt	600
tgtttacata	gttctttggg	attttactgt	tcctaatttt	attctgaaac	tcaattttac	660
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<210> 607

<211> 687

<212> DNA

<213> Homo Sapiens

<400> 607

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tttaaaaaata	agcctgtgtt	caagctctga	tcataatttct	tttattttga	tttggaaga	360
aaatactgtt	tctgatagca	tgaaatgcaa	aattttttaga	tttttaattct	cnctaatttt	420
aagaactatt	gagaaattga	ttaatgacat	gaagtgcaca	acactaatta	ctggccagct	480
gttggcattg	tgtttcttac	ttagtctctc	caaggaaaaa	tcttaaaactg	aatcttcagc	540
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ggattttact	gttcctaatt	ttattctgaa	actccatttt	tcccagacc	ataattacc	660
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<210> 608

<211> 994

<212> DNA

<213> Homo Sapiens

<400> 608

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caccaaata	tattgacgta	atagaacttc	acgattgctt	ttctaccaac	gaactcctta	480
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accactagg	cgctacaggt	cttgcctcagt	gtgcagaact	ctgctggcag	ctgagagggg	660
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<210> 609

<211> 843

<212> DNA

<213> Homo Sapiens

<400> 609

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tnngcaatan	ttaaccttnc	ttgaaaangg	aaatttntac	caanggacng	aaancnttnt	180
aattngaant	naaattatan	ttngaaancg	gcnnncgaaa	ccaancttna	tggtccaatt	240
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aaaantnttt	tnatttttaa	aataacceng	tnccaacccc	cngatcanat	tccttttnatt	360
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ttncnggcca	ccngtgggcn	tngtnttcc	tacttantcc	cccccaaggaa	annccctaan	540
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tttacntant	ccttgggatt	taacgggtcc	ccaatttnat	ccngaaccce	nttttcccc	660
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aaaacaacct	ccccccnctt	ttggcccagg	nttntttccc	gtctaaatcc	gaacaataaa	840
aag						843

<210> 610

<211> 707

<212> DNA

<213> Homo Sapiens

<400> 610

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gttcagtgtt	ttaatctgac	gcaggcttat	gcggaggana	atgttttcat	gttacttata	180
ctaacattag	ttcttctata	gggtgataga	ttggtccaat	tgggtgtgag	gagttcagtt	240
atatgttttg	gatttttttag	gtantgggtg	ttgagcttga	acgctttctt	aattgggtggc	300
tgtcttttag	cctactatgg	gtgttaaatt	ttttactctc	tctacaaggt	tttttccctag	360
tgtccaaana	gctgttcctc	tttgactaa	cagttaaatt	tacaagggga	tttagagggg	420
tctgtgggca	aattttaaagt	tgaactaaga	ttctatcttg	gacaaccagc	tatcaccagg	480
ctcggtagg	ttgtgccttc	tacctataaa	tcttcccact	attttgctac	atagacgggg	540
tgtgtctttt	tanctgttct	tangtanctc	gtctggtttc	gggggtctta	gctttggctc	600
tccttgcaaa	gttattttcta	agttnaattc	attatgcnc	angtatagg	gttagtcctt	660
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<210> 611

<211> 663
 <212> DNA
 <213> Homo Sapiens

<400> 611

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aaagtaatct	canaaaaaaaa	aggttttttg	aaattaaact	tgacttttaa	aaaatcatac	180
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caattccaca	cacagccatt	tatgtgtgag	tgctctgctt	caagcacagt	acgctctttg	420
cagggaaggc	cagatgttca	gagtgggagt	ggtacttttc	aaccagctaa	aagtgcagaa	480
gtcatctant	cgtctgcctc	ttcccactgc	cagtgcctgc	agccttgcag	caaettttaa	540
ccacccccta	tgggactgga	atnttgagtt	aaaaagccaa	ngctgaactg	gctgacgctg	600
tantctccan	tgaaaaggaa	atgggatgaa	atggaaaccg	aaaaaccccc	ngtnacntga	660
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<210> 612
 <211> 621
 <212> DNA
 <213> Homo Sapiens

<400> 612

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aagtaatctc	anaaaaaaaa	ggttttttga	aattaaactt	gactttttaa	aaatcatacg	180
gacaaacaa	tttcaaaca	aactggatta	gtaggatttc	ttgcctgctt	aactaacatg	240
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aattccacnc	acagccattt	atgtgtgagt	gctctgcttc	aagcacanta	cgctctttgc	420
agggaaggcc	anatgttcnn	antgggagt	gtacttttca	accagctaaa	antgcanaag	480
tcatctantc	gtctgcctct	tccaactgcc	agttgcctgc	agccttgcag	catcttttaa	540
ccacccctat	nggactggaa	tattgaatta	taaaccnngg	ntgaactggc	tgangctggt	600
tctcccttga	aaaggaaatg	g				621

<210> 613
 <211> 637
 <212> DNA
 <213> Homo Sapiens

<400> 613

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tantntnctn	aaaaaaaaaga	ggtttganga	aattaaactt	gactttttaa	anatcatgng	180
gacaaacnac	tttcaaaca	agctggatta	gnaggatttc	tngnctgctt	aactaacatn	240
aaanacttct	tgtcccaggc	cctnctnaaa	aaaacctctt	gtggaaaccn	agcnaaaaat	300
aanantttct	ccctgatgca	ntggggggag	anggagaggc	taaaaacttc	tntggaanc	360
anttccacnc	acngccattt	ttntntnagt	gcnetgctnc	nancnnagta	cgctctttgg	420
gnggacggcn	anntnttnat	agngggagt	gtnttttcaa	ccagctaata	ntgaagaaat	480
catctagtgc	netgcctctn	cccactgcc	gtgcctgcnt	ccttgcaacn	tcttttaacc	540
ccccctangg	acnggattat	nnagttaana	ccgaggntga	gctggntgac	gctntctcct	600
ccatttgaaa	angaaatgga	taagatggaa	ccgaaaa			637

<210> 614

<211> 673
<212> DNA
<213> Homo Sapiens

<400> 614
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agtttgcttt ggaatctgag aatatttctc aaccatactt tacgaacaga aggactattc 600
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<210> 615
<211> 714
<212> DNA
<213> Homo Sapiens

<400> 615
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acagaatctt cctcgtcact tgtacccttc aagggtgggt gttcttgana anacacttct 180
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<210> 616
<211> 688
<212> DNA
<213> Homo Sapiens

<400> 616
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tctcccttg ttncccttca anggtgggtg gtttctcgaa aaaaanactg tcttanaatt 660
ttctccttc ctttttttct tctgggtt 688

<210> 617
 <211> 721
 <212> DNA
 <213> Homo Sapiens

<400> 617

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c						721

<210> 618
 <211> 461
 <212> DNA
 <213> Homo Sapiens

<400> 618

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cttatcccc	ctngccccct	gaatggetgg	gggtccgcgcg	tccttggggn	aggcnctcca	420
ccaacncaaa	atgcaatcnt	cncagnaac	ccntgccgcc	t		461

<210> 619
 <211> 751
 <212> DNA
 <213> Homo Sapiens

<400> 619

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cccagggcct	ggcaggaacg	tcacagtggc	ctcgagcagg	agcccccggt	gccttatcgc	180
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aactgaaggc	ccccggggcc	ggaccattac	ggaacaagtg	ctgtcccttg	naggagaaaa	660
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<210> 620
 <211> 556
 <212> DNA
 <213> Homo Sapiens

<400> 620
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 gcaaaaaaag cttaaaaaaa ccaaaaacca aaggcagcat ccttgctaata tttcatctac 180
 attaanaaaa aaaaaatctt gtaactaatg tttttatttn ccttaaaaaa aatatttcgc 240
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<210> 621
 <211> 708
 <212> DNA
 <213> Homo Sapiens

<400> 621
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 aaaaactnat atattccaaa ttcnccgcat ntggnaatnt tncatggac nctgnatctt 300
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 caaanctcac aagnaattgt aattngcngt ngggantcaa tgttncggg tnaattatct 600
 tggatnanaa cnttttcta catnactatt gaaaaaacct gtggtttctt gctttttaac 660
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<210> 622
 <211> 675
 <212> DNA
 <213> Homo Sapiens

<400> 622
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 gattctcaaa acttaaatcc aagaaggagc cctgtcccag ctcaaatagc tataactgta 180
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 gctgtggaag aaantggaga anaagctgag ccagtncgta ntgggtgctga gagtgtctct 420
 gaggggtgaag gantagatgc tacttcaggc tccncagata gttctggtga tggggttacn 480
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 ngggagttct gctggacttc cagttcatgc ctgcctggta tnccttncce gagggcctgc 600
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<210> 623
<211> 713
<212> DNA
<213> Homo Sapiens

<400> 623

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cagtgtccac	tctgaaggta	naagaatcng	gttattatag	cttgctttta	caaacagcng	660
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<210> 624
<211> 554
<212> DNA
<213> Homo Sapiens

<400> 624

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aattaaagct	gaattagcta	aaaccaatgg	agaattaatc	tcnaccncnc	acnanttcnc	300
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aattncacaa	aatctggaga	attnnagaat	tgatnaatat	nattgatcnn	tcgaagatac	420
tatcanogaa	tttcagaacc	tnangtctca	tatggaaaac	tcnttttaaat	gcnatgacaa	480
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acctaaggga	cagc					554

<210> 625
<211> 551
<212> DNA
<213> Homo Sapiens

<400> 625

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tggggatggt	taatgggtac	aaaaacaaat	aagatnaaaa	gaatgattta	atatctgata	180
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agactgaaat	ctttttctaa	ataatgtata	tacatgtttt	gtgatctgta	cacacttatt	480
ctccaaatcc	taactntant	cccaacanat	atnttaaate	cttgttttanc	ngaataagtt	540
aaaaaaatcc	t					551

<210> 626
<211> 680

<212> DNA

<213> Homo Sapiens

<400> 626

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cgactcgatc	aatgcccattg	ccccagccag	ctgtgggggg	cagcccatat	tccagggcag	360
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<210> 627

<211> 753

<212> DNA

<213> Homo Sapiens

<400> 627

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cccaagagag	gaaggctgca	atgaagacag	ctgaagaatt	tctacagcaa	atgaattatt	420
ccaagaatac	ccaaattcaa	gttcttcag	aaggaggtga	aacaccaatc	ttcaaacagt	480
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gtncaaaaca	atggtaggat	ccaagttgac	cnnaactcct	atggtgactc	ccatgggtgg	720
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<210> 628

<211> 675

<212> DNA

<213> Homo Sapiens

<400> 628

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gttaaancca	ccttaacata	aaccttatng	caattntaca	cntcttttga	acncaatcta	180
taaaaaaaaa	aataactncc	anggcattac	aacttttnct	ctggcatntt	aaaaaacaac	240
tctnactaat	ggctaattgca	ttataaaaatt	ncctatctna	caaactctnc	taaattatgc	300
atagtatttt	acttttnaaa	ggtcntaaaa	aaaatataaa	tcanttncca	taaaanctaa	360
tatnggccca	taacaaaant	tcctnccagg	ttattttaat	ntnttaacnt	aaaaaaacnc	420
cagntgaaaa	aaaattncaa	nccaaaacta	accnttaaaa	aataggcntt	nggttnaggt	480
taattttttt	tttttttttt	ttgnaaaaaa	antcncnttt	gccagncctg	gattgtgggtg	540
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<210> 629
 <211> 677
 <212> DNA
 <213> Homo Sapiens

<400> 629

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agaagctgga	gctggtgccc	gtgccccaga	gcgctcacgg	cgactttctac	gtcggggatg	180
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tggatgacta	tttgggtggc	aagccagtgc	agaatagaga	acttcaagga	tatgagtcta	360
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<210> 630
 <211> 665
 <212> DNA
 <213> Homo Sapiens

<400> 630

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ttccagaagg	gtctgtctca	aggtacattt	tggcanactt	caaagattct	ttttctcaa	540
cttcattagc	atctttgcca	atccaaataa	atatctgttc	ccaagcatct	agtaacatga	600
catcatcttc	agctaaatca	tcctgggtga	actctccctg	gaatctcttc	aataacaaat	660
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<210> 631
 <211> 698
 <212> DNA
 <213> Homo Sapiens

<400> 631

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tgatgttact	ggtcaatggc	agtaatcctg	aagggtgaaga	tcctgagagg	gaacctgtan	180
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ctcagcagcc	tcccagataac	caggaaaagg	aacgactaaa	tacatccatt	ccacaaaaaa	300
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aatatgtaga	catcantatt	attgccctta	ctcgaaatcg	gaggacaagg	agatggtaca	420
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cccacactgg	agaaaaaccc	tatgactgtg	ntcactgtgg	gaaaagcttc	aatcatnaaa	540
caaacctcaa	taaacatgag	cgaattcnta	caggagagaa	accttattcc	tgttctcagt	600
gtggaaaaaa	cttcocgtcng	aattctcatc	ggagtcgtcc	tgaaggaatc	catntaacgg	660

agaagatatt aagtgtccan aatgtgggaa aacctccc

698

<210> 632
<211> 466
<212> DNA
<213> Homo Sapiens

<400> 632

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cagtaatttg gttctttcac canaacacag ttccagataa gcatctttgc actatttctc	240
aantatgaat ccccatgtgg ggggaaaacg gatatacttt caatagacac aagtcactct	300
ttgccttcca agtaagcana ctccagattc atcttcaaag tgttgggaaa ngggatctgt	360
gacctgtncat ttatcatata acttcaaaaa ggaaagctcc ttantccaaa aagcctanat	420
gctgaggtat agcccttgaa atgttttctt cctgtnaat ttccta	466

<210> 633
<211> 734
<212> DNA
<213> Homo Sapiens

<400> 633

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gcctccaagt gaacttaaca tattgcctat gcatctgatt ctttatanac ttttanattt	180
taaaactaaa tttganaaac catgcatact gtatacctta tttaataatc caaanaattg	240
tttgcacttt caaaaaagtt acaaaaaggc tgaacacaag ttaataaacc tatatgatgt	300
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gattgtcaga nacgcttcag taaattatct ctactttaaa attatatctg aatccccctt	420
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ncacctatgg tatgetgcat attaaattta acatttcaag taacatatat atagcaaaaa	600
ttcagccaaa tactctttca tgaaaagata ctgtccttaa aataaaaagt tantgaaaag	660
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<210> 634
<211> 822
<212> DNA
<213> Homo Sapiens

<400> 634

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tgtaaataatt gtacttttca aactccagat ctaaatatgt ttacttttca tgtggattcg	180
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tctaatacaa gtacttccat tgtaaacaga atacatccaa gtactgccag caccgtagtg	660
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agaattctaa tttgattccc naagtcttaa tccctgttna tancatcccc cctacaatgc 780
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<210> 635
 <211> 819
 <212> DNA
 <213> Homo Sapiens

<400> 635

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gaatatgagg	acaagctcta	gtgggtcatta	aacccccctca	gaaagtctaa	gattcagaat	180
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<210> 636
 <211> 704
 <212> DNA
 <213> Homo Sapiens

<400> 636

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<210> 637
 <211> 693
 <212> DNA
 <213> Homo Sapiens

<400> 637

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<210> 638
 <211> 619
 <212> DNA
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<400> 638						
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gcaacagtgg	ggatctanag	gaggatttgc	angaagagct	cgtggaagan	gtgggtggcc	480
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<210> 639
 <211> 694
 <212> DNA
 <213> Homo Sapiens

<400> 639						
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<210> 640
 <211> 728
 <212> DNA
 <213> Homo Sapiens

<400> 640						
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tcacagatca	ggtgatgcag	aatcctcgag	ttctggcagc	tttacaggag	cgacttgaca	180
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 acacctgcag gatnttaaag ttgaaatttt ctgacctggg acagcctatg tcttttgtgt 660
 tagaattcca ctttgaaccc cagcactact ttaccaactc agtcctgaca aaaaccttac 720
 cagatgaa 728

<210> 641
 <211> 732
 <212> DNA
 <213> Homo Sapiens

<400> 641
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 ctgtgttcac aagttccctg aagcttaggt tttgagagaa tattgttgag tcaactaggca 180
 gggctcacat aggaaactgg caatcacctc tgaaactgct tcacagacac ctgcttttcc 240
 tgctctgttc ctcanacttc tctcttcaa gcgtattccc cccacaacaa ggacagcagc 300
 ttggactaca tatctggctg atgatgtaat aaaaagatta ggcattggggg tttcctaagc 360
 cacaattcag ggccactctg caccaacaga gataagcacc caggtggaag ccccccttcc 420
 ccgagcctca tacattgtca tcatcttcta tggcctcccc agtgaagtac agcacagccc 480
 gcgggactat ccgctcacgg aaaaagtgtc caatttcaaa atcagaagct aatgtgaatt 540
 caaaatcttc atccagtgat ctccatcccc ggatgctttc caatggattg aagaaattga 600
 aaaaggactc attgggtact gtttcgtaat tgttctaaca gtgcctcaac cttatgcttc 660
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 ccccgttcac aa 732

<210> 642
 <211> 582
 <212> DNA
 <213> Homo Sapiens

<400> 642
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 naaggcgctg cctgatttcc tcaagctcct ccttctctct ctctctatct cgttcatctg 180
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 tggccatttc tcttcttctt tcttcttctc tttcagcttc tttctcatat tcccgggttt 360
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 gganttttct ttcaagtttt cttegttctg atgcattctc ttcattctct tctcgggtccc 480
 gttttttgtc tttttctctt tctcgtctcc gttectctct cnetctctct ctcgtctccc 540
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<210> 643
 <211> 784
 <212> DNA
 <213> Homo Sapiens

<400> 643
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 aagaaattct tcttgaaaga gccagtcaga aacgtggaga attgcaaact aaactcaaga 180

cagaaggacc	ttcaaaaact	gatgattcta	cttcagggag	caagaagctc	ctccactatc	240
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gagacnaaaa	agcnaaaagg	gatacaactt	gcatacaagct	aaagattgat	agtgaatta	360
aaaaaacagt	agttttgcc	ccattgttg	ccagcagagg	acaatcagag	gagcctgcag	420
gtaaaacaaa	gtctatgcag	ggaggtgcac	atcaagacgc	tggaaganat	taaactggag	480
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gccactccag	ggggcnaggc	ggctgctgcg	aatcacnnn	agaaccggga	tgaaagaaga	600
gaagancctt	cgggaagg	aatgaagt	attctcagag	cngtattaga	acngaagcta	660
aanganctcc	gggtgagaac	nccggggtg	acctccctaa	aattccagtc	cagagatgtn	720
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cttc						784

<210> 644

<211> 749

<212> DNA

<213> Homo Sapiens

<400> 644

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tatttttttaa	aaaagcaaaa	naataaagaa	tatatataaaa	agggacctgn	aatctgtaag	180
gtgattccaa	aaacnaaata	antagaaaat	ccatggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggtatcat	acaacattca	gtcagctgaa	natggattgg	tanagggtg	300
tctatacata	aacttcagtc	atTTTTgctt	gtgcanaatc	atcccaatct	tcccaanact	360
gaatgggcag	tcctgtggct	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagcgcgtt	acaacagcag	ttccttaggg	agccaacatg	acagggtgggt	480
canatttccc	tatgagaac	aaaactggcc	acctacagca	aaatatcaaa	atgggtaagt	540
ccttccttcc	tcttcctcct	gatttatatac	aacatatctc	ctttcaagac	tattatttcc	600
atcatgctta	ttccttcaca	aatctaaacc	ttgaggatgat	atgaaggaaa	ccancntcaa	660
aaaaaagaaa	actcaattcc	gaaatgaana	aaactgggcn	nggtatncaa	tacnccccan	720
aacatctcca	tatccttggc	ccagttacc				749

<210> 645

<211> 751

<212> DNA

<213> Homo Sapiens

<400> 645

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acaaaattat	tttttaaaaa	agcaaaaagaa	taaagaatat	atacaaaaagg	gacctggaat	180
ctgtaagggtg	attccaaaaa	cgaaataagt	agaaaatcca	tggtgaaacc	tgaacattct	240
acctctgctt	tggagaagg	ctatcataca	acattcagtc	agctgaagat	ggattggtag	300
agggtgtgtct	atacataaac	ttcagtcatt	tttgcttggtg	cagaatcatc	ccaatcttcc	360
caanactgaa	tgggcagtc	tgtggcttcc	ttccttttcc	atattcccaa	caaggctacg	420
tgaagttcaa	ctcttgatga	gccgcttaca	acagcagttc	cttaggancc	caacatgaca	480
gggtgggtcag	atttccctat	gagaaacaaa	actggncacc	tacagcaaaa	tntcaaaatg	540
ggtaagtcct	tccttctctc	tcctcctgat	tatntacaac	atatctcctt	tcaagantat	600
tatttccatc	atgcttattc	cttcccaaat	ctaaaccttg	aagggtgattt	gaagggaaac	660
cnccatccnn	aaaaagaaaa	acccattccc	aaattgaaaa	aaaactnggc	agggtataca	720
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<210> 646

<211> 760

<212> DNA

<213> Homo Sapiens

<400> 646

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tattttttta	aaaagcaaaa	gaataaagaa	tatatataaa	agggacctgg	aatctgtaag	180
gtgattccaa	aaacnaaata	agtagaaaat	ccatgggtgaa	acctgaacat	tctacctctg	240
ctttggagaa	gggctatcat	acaacattca	gtcagctgaa	natggattgg	tagagggtgtg	300
tctatacata	aacttcagtc	atTTTTgtct	gtgcanaatc	atcccaatct	tcccaanact	360
gaatgggcag	tctgtgggt	ttcttccttt	tccatattcc	caacaaggct	acgtgaagtt	420
caactcttga	tgagccgctt	acaacagcag	ttccttagga	gccaaatga	cagggtgggtc	480
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catgcttatt	ccttcacaaa	tctaaacctt	gaagtgatat	gaangaaacc	nccntccaga	660
aaagaaaact	cnantcanaa	atgaaaaaaa	ctggcaggta	tncaatacac	cccaaaacnt	720
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<210> 647

<211> 1041

<212> DNA

<213> Homo Sapiens

<400> 647

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tgataaaaaa	cgcagtgaat	ttccttggtt	ttgggaaaat	cagccaacag	gatgtcaaaa	180
attaaactgc	gctttccatc	acaatagagg	acgatatggt	gatggccttt	tctacctcc	240
gagcaaaact	gtgttgccca	ctgtgcctga	gtcaccagaa	gaggaagtga	aggctagcca	300
actttcagtt	cagcagaaca	aattgtctgt	ccagtccaat	ccttcccttc	agctgaggag	360
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taatgctgca	gatgatgatg	aagatgatga	tgatcagttt	tctgaggaag	gtgatgaaac	480
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ccggaaacct	gcagtcaata	ttaaagcaagg	tgaatgtttg	aatttttgaa	taaaaactct	600
tgaggaaatt	aagtcaaaga	aatgaagga	aaaatctaag	aagcaagggtg	agggttcttc	660
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tcaggactgt	ggtgaaggac	agtaactctc	tccaacaaac	aanggagaaa	gaanccttgg	780
gtagattgag	tctactgan	agacggggga	aacgaaaant	tcagcaagcg	gtgacaagtg	840
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actaacattg	acaaaaccac	caaagaaagc	tcaagnttcc	aagtccctta	agggaccgan	960
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<210> 648

<211> 810

<212> DNA

<213> Homo Sapiens

<400> 648

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ttatttttta	aaaaagcaaa	agaataaana	atatatacaa	aagggacctg	naatctgtaa	180
gctgattcca	aaaacnaaat	aantanaaaa	tccatgggtga	aacctgaaca	ttctacctct	240
gctttggana	agggctatca	tacaacattc	antcagctga	aaatggattg	gtaaagggtgt	300
gtctatacat	aaacttcant	catttttggc	tgtgcaaaat	catcccaatc	ttcccaaaac	360
tgaatgggca	gtcctgtggc	ttcttccttt	ttccatattc	ccaacaaggc	tacntgaant	420

tcaactcttg atnagccgct tacaacagca gttccttagg agccaacatg acagggtgggt 480
 caaatttccc tatgaanaaa caaaactggc cacctacagc aaaatatcaa aatgggtaag 540
 tccttccttc ctcttcctcc tgattatata caacatatct cctttcaaga ctattatttc 600
 catcatgctt attccttcac aaatctaaac cttgaggtga tatgaaggaa accancatca 660
 agaaaagaaa accaattcan aaatgaanaa aactggcagg tntacaatac accccananc 720
 atctcaatat ccttggcaca gttacaattc agtgttctgc tacagcccat aaaataaata 780
 ttggcagctt gaataancnc attttttccc 810

<210> 649
 <211> 656
 <212> DNA
 <213> Homo Sapiens

<400> 649

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 nctnatncca aaaacaaaaat aattaaaaaa tccatggtna aacctnaacn tntacctct 240
 gcttnggaaa agggctatca tacaacntnc antcanctna aaatggatng gtaaaggtn 300
 ntctatacat aaacttcant cattttngct tgtgcaaaat cancccaatc tncctaaaac 360
 tnaatgggca ntctgtggc ttntctnctt tncctatncc ccaacaaggc tacttnaatt 420
 tcaactcttn ataancgct tacaacagca ntnccttagn anccaacatn acagggtgggt 480
 caaattcccc tataaaaaac aaaactggcc nctacanca aaatatcaaa atgggtaatt 540
 ccttctncc tctnccnct nattatatac aacatttctc ctttcaaaac tattattncc 600
 atcatgcttn ttctnccaca aatctaaacc ttgangtgat ttgaagggaac cacctc 656

<210> 650
 <211> 645
 <212> DNA
 <213> Homo Sapiens

<400> 650

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 ncaaannttat tttttaaaaa accaaaaaaa taaaaaatnt ttccaaangg gacctgaaan 180
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 naattncac ncttnataac ccccttaca caccattncc ttagnacca cataacagg 480
 gggtaaaatt nccnataaa aaacaaanct ggccccncc ccaaaatncc caaatgggta 540
 ttctnctn ccttcccc ngnatatata caacatntcc cctttcanaa atatattccc 600
 ccacgcttat tcncccaaa nntaancctt gaagttattt aagga 645

<210> 651
 <211> 780
 <212> DNA
 <213> Homo Sapiens

<400> 651

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 cagccatat gtatgcagaa cacttaacag aattatgcta tgttgtctgt ttttgtttgt 180
 atttcttgct cttgtgaag attgaactga aatcttaaac taagttctcc ctctttatag 240
 ggggtgacag tgatctcca ttaaagcgta gctggcaca gaggctaggg aagaaagttg 300

aagctccaga	aactaacatt	gacaaaaac	caaagaaagc	tcaagtttcc	aagtctctta	360
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aaaaaaaaa	tcngcagcag	ggaactgaag	agacaaaaaa	gccnaaagga	tacaacttgc	660
atcaagctaa	agattgatag	tgaaattaaa	aaaaacagta	atcttngcca	ccattgtttg	720
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<210> 652

<211> 518

<212> DNA

<213> Homo Sapiens

<400> 652

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acaaaattat	tttttataaaa	ancaaaaaaa	taaaaaatnt	ttncaaaang	gacctgaaat	180
ctntaanctn	atnccaaaaa	caaaataatt	naaaaaatcc	nggtgaaacc	tnaactnct	240
ncnctgctt	tggaaaagg	ctntcataca	acnttcattc	ncctaaaaat	ggattggtaa	300
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tnaatttcaa	cncttnataa	ncgctttaca	acancatttc	cttaggancc	aacatnacgg	480
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<210> 653

<211> 490

<212> DNA

<213> Homo Sapiens

<400> 653

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gattctactt	caggagcaag	aagctcctcc	actatccgta	tcaaaacctt	ctctgaggtc	180
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<210> 654

<211> 359

<212> DNA

<213> Homo Sapiens

<400> 654

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tnntttttta	aaaagccaaa	naattaagaa	ttttttccaa	agggaaacng	aatccnttag	180
ggtaatccca	aaaccaaatt	agttaaaaat	ccctggntaa	accnaacnt	tcnccnccn	240
ccttgaaaaa	agggnnnccn	ncnaccttcc	atnccnntaa	aatgaatgg	ntaaagnttt	300
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<210> 655

<211> 611
 <212> DNA
 <213> Homo Sapiens

<400> 655
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 cncnaaaga ncagggatga angaagagaa gaaccttcag gaaggaaatg aatttgattc 360
 tcagancatt attataactg aagctnnana ngcttcnggt gagaccacng ganttgacat 420
 cactaaaatt ccagtcaaga gatgtgagac catgagagag aagcacatgc acaaaacanc 480
 nngagaggga aaaatcagtc ttgacacctc ttcggggaga tgtagcatct tgcggnaccc 540
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 ggcttccac a 611

<210> 656
 <211> 634
 <212> DNA
 <213> Homo Sapiens

<400> 656
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 ctgattccaa aaacnaaata anttnaaaat centggtgaa acctgaacat tctacctctg 240
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 aatttcccta tnaaaaacaa aactgggcc tacagcaaaa tatccaaatg ggtnagtcct 540
 tcttccctct tcccctgant atatacacat atctcctttc aanaatanta tttccccatg 600
 cttattccctt ccnaatcta aaccttgaag tgat 634

<210> 657
 <211> 958
 <212> DNA
 <213> Homo Sapiens

<400> 657
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 aggcagtgtg catcaagata ctgctgaaaa gaatgcatct tccccagaga aagccaaggg 180
 tagacatact gtgccttgta tgccacctgc aaagcagaag tttctaaaaa gtactgagga 240
 gcaagagctg gagaagagta tgaaaatgca gcaagagggtg gtggagatgc ggaaaaagaa 300
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 ccaggtcacc aaatcagttg acttccactt ccgcacagat gagcgaatca aacaacatcc 420
 taagaaccag gaggaatata aggaagtga ctttacatct gaactacgaa agcatccttc 480
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 agacttccat aaacgaaccc ctaacagata tcatttgagg agcaagaagg atgatattaa 660
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 gaggagctnc gagaaattgc aaccantaca anttccaaag cacgtngaac cttgattccc 840

agaataactt ganggggtggg cccaaccttg cccaagaaaa ccaccngtga aancaancca 900
acggagccct antnggcttt gatttgggaa tttgggaaan gaatncaagg gagngag 958

<210> 658
<211> 816
<212> DNA
<213> Homo Sapiens

<400> 658
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gcctgctgctg tggctgctgt gaggtcccc atgaatccac gcagtcttct tctcactggt 180
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gggtaggtaa aagtcgtgan aaatgggttc tctccatgcc caatgacaaa gcaagacggt 660
cctaggtttg aagttaaaaa caggccccaa ttgcccgggc ggtatccgcc agctcacagc 720
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ggtcctttga cttatctcca naaccgggt actggc 816

<210> 659
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 659
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cttggatgat gaaggagata ctcaaaacat agattcatgg tttgaggaga aggccaattt 180
ggagaataag ttactgggga agaatggaac tggagggtct tttcagggca aaactccttt 240
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ttccctggaa gttgaggcag ccatatcaag aaaaactcca gccagcctc agagaagatc 420
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agccaagaga tgtgccactc ctgtaatcat cgatgaaatt ctacctcta agaaaatgaa 540
agtttctaac ancacaaaga agccagagga agaaggcagt gctcatcaag atactgctga 600
aaagaatgca tcttcccaa gagaaagcca agggtagaca tactgtgcct tgtatgccac 660
ctgcanagca gaagtttcna aaangtactg angagcaang aatctggaga agagtatgaa 720
aatgc 726

<210> 660
<211> 824
<212> DNA
<213> Homo Sapiens

<400> 660
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tcagagtga naccatata aaaggccggc tgatggttta aaggaagtaa ctacatggag 180
tctaactgag acattcatga gttacatctc attattagcc ttagtaatgt aagaaaacaa 240
ttctcaacaa aactggagtc cacagttgtc aagtatgctt tctcaggcac gggtaggtaa 300

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ggaatcgagt	ggagaatttg	gggagataca	ggcncagtc	gaggctgggc	acttgacttt	480
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ctggccanct	cctctttttt	ctgctcttcc	tctgttagtc	tggcctcctc	caactgctgg	600
gctttctggg	cttctacctc	agccattctc	ttctccagct	ccctgccgct	ctttggctct	660
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ctgatttcnt	ctctttcttg	gggaaccaag	ggccccgtga	aaaanaaacg	gtgtttggaa	780
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<210> 661
 <211> 399
 <212> DNA
 <213> Homo Sapiens

<400> 661						
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caaaaacctnc	tgcttggttg	ctttaaggnc	cccataannc	ccccatnnt	cctccccccac	180
tggtncattg	gtnaggtttc	ctcccccccn	ccaaaggnt	ccttacntat	aaatcccngg	240
tttncaaaaa	aaaananaaa	accaatttcn	gatntcccc	cttnaancca	gnacttaatc	300
cctntctnag	gattnaacaa	cctttttttt	cgggttaaaa	tttttaaaaa	aattngggaa	360
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<210> 662
 <211> 826
 <212> DNA
 <213> Homo Sapiens

<400> 662						
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gccttgatg	ccacctgcaa	agcagaagtt	tctaaaaagt	actgaggagc	aagagctgga	360
gaagagtatg	aaaatgcagc	aagaggtggt	ggagatgcgg	aaaaagaatg	aagaattcaa	420
gaaacttgct	ctggctggaa	tagggcaacc	tgtgaagaaa	tcagtgaagc	aggtcaccaa	480
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taancgaacc	ctnactgatt	tcttttgang	aaccagaang	gntgattttt	ccctgtttcc	780
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<210> 663
 <211> 770
 <212> DNA
 <213> Homo Sapiens

<400> 663						
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anagaanagg	acagaatctg	atttactgat	tgttcctcat	ttaaaccatg	acttaatctc	300
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ggtgagagtc	gtaaggggca	atagcaatag	agattacact	gtgctgacac	agagactaaa	420
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<210> 664
 <211> 593
 <212> DNA
 <213> Homo Sapiens

<400> 664						
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aagatgattc	cagaacggaa	acagcttgcc	atcccaaaga	cggagtctcc	agagggtac	300
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tctctagagt	cctacgatga	anaggacggc	agcaagggca	agtcggcccc	ttaccantgg	420
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<210> 665
 <211> 1024
 <212> DNA
 <213> Homo Sapiens

<400> 665						
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<210> 666
 <211> 734
 <212> DNA

<213> Homo Sapiens

<400> 666

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caccatgccc agctaatttt tattttggta nanacaaggt ttcacatgt tgcttaggta	180
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cccagtatat tctcttgatc tgtacaagct aggattttta ttctctttgg gagaggaagc	480
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caggttctta aggggtctct tccaccaatg tgcaggga gggctgccat cactctgtt	660
taacacatag ctactttctt aaaccnataa gcttaaaaaa gangactatg gaattaccaa	720
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<210> 667

<211> 592

<212> DNA

<213> Homo Sapiens

<400> 667

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acgaattttt tttatanatc tatgataaat gcattctccc tntaggagggt agaanagtat	180
acagctgtnt ataataagct tcgctatgaa catacatttc tcaagtcaga atttgaacac	240
cagaaggaag agtatgcacg tnttttagat gaangaaacn ataaactatg aatcagagat	300
ngcaanactg gaggaagatn aagaagaact acgtanccag ctgcttaatg tngatctcac	360
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ggtggaaaat gcccanaaa tacacgtgcg gcagttggct gagatgcacg ctacagtcag	540
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<210> 668

<211> 373

<212> DNA

<213> Homo Sapiens

<400> 668

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gtttttgtnt atagtaaacc anaanatgtg tntggacct gttatggna agcatctcaa	180
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<210> 669

<211> 661

<212> DNA

<213> Homo Sapiens

<400> 669

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<210> 670

<211> 401

<212> DNA

<213> Homo Sapiens

<400> 670

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<210> 671

<211> 1347

<212> DNA

<213> Homo Sapiens

<400> 671

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<210> 672
 <211> 3441
 <212> DNA
 <213> Homo Sapiens

<400> 672

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<211> 1016

<212> DNA

<213> Homo Sapiens

<400> 673

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<210> 674

<211> 1135

<212> DNA

<213> Homo Sapiens

<400> 674

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<210> 675

<211> 1067

<212> DNA

<213> Homo Sapiens

<400> 675

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<211> 784

<212> DNA

<213> Homo Sapiens

<400> 676

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<210> 677

<211> 1362

<212> DNA

<213> Homo Sapiens

<400> 677

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<211> 1771

<212> DNA

<213> Homo Sapiens

<400> 678

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<210> 679

<211> 1367

<212> DNA

<213> Homo Sapiens

<400> 679

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<210> 680

<211> 2545

<212> DNA

<213> Homo Sapiens

<400> 680

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<213> Homo Sapiens

<400> 681

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 <213> Homo Sapiens

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<212> PRT
<213> Homo Sapiens

<400> 684

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Gln Val Ser Ala Asn Asn Gln Phe Ser Ile Thr Lys Asn Arg Asp Gly
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Arg Glu Asn Arg Arg Arg Asn Ser Lys Ile Gly Asp Asp Asn Glu Asn
65      70      75      80
Leu Thr Phe Lys Leu Glu Val Asn Glu Leu Ser Gly Lys Leu Asp Asn
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Ser Arg Ser Tyr Glu Val Met Gly Ser Met Glu Glu Thr Leu Cys Asn
115     120     125
Ile Asp Asp Arg Asp Gly Asn Arg Asn Val His Leu Glu Phe Thr Glu
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Arg Glu Ser Arg Lys Asp Gly Glu Asp Glu Phe Val Lys Glu Met Arg
145     150     155     160
Glu Glu Arg Lys Phe Gln Lys Leu Lys Asn Lys Glu Glu Val Leu Lys
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Ala Ser Arg Glu Glu Lys Val Leu Met Asp Glu Gly Ala Val Leu Thr
180     185     190
Leu Ala Ala Asp Leu Ser Ser Ala Thr Leu Asp Ile Ser Lys Gln Trp
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Ser Asn Val Phe Asn Ile Leu Arg Glu Asn Asp Phe Glu Pro Lys Phe
210     215     220
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275     280     285
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Glu Glu Ala Ser Gly Met Glu Asp Asp Glu Asp Thr Ser Gly Leu Glu
340     345     350
Glu Glu Glu Glu Glu Glu Ala Ser Gly Leu Glu Glu Asp Xaa Ser Ser
355     360     365
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Xaa Gly His Thr Leu Val Asp Ala Lys His Glu Val Glu Ile Thr Ser

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Phe Ser Tyr Leu Val Gly Asp Ser Gly Lys Lys Lys Leu Val Lys His						
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Ser Lys Ser Leu Glu Met Ser His Asp Glu His Lys Lys His Ser His						
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Glu Lys Lys His Arg Thr Leu His Thr Glu Glu Leu Thr Ser Lys Glu						
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Ala Asp Leu Thr Glu Glu Thr Glu Glu Asn Leu Arg Ser Ser Val Ile						
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Asn Ser Ile Arg Glu Ile Lys Glu Glu Ile Gly Asn Leu Lys Ser Ser						
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His Ser Gly Val Leu Glu Ile Glu Asn Ser Val Asp Asp Leu Ser Ser						
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Arg Met Asp Ile Leu Glu Glu Arg Ile Asp Ser Leu Glu Asp Gln Ile						
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	610		615			620
Lys Glu Gly Pro Arg Asp Ile Glu Glu Arg Ser Arg Ser Cys Asn Ile						
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Arg Leu Ile Gly Ile Pro Glu Lys Glu Ser Tyr Glu Asn Arg Ala Glu						
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Asp Ile Ile Lys Glu Ile Ile Asp Glu Asn Phe Ala Glu Leu Lys Lys						
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Gly Ser Ser Leu Glu Ile Val Ser Ala Cys Arg Val Pro Ser Lys Ile						
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Asp Glu Lys Arg Leu Thr Pro Arg His Ile Leu Val Lys Phe Trp Asn						
	690		695			700
Ser Ser Asp Lys Glu Lys Ile Ile Arg Pro Ser Arg Glu Arg Arg Glu						
	705		710			715
Ile Thr Tyr Gln Gly Thr Arg Ile Arg Leu Thr Ala Asp Leu Ser Leu						
	725		730			735
Asp Thr Leu Asp Ala Arg Ser Lys Trp Ser Asn Val Phe Lys Val Leu						
	740		745			750
Leu Glu Lys Gly Phe Asn Pro Arg Thr Leu Tyr Pro Ala Lys Met Ala						
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Phe Asp Phe Arg Gly Lys Thr Lys Val Phe Leu Ser Ile Glu Glu Phe						
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<211> 947
 <212> PRT
 <213> Homo Sapiens

<400> 685

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 35 40 45
 Ser Trp Pro Phe Gln Arg Pro Val Asp Ala Val Lys Leu Lys Leu Pro
 50 55 60
 Asp Tyr Tyr Thr Ile Ile Lys Asn Pro Met Asp Leu Asn Thr Ile Lys
 65 70 75 80
 Lys Arg Leu Glu Asn Lys Tyr Tyr Ala Lys Ala Ser Glu Cys Ile Glu
 85 90 95
 Asp Phe Asn Thr Met Phe Ser Asn Cys Tyr Leu Tyr Asn Lys Pro Gly
 100 105 110
 Asp Asp Ile Val Leu Met Ala Gln Ala Leu Glu Lys Leu Phe Met Gln
 115 120 125
 Lys Leu Ser Gln Met Pro Gln Glu Glu Gln Val Val Gly Val Lys Glu
 130 135 140
 Arg Ile Lys Lys Gly Thr Gln Gln Asn Ile Ala Val Ser Ser Ala Lys
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 Ile Pro Ser Val Phe Pro Lys Thr Ser Ile Ser Pro Leu Asn Val Val
 180 185 190
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 Val Lys Ala Ser Ser Glu Phe Ser Pro Thr Phe Thr Glu Lys Ser Val
 225 230 235 240
 Ala Leu Pro Pro Ile Lys Glu Asn Met Pro Lys Asn Val Leu Pro Asp
 245 250 255
 Ser Gln Gln Gln Tyr Asn Val Val Glu Thr Val Lys Val Thr Glu Gln
 260 265 270
 Leu Arg His Cys Ser Glu Ile Leu Lys Glu Met Leu Ala Lys Lys His
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 290 295 300
 Gly Leu His Asn Tyr Tyr Asp Val Val Lys Asn Pro Met Asp Leu Gly
 305 310 315 320
 Thr Ile Lys Glu Lys Met Asp Asn Gln Glu Tyr Lys Asp Ala Tyr Ser
 325 330 335
 Phe Ala Ala Asp Val Arg Leu Met Phe Met Asn Cys Tyr Lys Tyr Asn
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 355 360 365
 Phe Glu Thr His Phe Ser Lys Ile Pro Ile Glu Pro Val Glu Ser Met
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 385 390 395 400

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Val His Gln Gln Leu Gln Val Leu Ser Gln Val Pro Phe Arg Lys Leu	435	440	445
Asn Lys Lys Lys Glu Lys Ser Lys Lys Glu Lys Lys Lys Glu Lys Val	450	455	460
Asn Asn Ser Asn Glu Asn Pro Arg Lys Met Cys Glu Gln Met Arg Leu	465	470	475
Lys Glu Lys Ser Lys Arg Asn Gln Pro Lys Lys Arg Lys Gln Gln Phe	485	490	495
Ile Gly Leu Lys Ser Glu Asp Glu Asp Asn Ala Lys Pro Met Asn Tyr	500	505	510
Asp Glu Lys Arg Gln Leu Ser Leu Asn Ile Asn Lys Leu Pro Gly Asp	515	520	525
Lys Leu Gly Arg Val Val His Ile Ile Gln Ser Arg Glu Pro Ser Leu	530	535	540
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Ala Ser Thr Leu Arg Glu Leu Glu Lys Tyr Val Ser Ala Cys Leu Arg	565	570	575
Lys Arg Pro Leu Lys Pro Pro Ala Lys Lys Ile Met Met Ser Lys Glu	580	585	590
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Ser Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Ser Ser Asp	645	650	655
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Phe Thr Glu Val Lys Pro Asn Asp Ser Pro Ser Lys Glu His Val Lys	675	680	685
Lys Met Lys Asn Glu Cys Ile Leu Pro Glu Gly Arg Thr Gly Val Thr	690	695	700
Gln Ile Gly Tyr Cys Val Gln Asp Thr Thr Ser Ala Asn Thr Thr Leu	705	710	715
Val His Gln Thr Thr Pro Ser His Val Met Pro Pro Asn His His Gln	725	730	735
Leu Ala Phe Asn Tyr Gln Glu Leu Glu His Leu Gln Thr Val Lys Asn	740	745	750
Ile Ser Pro Leu Gln Ile Leu Pro Pro Ser Gly Asp Ser Glu Gln Leu	755	760	765
Ser Asn Gly Ile Thr Val Met His Pro Ser Gly Asp Ser Asp Thr Thr	770	775	780
Met Leu Glu Ser Glu Cys Gln Ala Pro Val Gln Lys Asp Ile Lys Ile	785	790	795
Lys Asn Ala Asp Ser Trp Lys Ser Leu Gly Lys Pro Val Lys Pro Ser	805	810	815
Gly Val Met Lys Ser Ser Asp Glu Leu Phe Asn Gln Phe Arg Lys Ala	820	825	830
Ala Ile Glu Lys Glu Val Lys Ala Arg Thr Gln Glu Leu Ile Arg Lys			

835	840	845
His Leu Glu Gln Asn Thr Lys Glu Leu Lys Ala Ser Gln Glu Asn Gln		
850	855	860
Arg Asp Leu Gly Asn Gly Leu Thr Val Glu Ser Phe Ser Asn Lys Ile		
865	870	875
Gln Asn Lys Cys Ser Gly Glu Glu Gln Lys Glu His Pro Gln Ser Ser		
885	890	895
Glu Ala Gln Asp Lys Ser Lys Leu Trp Leu Leu Lys Asp Arg Asp Leu		
900	905	910
Ala Arg Pro Lys Glu Gln Glu Arg Arg Arg Arg Glu Ala Met Val Gly		
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Thr Ile Asp Met Thr Leu Gln Ser Asp Ile Met Thr Met Phe Glu Asn		
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Asn Phe Asp		

945

<210> 686
 <211> 3106
 <212> DNA
 <213> Homo Sapiens

<400> 686

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<210> 687

<211> 1759

<212> DNA

<213> Homo Sapiens

<400> 687

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<210> 688
 <211> 207
 <212> PRT
 <213> Homo Sapiens

<400> 688

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 35          40          45
Thr Glu Ala Leu Ser Val Ser Gln Glu Arg Val Gly Met Ser Leu Val
 50          55          60
Ala Leu Lys Lys Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys Asn
 65          70          75          80
Asn Ser Arg Ile Lys Leu Ser Leu Lys Ser Leu Val Asn Lys Gly Ile
 85          90          95
Leu Val Gln Thr Arg Gly Thr Gly Ala Ser Gly Ser Phe Lys Leu Ser
100          105          110
Lys Lys Val Ile Pro Lys Ser Thr Arg Ser Lys Ala Lys Lys Ser Val
115          120          125
Ser Ala Lys Thr Lys Lys Leu Val Leu Ser Arg Asp Ser Lys Ser Pro
130          135          140
Lys Thr Ala Lys Thr Asn Lys Arg Ala Lys Lys Pro Arg Ala Thr Thr
145          150          155          160
Pro Lys Thr Val Arg Ser Gly Arg Lys Ala Lys Gly Ala Lys Gly Lys
165          170          175
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<210> 689
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 <212> DNA
 <213> Homo Sapiens

<400> 689

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<210> 690

<211> 363

<212> PRT

<213> Homo Sapiens

<400> 690

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35 40 45
Glu Asn Thr Glu Glu Asn Arg Arg Phe Tyr Arg Gln Leu Leu Leu Thr
50 55 60
Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe His
65 70 75 80
Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln Val
85 90 95
Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly Val
100 105 110
Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp
115 120 125
Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe
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Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala
145 150 155 160
Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile
165 170 175
Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro
180 185 190
Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys Val
195 200 205
Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu Glu
210 215 220
Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys Thr
225 230 235 240
Gln Lys Phe Ser His Glu Glu Ile Ala Met Ala Thr Val Thr Ala Leu
245 250 255
Arg Arg Thr Val Pro Pro Ala Val Thr Gly Ile Thr Phe Leu Ser Gly
260 265 270
Gly Gln Ser Glu Glu Glu Ala Ser Ile Asn Leu Asn Ala Ile Asn Lys
275 280 285
Cys Pro Leu Leu Lys Pro Trp Ala Leu Thr Phe Ser Tyr Gly Arg Ala

290 295 300
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 305 310 315 320
 Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser Leu
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<210> 691
 <211> 1216
 <212> DNA
 <213> Homo Sapiens

<400> 691

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<210> 692
 <211> 1958
 <212> DNA
 <213> Homo Sapiens

<400> 692

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<210> 693
 <211> 505
 <212> PRT
 <213> Homo Sapiens

<400> 693

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Phe	Asn	Gln	Asp	Tyr	Leu	Ser	Gly	Met	Ala	Ala	Asn	Met	Ser	Gly	Thr
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Gln	Gln	Pro	Val	Pro	Pro	Tyr	Gly	Met	Tyr	Pro	Pro	Pro	Gly	Gly	Asn
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		115					120					125			
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Pro	Gly	Gln	Gln	Gln	Pro	Val	Pro	Ser	Tyr	Pro	Gly	Tyr	Pro	Gly	Ser
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Leu Arg Lys Ala Met Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Ile
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 Pro Val Leu Phe Asp Ile Tyr Glu Ile Lys Glu Ala Ile Lys Gly Val
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 Thr Leu Glu Glu Ala Ile Arg Ser Asp Thr Ser Gly His Phe Gln Arg
 325 330 335
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 Asp Met Ser Leu Ala Gln Arg Asp Ala Gln Glu Leu Tyr Ala Ala Gly
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 Met Thr Gly Arg Asp Ile Glu Lys Ser Ile Cys Arg Glu Met Ser Gly
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 Asp Leu Glu Glu Gly Met Leu Ala Val Lys Cys Leu Lys Asn Thr
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 Pro Ala Phe Phe Ala Glu Arg Leu Asn Lys Ala Met Arg Gly Ala Gly
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 Thr Lys Asp Arg Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Thr
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 Asp Leu Leu Asp Ile Arg Ser Glu Tyr Lys Arg Met Tyr Gly Lys Ser
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<210> 694
 <211> 1141
 <212> DNA
 <213> Homo Sapiens

<400> 694

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gagagcagtt tcgcaacttt gttcccaaaa tacagggaag cttacttgaa agagtgttg	240
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<210> 695

<211> 288

<212> PRT

<213> Homo Sapiens

<400> 695

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35 40 45
Asp Asn Pro Arg Gly Leu Leu Glu Glu Ser Ser Phe Ala Thr Leu Phe
50 55 60
Pro Lys Tyr Arg Glu Ala Tyr Leu Lys Glu Cys Trp Pro Leu Val Gln
65 70 75 80
Lys Ala Leu Asn Glu His His Val Asn Ala Thr Leu Asp Leu Ile Glu
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Gly Ser Met Thr Val Cys Thr Thr Lys Lys Thr Phe Asp Pro Tyr Ile
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Ile Ile Arg Ala Arg Asp Leu Ile Lys Leu Leu Ala Arg Ser Val Ser
115 120 125
Phe Glu Gln Ala Val Arg Ile Leu Gln Asp Asp Val Ala Cys Asp Ile
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<210> 696

<211> 1008
<212> DNA
<213> Homo Sapiens

<400> 696

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<210> 697
<211> 685
<212> DNA
<213> Homo Sapiens

<400> 697

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<212> DNA
<213> Homo Sapiens

<400> 698

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<210> 699

<211> 1427

<212> DNA

<213> Homo Sapiens

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<210> 700

<211> 1967

<212> DNA

<213> Homo Sapiens

<400> 700

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<211> 3423

<212> DNA

<213> Homo Sapiens

<400> 701

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 <211> 1106
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 <213> Homo Sapiens

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<211> 1095

<212> DNA

<213> Homo Sapiens

<400> 703

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<210> 704

<211> 1968

<212> DNA

<213> Homo Sapiens

<400> 704

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<211> 800

<212> DNA

<213> Homo Sapiens

<400> 705

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<210> 706

<211> 487

<212> DNA

<213> Homo Sapiens

<400> 706

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<210> 707

<211> 3599

<212> DNA

<213> Homo Sapiens

<400> 707

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 <211> 1123
 <212> PRT
 <213> Homo Sapiens

<400> 708

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 275 280 285
 Asp Pro Asn Ile Leu Asp Tyr Ile Gln Pro Ser Thr Gln Asp Arg Glu
 290 295 300
 His Ser Gly Met Asn Val Asn Arg Arg Glu Glu Ser Thr His Asp His
 305 310 315 320
 Thr Ile Glu Arg Pro Ala Phe Gly Ile Gln Lys Gly Glu Phe Glu His
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Lys Ser Gln Leu Ser Gly Arg Glu Glu Gln Ser Ser Asp Ala Gly Leu
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 385 390 395 400
 Tyr Arg Ser Met Glu Tyr Arg Asp Val Asp His Arg Leu Pro Gly Ser
 405 410 415
 Gln Met Phe Gly Tyr Gly Gln Ser Lys Ser Phe Pro Glu Gly Lys Thr
 420 425 430
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 Glu Arg Glu Ser Trp Ser Gly Glu Thr Arg Gln Asp Gly Glu Ser Lys
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 Thr Ile Met Leu Lys Arg Ile Tyr Arg Ser Thr Pro Pro Glu Val Ile
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 Val Glu Val Leu Glu Pro Tyr Val Arg Leu Thr Thr Ala Asn Val Arg
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 Ile Ile Lys Asn Arg Thr Gly Pro Met Gly His Thr Tyr Gly Phe Ile

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Leu Ala Thr Gly Lys Arg	Arg Asn Asp Ser Gly Asp	His Ser Asp His
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Arg Arg Gln Phe Pro Asn	Lys Glu Val Leu Ile Lys	His Gln Gln Leu
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Ser Asp Leu His Lys Gln	Asn Leu Glu Ile His Arg	Lys Ile Lys Gln
980	985	990
Ser Glu Gln Glu Leu Ala	Tyr Leu Glu Arg Arg Glu	Arg Glu Gly Lys
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 <212> DNA
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<400> 709

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 <213> Homo Sapiens

<400> 710

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Tyr	Gly	Ala	Arg	Asp	Gly	Pro	His	Gly	Asp	Tyr	Arg	Gly	Gly	Glu	Gly
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Pro	Gly	His	Asp	Phe	Arg	Gly	Gly	Asp	Phe	Ser	Ser	Ser	Asp	Phe	Gln
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Arg Glu Met Pro Pro Val Asp Pro Asn Ile Leu Asp Tyr Ile Gln Pro		
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Ser Thr Gln Asp Arg Glu His Ser Gly Met Asn Val Asn Arg Arg Glu		
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Glu Ser Thr His Asp His Thr Ile Glu Arg Pro Ala Phe Gly Ile Gln		
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Lys Gly Glu Phe Glu His Ser Glu Thr Arg Glu Gly Glu Thr Gln Gly		
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Val Ala Phe Glu His Glu Ser Pro Ala Asp Phe Gln Asn Ser Gln Ser		400
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Pro Val Gln Asp Gln Asp Lys Ser Gln Leu Ser Gly Arg Glu Glu Gln		
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Ser Ser Asp Ala Gly Leu Phe Lys Glu Glu Gly Gly Leu Asp Phe Leu		
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His Arg Leu Pro Gly Ser Gln Met Phe Gly Tyr Gly Gln Ser Lys Ser		
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Phe Pro Glu Gly Lys Thr Ala Arg Asp Ala Gln Arg Asp Leu Gln Asp		
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Gln Asp Tyr Arg Thr Gly Pro Ser Glu Glu Lys Pro Ser Arg Leu Ile		
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Ala Phe Arg Thr Pro Asp Gly Met Pro Val Lys Asn Leu Gln Leu Lys		
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Glu Tyr Asn Thr Gly Tyr Asp Tyr Gly Tyr Val Cys Val Glu Phe Ser		
545	550	555
Leu Leu Glu Asp Ala Ile Gly Cys Met Glu Ala Asn Gln Gly Thr Leu		
565	570	575
Met Ile Gln Asp Lys Glu Val Thr Leu Glu Tyr Val Ser Ser Leu Asp		
580	585	590
Phe Trp Tyr Cys Lys Arg Cys Lys Ala Asn Ile Gly Gly His Arg Ser		
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Ser Cys Ser Phe Cys Lys Asn Pro Arg Glu Val Thr Glu Ala Lys Gln		
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Glu Leu Ile Thr Tyr Pro Gln Pro Gln Lys Thr Ser Ile Pro Ala Pro		
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Leu Glu Lys Gln Pro Asn Gln Pro Leu Arg Pro Ala Asp Lys Glu Pro		
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Glu Pro Arg Lys Arg Glu Glu Gly Gln Glu Ser Arg Leu Gly His Gln		
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Lys Arg Glu Ala Glu Arg Tyr Leu Pro Pro Ser Arg Arg Glu Gly Pro		
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Thr Phe Arg Arg Asp Arg Glu Arg Glu Ser Trp Ser Gly Glu Thr Arg		
690	695	700

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<400> 711

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<213> Homo Sapiens

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<213> Homo Sapiens

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<211> 609

<212> PRT

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<400> 804

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210	215	220
Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val		
225	230	235
Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser		
245	250	255
Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly		
260	265	270
Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile		
275	280	285
Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu		
290	295	300
Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp		
305	310	315
Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser		
325	330	335
Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly		
340	345	350
Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val		
355	360	365
Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys		
370	375	380
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu		
385	390	395
Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys		
405	410	415
Glu Leu Phe Lys Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu		
420	425	430
Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val		
435	440	445
Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His		
450	455	460
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val		
465	470	475
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg		
485	490	495
Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe		
500	505	510
Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala		
515	520	525
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu		
530	535	540
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys		
545	550	555
Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala		
565	570	575
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595	600	605
Leu		

<211> 1356
 <212> DNA
 <213> Homo Sapiens

<400> 805

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ctctttgtag	acattcctgc	aaaaaagggt	tgccgggtggg	attcattcac	caagcaagta	240
cagecgagtga	ccatggatgc	cccagtcagc	tccgtggctc	ttcgccagtc	gggaggctat	300
gttgccacca	ttggaacaaa	gttctgtgct	ttgaactgga	aagaacaatc	agcagttgtc	360
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<210> 806
 <211> 299
 <212> PRT
 <213> Homo Sapiens

<400> 806

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			20					25					30		
Asp	Ile	Pro	Ala	Lys	Lys	Val	Cys	Arg	Trp	Asp	Ser	Phe	Thr	Lys	Gln
			35				40					45			
Val	Gln	Arg	Val	Thr	Met	Asp	Ala	Pro	Val	Ser	Ser	Val	Ala	Leu	Arg
			50			55				60					
Gln	Ser	Gly	Gly	Tyr	Val	Ala	Thr	Ile	Gly	Thr	Lys	Phe	Cys	Ala	Leu
65				70					75				80		
Asn	Trp	Lys	Glu	Gln	Ser	Ala	Val	Val	Leu	Ala	Thr	Val	Asp	Asn	Asp
			85					90					95		
Lys	Lys	Asn	Asn	Arg	Phe	Asn	Asp	Gly	Lys	Val	Asp	Pro	Ala	Gly	Arg
			100					105					110		
Tyr	Phe	Ala	Gly	Thr	Met	Ala	Glu	Glu	Thr	Ala	Pro	Ala	Val	Leu	Glu
			115				120					125			
Arg	His	Gln	Gly	Ala	Leu	Tyr	Ser	Leu	Phe	Pro	Asp	His	His	Val	Lys
			130			135				140					
Lys	Tyr	Phe	Asp	Gln	Val	Asp	Ile	Ser	Asn	Gly	Leu	Asp	Trp	Ser	Leu
145				150						155				160	

Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Ser Val Asp
 165 170 175
 Ala Phe Asp Tyr Asp Leu Gln Thr Gly Gln Ile Ser Asn Arg Arg Ser
 180 185 190
 Val Tyr Lys Leu Glu Lys Glu Glu Gln Ile Pro Asp Gly Met Cys Ile
 195 200 205
 Asp Ala Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
 210 215 220
 Ile Arg Leu Asp Pro Val Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
 225 230 235 240
 Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asn Tyr Ser
 245 250 255
 Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Asp Pro Glu Gly Leu
 260 265 270
 Leu Arg Gln Pro Glu Ala Gly Gly Ile Phe Lys Ile Thr Gly Leu Gly
 275 280 285
 Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
 290 295

<210> 807

<211> 1980

<212> DNA

<213> Homo Sapiens

<400> 807

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 aaaattggag agacagaaaag agagtatgaa aaatcactta ctgaaatcag acagttaagg 1920
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<210> 808
 <211> 659
 <212> PRT
 <213> Homo Sapiens

<400> 808
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 Met Asn Cys Trp Phe Ser Cys Ala Pro Lys Asn Arg His Ala Ala Asp
 20 25 30

Trp Asn Lys Tyr Asp Asp Arg Leu Met Lys Ala Ala Glu Arg Gly Asp
 35 40 45
 Val Glu Lys Val Ser Ser Ile Leu Ala Lys Lys Gly Ile Asn Pro Gly
 50 55 60
 Lys Leu Asp Val Glu Gly Arg Ser Ala Phe His Val Val Ala Ser Lys
 65 70 75 80
 Gly Asn Leu Glu Cys Leu Asn Ala Ile Leu Ile His Gly Val Asp Ile
 85 90 95

Thr Thr Ser Asp Thr Ala Gly Arg Asn Ala Leu His Leu Ala Ala Lys
 100 105 110
 Tyr Gly His Ala Leu Cys Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro
 115 120 125
 Thr Glu His Ala Asp Leu Gln Gly Arg Thr Ala Leu His Asp Ala Ala
 130 135 140
 Met Ala Asp Cys Pro Ser Ser Ile Gln Leu Leu Cys Asp His Gly Ala
 145 150 155 160
 Ser Val Asn Ala Lys Asp Val Asp Gly Arg Thr Pro Leu Val Leu Ala
 165 170 175
 Thr Gln Met Cys Arg Pro Ala Ile Cys Gln Leu Leu Ile Asp Arg Gly
 180 185 190
 Ala Glu Ile Asn Ser Arg Asp Lys Gln Asn Arg Thr Ala Leu Met Leu
 195 200 205
 Gly Cys Glu Tyr Gly Cys Lys Asp Ala Val Glu Val Leu Leu Lys Asn
 210 215 220
 Gly Ala Asp Val Ser Leu Leu Asp Ala Leu Gly His Asp Ser Ser Tyr
 225 230 235 240
 Tyr Ala Arg Ile Gly Asp Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr
 245 250 255
 Ala Ser Glu Asn Thr Asn Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro
 260 265 270
 Ser Leu Gln Gln Arg Asn Leu Pro Tyr Met Leu Asp Glu Val Asn Val
 275 280 285
 Lys Ser Ser Gln Arg Glu His Arg Asn Ile Gln Glu Leu Glu Ile Glu
 290 295 300
 Asn Glu Asp Leu Lys Asp Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg
 305 310 315 320
 Ile Leu Leu Asp Lys Val Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu
 325 330 335
 Val Met Val Ala Asp Asp Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser
 340 345 350
 Leu Leu Val Ala Lys Glu Lys Gln His Glu Glu Ser Leu Arg Thr Ile

355		360		365
Glu Ser Leu Lys Asn Arg Phe Lys Tyr Phe Glu Cys Thr Ser Pro Gly				
370		375		380
Val Pro Ala His Met Gln Ser Arg Ser Met Leu Arg Pro Leu Glu Leu				
385		390		400
Ser Leu Pro Asn Gln Thr Ser Tyr Ser Glu Asn Asp Leu Leu Lys Lys				
	405		410	415
Glu Leu Glu Ala Met Arg Thr Phe Cys Glu Ser Ala Lys Gln Asp Arg				
	420		425	430
Leu Lys Leu Gln Asn Gly Val Ala His Lys Val Ala Glu Cys Lys Ala				
	435		440	445
Leu Gly Leu Glu Cys Glu Arg Ile Lys Glu Asp Ser Asp Glu Gln Ile				
	450		455	460
Lys Gln Leu Glu Asp Ala Leu Lys Asp Val Gln Lys Arg Met Tyr Glu				
465		470		475
Ser Glu Gly Lys Val Lys Gln Met Gln Thr His Phe Leu Ala Leu Lys				
	485		490	495
Glu His Leu Thr Ser Glu Ala Ala Ile Gly Asn His Arg Leu Met Glu				
	500		505	510
Glu Leu Lys Asp Gln Leu Lys Asp Met Lys Ala Lys Tyr Glu Gly Ala				
	515		520	525
Ser Ala Glu Val Gly Lys Leu Arg Asn Gln Ile Lys Gln Asn Glu Leu				
530		535		540
Leu Val Glu Gln Phe Arg Arg Asp Glu Gly Lys Leu Val Glu Glu Asn				
545		550		555
Lys Arg Leu Gln Lys Glu Leu Ser Met Cys Glu Thr Glu Arg Asp Lys				
	565		570	575
Lys Gly Arg Arg Val Ala Glu Val Glu Gly Gln Val Lys Glu Leu Leu				
580		585		590
Ala Lys Leu Thr Leu Ser Val Pro Thr Glu Lys Phe Glu Ser Met Lys				
595		600		605
Ser Leu Leu Ser Ser Glu Val Asn Glu Lys Val Lys Lys Ile Gly Glu				
610		615		620
Thr Glu Arg Glu Tyr Glu Lys Ser Leu Thr Glu Ile Arg Gln Leu Arg				
625		630		635
Arg Glu Leu Glu Asn Cys Lys Arg Gln Thr Ser Ser Ala Cys Gln Ala				
	645		650	655
Arg Gly Ala				

<210> 809
 <211> 1725
 <212> DNA
 <213> Homo Sapiens

<400> 809	
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<210> 810

<211> 355

<212> PRT

<213> Homo Sapiens

<400> 810

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			20					25					30		
Val	Asn	Gly	Thr	Val	Leu	Ser	Ser	Ser	Gly	Thr	Arg	Phe	Ala	Val	Asn
		35						40					45		
Phe	Gln	Thr	Gly	Phe	Ser	Gly	Asn	Asp	Ile	Ala	Phe	His	Phe	Asn	Pro
		50				55					60				
Arg	Phe	Glu	Asp	Gly	Gly	Tyr	Val	Val	Cys	Asn	Thr	Arg	Gln	Asn	Gly
65				70					75					80	
Ser	Trp	Gly	Pro	Glu	Glu	Arg	Lys	Thr	His	Met	Pro	Phe	Gln	Lys	Gly
			85					90						95	
Met	Pro	Phe	Asp	Leu	Cys	Phe	Leu	Val	Gln	Ser	Ser	Asp	Phe	Lys	Val
		100						105					110		
Met	Val	Asn	Gly	Ile	Leu	Phe	Val	Gln	Tyr	Phe	His	Arg	Val	Pro	Phe
		115					120					125			
His	Arg	Val	Asp	Thr	Ile	Ser	Val	Asn	Gly	Ser	Val	Gln	Leu	Ser	Tyr
	130					135						140			
Ile	Ser	Phe	Gln	Asn	Pro	Arg	Thr	Val	Pro	Val	Gln	Pro	Ala	Phe	Ser
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Thr	Val	Pro	Phe	Ser	Gln	Pro	Val	Cys	Phe	Pro	Pro	Arg	Pro	Arg	Gly
			165					170						175	
Arg	Arg	Gln	Lys	Pro	Pro	Gly	Val	Trp	Pro	Ala	Asn	Pro	Ala	Pro	Ile
		180						185					190		
Thr	Gln	Thr	Val	Ile	His	Thr	Val	Gln	Ser	Ala	Pro	Gly	Gln	Met	Phe
	195						200					205			
Ser	Thr	Pro	Ala	Ile	Pro	Pro	Met	Met	Tyr	Pro	His	Pro	Ala	Tyr	Pro
210						215						220			

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
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 Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
 245 250 255
 Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
 260 265 270
 Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
 275 280 285
 Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
 290 295 300
 Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
 305 310 315 320
 Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
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Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
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 Val Gln Thr
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<210> 811
 <211> 1022
 <212> DNA
 <213> Homo Sapiens

<400> 811
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 ca 1022

<210> 812
 <211> 317
 <212> PRT
 <213> Homo Sapiens

<400> 812
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 20 25 30
 Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Leu

35	40	45
Gly Thr Leu Glu Lys Val Pro Ala Ala Glu Ser Ala Asp Pro Pro Gln		
50	55	60
Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys		
65	70	75
Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Ala		
85	90	95
Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn		
100	105	110
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Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys		
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Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr		
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Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly		
180	185	190
Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly		
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Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu		
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Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr		
225	230	235
Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr		
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Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe		
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Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu		
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Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser		
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<210> 813
 <211> 5175
 <212> DNA
 <213> Homo Sapiens

<400> 813

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<210> 814
 <211> 1392
 <212> PRT
 <213> Homo Sapiens

<400> 814

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Val	Glu	Lys	Thr	Ile	Ser	Ser	Glu	Lys	Ala	Ser	Ser	Thr	Pro	Ser	Ser
			35				40					45			
Glu	Thr	Gln	Glu	Glu	Phe	Val	Asp	Asp	Phe	Arg	Val	Gly	Glu	Arg	Val
			50			55				60					
Trp	Val	Asn	Gly	Asn	Lys	Pro	Gly	Phe	Ile	Gln	Phe	Leu	Gly	Glu	Thr
			65		70				75					80	
Gln	Phe	Ala	Pro	Gly	Gln	Trp	Ala	Gly	Ile	Val	Leu	Asp	Glu	Pro	Ile
			85					90					95		
Gly	Lys	Asn	Asp	Gly	Ser	Val	Ala	Gly	Val	Arg	Tyr	Phe	Gln	Cys	Glu
			100					105					110		
Pro	Leu	Lys	Gly	Ile	Phe	Thr	Arg	Pro	Ser	Lys	Leu	Thr	Arg	Lys	Val
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Gln	Ala	Glu	Asp	Glu	Ala	Asn	Gly	Leu	Gln	Thr	Thr	Pro	Ala	Ser	Arg
			130			135				140					
Ala	Thr	Ser	Pro	Leu	Cys	Thr	Ser	Thr	Ala	Ser	Met	Val	Ser	Ser	Ser
			145		150				155					160	
Pro	Ser	Thr	Pro	Ser	Asn	Ile	Pro	Gln	Lys	Pro	Ser	Gln	Pro	Ala	Ala
			165					170					175		
Lys	Glu	Pro	Ser	Ala	Thr	Pro	Pro	Ile	Ser	Asn	Leu	Thr	Lys	Thr	Ala
			180					185					190		
Ser	Glu	Ser	Ile	Ser	Asn	Leu	Ser	Glu	Ala	Gly	Ser	Ile	Lys	Lys	Gly
			195			200						205			
Glu	Arg	Glu	Leu	Lys	Ile	Gly	Asp	Arg	Val	Leu	Val	Gly	Gly	Thr	Lys

210	215	220
Ala Gly Val Val Arg Phe	Leu Gly Glu Thr Asp	Phe Ala Lys Gly Glu
225	230	235
Trp Cys Gly Val Glu Leu	Asp Glu Pro Leu Gly	Lys Asn Asp Gly Ala
245	250	255
Val Ala Gly Thr Arg Tyr	Phe Gln Cys Gln Pro	Lys Tyr Gly Leu Phe
260	265	270
Ala Pro Val His Lys Val	Thr Lys Ile Gly Phe	Pro Ser Thr Thr Pro
275	280	285
Ala Lys Ala Lys Ala Asn	Ala Val Arg Arg Val	Met Ala Thr Thr Ser
290	295	300
Ala Ser Leu Lys Arg Ser	Pro Ser Ala Ser Ser	Leu Ser Ser Met Ser
305	310	315
Ser Val Ala Ser Ser Val	Ser Ser Arg Pro Ser	Arg Thr Gly Leu Leu
325	330	335
Thr Glu Thr Ser Ser Arg	Tyr Ala Arg Lys Ile	Ser Gly Thr Thr Ala
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Leu Gln Glu Ala Leu Lys	Glu Lys Gln Gln His	Ile Glu Gln Leu Leu
355	360	365
Ala Glu Arg Asp Leu Glu	Arg Ala Glu Val Ala	Lys Ala Thr Ser His
370	375	380
Val Gly Glu Ile Glu Gln	Glu Leu Ala Leu Ala	Arg Asp Gly His Asp
385	390	395
Gln His Val Leu Glu Leu	Glu Ala Lys Met Asp	Gln Leu Arg Thr Met
405	410	415
Val Glu Ala Ala Asp Arg	Glu Lys Val Glu Leu	Leu Asn Gln Leu Glu
420	425	430
Glu Glu Lys Arg Lys Val	Glu Asp Leu Gln Phe	Arg Val Glu Glu Glu
435	440	445
Ser Ile Thr Lys Gly Asp	Leu Glu Val Ala Thr	Val Ser Glu Lys Ser
450	455	460
Arg Ile Met Glu Leu Glu	Lys Asp Leu Ala Leu	Arg Val Gln Glu Val
465	470	475
Ala Glu Leu Arg Arg Arg	Leu Glu Ser Asn Lys	Pro Ala Gly Asp Val
485	490	495
Asp Met Ser Leu Ser Leu	Leu Gln Glu Ile Ser	Ser Ser Leu Gln Glu Lys
500	505	510
Leu Glu Val Thr Arg Thr	Asp His Gln Arg Glu	Ile Thr Ser Leu Lys
515	520	525
Glu His Phe Gly Ala Arg	Glu Glu Thr His Gln	Lys Glu Ile Lys Ala
530	535	540
Leu Tyr Thr Ala Thr Glu	Lys Leu Ser Lys Glu	Asn Glu Ser Leu Lys
545	550	555
Ser Lys Leu Glu His Ala	Asn Lys Glu Asn Ser	Asp Val Ile Ala Leu
565	570	575
Trp Lys Ser Lys Leu Glu	Thr Ala Ile Ala Ser	His Gln Gln Ala Met
580	585	590
Glu Glu Leu Lys Val Ser	Phe Ser Lys Gly Leu	Gly Thr Glu Thr Ala
595	600	605
Glu Phe Ala Glu Leu Lys	Thr Gln Ile Glu Lys	Met Arg Leu Asp Tyr
610	615	620
Gln His Glu Ile Glu Asn	Leu Gln Asn Gln Gln	Asp Ser Glu Arg Ala
625	630	635
Ala His Ala Lys Glu Met	Glu Ala Leu Arg Ala	Lys Leu Met Lys Val
645	650	655

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Lys	Ala	Glu	Asp	Gln	His	Leu	Val	Glu	Met	Glu	Asp	Thr	Leu	Asn	Lys	
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	690					695						700				
Lys	Cys	Asn	Glu	Gln	Thr	Lys	Val	Ile	Asp	Asn	Phe	Thr	Ser	Gln	Leu	
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Lys	Ala	Thr	Glu	Glu	Lys	Leu	Leu	Asp	Leu	Asp	Ala	Leu	Arg	Lys	Ala	
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Ser	Ser	Glu	Gly	Lys	Ser	Glu	Met	Lys	Lys	Leu	Arg	Gln	Gln	Leu	Glu	
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Ala	Ala	Glu	Lys	Gln	Ile	Lys	His	Leu	Glu	Ile	Glu	Lys	Asn	Ala	Glu	
		755					760					765				
Ser	Ser	Lys	Ala	Ser	Ser	Ile	Thr	Arg	Glu	Leu	Gln	Gly	Arg	Glu	Leu	
	770					775					780					
Lys	Leu	Thr	Asn	Leu	Gln	Glu	Asn	Leu	Ser	Glu	Val	Ser	Gln	Val	Lys	
785				790						795					800	
Glu	Thr	Leu	Glu	Lys	Glu	Leu	Gln	Ile	Leu	Lys	Glu	Lys	Phe	Ala	Glu	
			805						810					815		
Ala	Ser	Glu	Glu	Ala	Val	Ser	Val	Gln	Arg	Ser	Met	Gln	Glu	Thr	Val	
			820					825					830			
Asn	Lys	Leu	His	Gln	Lys	Glu	Glu	Gln	Phe	Asn	Met	Leu	Ser	Ser	Asp	
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Leu	Glu	Lys	Leu	Arg	Glu	Asn	Leu	Ala	Asp	Met	Glu	Ala	Lys	Phe	Arg	
	850					855					860					
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Glu	Asn	Asp	Ile	Ala	Glu	Ile	Met	Lys	Met	Ser	Gly	Asp	Asn	Ser	Ser	
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Gln	Leu	Thr	Lys	Met	Asn	Asp	Glu	Leu	Arg	Leu	Lys	Glu	Arg	Asp	Val	
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Glu	Glu	Leu	Gln	Leu	Lys	Leu	Thr	Lys	Ala	Asn	Glu	Asn	Ala	Ser	Phe	
		915					920					925				
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	930					935					940					
Gln	Glu	Ala	Ala	Lys	Lys	His	Glu	Glu	Glu	Lys	Lys	Glu	Leu	Glu	Arg	
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Lys	Leu	Ser	Asp	Leu	Glu	Lys	Lys	Met	Glu	Thr	Ser	His	Asn	Gln	Cys	
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Gln	Glu	Leu	Lys	Ala	Arg	Tyr	Glu	Arg	Ala	Thr	Ser	Glu	Thr	Lys	Thr	
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Lys	His	Glu	Glu	Ile	Leu	Gln	Asn	Leu	Gln	Lys	Thr	Leu	Leu	Asp	Thr	
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Glu	Leu	Glu	Glu	Leu	Arg	Lys	Gln	Ala	Glu	Lys	Ala	Lys	Ala	Ala	Gln	
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Thr	Ala	Glu	Asp	Ala	Met	Gln	Ile	Met	Glu	Gln	Met	Thr	Lys	Glu	Lys	
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Leu	Gln	Asn	Glu	Leu	Asp	Thr	Leu	Lys	Glu	Asn	Asn	Leu	Lys	Asn	Val	
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Ala Glu Glu Leu Gly Arg Ser Arg Asp Glu Val Thr Ser His Gln Lys		
1140	1145	1150
Leu Glu Glu Glu Arg Ser Val Leu Asn Asn Gln Leu Leu Glu Met Lys		
1155	1160	1165
Lys Arg Glu Ser Lys Phe Ile Lys Asp Ala Asp Glu Glu Lys Ala Ser		
1170	1175	1180
Leu Gln Lys Ser Ile Ser Ile Thr Ser Ala Leu Leu Thr Glu Lys Asp		
1185	1190	1195
Ala Glu Leu Glu Lys Leu Arg Asn Glu Val Thr Val Leu Arg Gly Glu		
1205	1210	1215
Asn Ala Ser Ala Lys Ser Leu His Ser Val Val Gln Thr Leu Glu Ser		
1220	1225	1230
Asp Lys Val Lys Leu Glu Leu Lys Val Lys Asn Leu Glu Leu Gln Leu		
1235	1240	1245
Lys Glu Asn Lys Arg Gln Leu Ser Ser Ser Ser Gly Asn Thr Asp Thr		
1250	1255	1260
Gln Ala Asp Glu Asp Glu Arg Ala Gln Glu Ser Gln Ile Asp Phe Leu		
1265	1270	1275
Asn Ser Val Ile Val Asp Leu Gln Arg Lys Asn Gln Asp Leu Lys Met		
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Lys Val Glu Met Met Ser Glu Ala Ala Leu Asn Gly Asn Gly Asp Asp		
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Leu Asn Asn Tyr Asp Ser Asp Asp Gln Glu Lys Gln Ser Lys Lys Lys		
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Pro Arg Leu Phe Cys Asp Ile Cys Asp Cys Phe Asp Leu His Asp Thr		
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Glu Asp Cys Pro Thr Gln Ala Gln Met Ser Glu Asp Pro Pro His Ser		
1345	1350	1355
Thr His His Gly Ser Arg Gly Glu Glu Arg Pro Tyr Cys Glu Ile Cys		
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 <211> 647
 <212> DNA
 <213> Homo Sapiens

<400> 815

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<210> 816
 <211> 152
 <212> PRT
 <213> Homo Sapiens

<400> 816

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		20					25						30		
Phe	Arg	Leu	Val	Ala	Met	Lys	Phe	Leu	Arg	Ala	Ser	Glu	Glu	His	Leu
		35					40					45			
Lys	Gln	His	Tyr	Ile	Asp	Leu	Lys	Asp	Arg	Pro	Phe	Phe	Pro	Gly	Leu
		50					55				60				
Val	Lys	Tyr	Met	Asn	Ser	Gly	Pro	Val	Val	Ala	Met	Val	Trp	Glu	Gly
65					70					75				80	
Leu	Asn	Val	Val	Lys	Thr	Gly	Arg	Val	Met	Leu	Gly	Glu	Thr	Asn	Pro
				85					90					95	
Ala	Asp	Ser	Lys	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Phe	Cys	Ile	Gln	Val
			100					105					110		
Gly	Arg	Asn	Ile	Ile	His	Gly	Ser	Asp	Ser	Val	Lys	Ser	Ala	Glu	Lys
		115					120					125			
Glu	Ile	Ser	Leu	Trp	Phe	Lys	Pro	Glu	Glu	Leu	Val	Asp	Tyr	Lys	Ser
		130				135					140				
Cys	Ala	His	Asp	Trp	Val	Tyr	Glu								
145						150									



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(57) Abstract			
<p>Tumor cell-specific antigens from melanoma cells have previously been identified using autologous cytolytic T cells clones from the patient, but the same approach did not work well with other tumour types. Here, screening of such antigens was successfully performed using antisera from the patient. Provided are several tumor cell-specific antigens, nucleic acids encoding them, antibodies and CTL's directed against these antigens, antigenic fragments diagnostic kits, etc.</p>			

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A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C12Q1/68 G01N33/53 C07K16/28
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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 97 17470 A (HOLLAND JAMES F) 15 May 1997</p> <p>Also against claims 82-84, 116, 117 see whole document, particularly the claims</p> <p>-/--</p>	<p>1,2, 4-10, 18, 21-23, 27, 28, 31, 32, 40, 42, 44, 45, 48-51, 58-60, 67-70, 76-79</p>



Further documents are listed in the continuation of box C.



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X	Also against claims 108,109,116,117. See whole document, particularly the claims and examples. --- WO 97 17441 A (KISHIMURA MASAOKI ; OSAKADA FUMIO (JP); OSAKI SHOICHI (JP); NAKAO K) 15 May 1997 see the whole document -& EP 0 869 176 A (KANEKA CORPORATION, OSAKA, JAPAN) 7 October 1998 Also against claims 68-72,74,76,77,82,116,117 see claims 10,12; examples 2,5 --- WO 97 02362 A (FOX CHASE CANCER CENTER) 23 January 1997 see the whole document, particularly the claims and seq. 1 and 2. Also against claims 70-72,74,76-80,82-85,88,89,99-104,108-111, 116,117. see page 18, line 20 - page 22, line 33 --- -/--	1,2,4-8, 13,18, 21,22, 24, 27-29, 31,32, 35,40, 42,44, 45, 47-50, 54,59, 60,63,67 1,2, 4-10,15, 18, 21-24, 27-29, 31,32, 37,40, 42-45, 47-50, 56, 58-60, 65,67

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	<p>ZWIJSEN, A. ET AL.: "Characterization of a rat C6 glioma-secreted follistatin-related protein (FRP); cloning and sequencing of the human homologue." EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 225, no. 3, November 1994, pages 937-46, XP002103181</p> <p>see page 945, right-hand column, paragraph 2-4; figure 3</p>	<p>18,21, 22,24, 27,28, 44,45, 47-50, 54,59, 60,63, 67-72, 74-80,82</p>
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X	<p>JIN, Y-J. ET AL.: "The 25-kDa FK506-binding protein is localized in the nucleus and associated with casein kinase II and nucleolin." PROC.NAT'L.ACAD.SCI.USA, vol. 90, August 1993, pages 7769-73, XP002104548</p> <p>see the whole document</p>	<p>31,32, JIN, Y-J. 35,40, FK506-bind 116,117 nucleol (stand biol Proc, 1993)</p>
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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	<p>DATABASE EMBL - EMHUM2 Entry HSU50839, Acc.no. U50839, 9 March 1997</p> <p>LATIF, F. ET AL.: "Homo sapiens gl6 protein (gl6) mRNA, complete cds." XP002103209 see the whole document</p> <p>---</p>	44,45, 60,64, 67,70
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X	<p>DATABASE EMBL - EMBEST11 Entry HS1188646, Acc.no. AA285170, 5 April 1997 STRAUSBERG, R.: "zs48f04.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:700735 3'." XP002103210 see the whole document</p> <p>---</p>	44,45, 59,60, 67-70
X	<p>FISHER, D.Z. ET AL.: "cDNA sequencing of nuclear lamins A and C reveals primary and secondary structural homology to intermediate filament proteins." PROC.NAT'L.ACAD.SCI.USA, vol. 83, September 1986, pages 6450-4, XP002103184 see figure 2</p> <p>---</p>	44,45, 59,60, 67-70
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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL - EMBEST11 Entry HS125289, Acc.no. AA454221, 11 June 1997 HILLIER, L. ET AL.: "zx48g12.r1 Soares testis NHT Homo sapiens cDNA clone 795526- 5' similar to TR:E243068 E243068 KINASE." XP002103190 see the whole document</p>	67,69
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	BOON T ET AL: "Tumor antigens recognized by T cells" IMMUNOLOGY TODAY, vol. 18, no. 6, June 1997, page 267-268 XP004068293 see the whole document	
A	SAHIN, U. ET AL.: "Human neoplasms elicit multiple specific immune responses in the autologous host." PROC.NATL.ACAD.SCI.USA, vol. 92, December 1995, pages 11810-3, XP002091914 cited in the application see the whole document	
P,X	DATABASE EMBL - EMHUM1 Entry/Acc.no. AC004022, 22 January 1998 HINDS, K. ET AL.: "Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence." XP002091837 from nt.330-810	1,2
P,X	ALAIYA, A.A. ET AL.: "Phenotypic analysis of ovarian carcinoma: polypeptide expression in benign, boderline and malignant tumors." JOURNAL OF CNACER, vol. 73, no. 5, 27 November 1997, pages 678-83, XP002104552 see abstract; figure 2	1-10,15
P,X	GÜRE, A.O. ET AL.: "Human lung cancer antigens recognized by autologous antibodies: definition of a novel cDNA derived from the tumor suppressor gene locus on chromosome 3p21.3" CANCER RESEARCH, vol. 58, 1 March 1998, pages 1034-41, XP002103188 see the whole document	1,2,4,5, 9,14,18, 21,22, 27,44, 45,49, 50,55, 59,60, 64, 67-70, 83,84
P,X	SCANLAN, M.J. ET AL.: "Characterization of human colon cancer antigens recognized by autologous antibodies" INTERNATIONAL JOURNAL OF CANCER, 29 May 1998, pages 652-8, XP002103186 see the whole document	31,32, 34,40, 59,60, 62, 67-70, 83,84, 116

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>NAGASE, T. ET AL.: "Prediction of the coding sequence of unidentified human genes. IX. The complete sequence of 100 new cDNA clones from brain which can code for large proteins in vivo."</p> <p>DNA RESEARCH, vol. 5, 28 February 1998, pages 31-39, XP002103187 see figure 1; table 3 -& DATABASE EMBL Entry/acc.no. AB011172, 10 April 1998</p>	44,45, 67-70, 83,84
P,X	<p>NAGASE, T. ET AL.: "Homo sapiens mRNA for KIAA0600 protein, partial cds." XP002104556 see the whole document</p> <p>-----</p> <p>JONES, M.H. ET AL.: "Identification and characterization of BRDT: a testis-specific gene related to the bromodomain genes RING3 and Drosophila fsh."</p> <p>GENOMICS, vol. 45, no. 3, 1 November 1997, pages 529-34, XP002103185 see page 529, right-hand column, paragraph 2 see page 530, left-hand column, paragraph 2; figure 1 see page 532, right-hand column, paragraph 2</p>	44,45, 59,60, 67-70, 83,84
P,X	<p>ISHIKAWA K ET AL: "Prediction of the coding sequences of unidentified human genes. X The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro"</p> <p>DNA RESEARCH, vol. 5, no. 321, 30 June 1998, pages 169-176, XP002089186 see abstract; figures 1,2; table 2</p> <p>-----</p>	44,59, 60,63, 67-70
E	<p>US 5 858 723 A (MUELLER-LANTZSCH NIKOLAUS ET AL) 12 January 1999</p> <p>Also against claims 108,109,116,117 see the whole document</p> <p>-----</p>	1,2, 4-10,31, 32,40, 42,43, 49,50, 58-60, 67,69, 71,72, 74-79, 82-84, 99-104

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 98 40483 A (HUMAN GENOME SCIENCES INC ;GREENE JOHN M (US); LI YI (US); ROSEN C) 17 September 1998	1,2, 4-10,14, 18, 21-24, 27,28, 31,32, 36,40, 44,45, 47-50, 55, 58-60, 64,67-72
	Also against claims 74,76-80,82-85,88,89, 99-104,108,109,111,116,117. See seq. 24 and the claims.	
E	WO 98 08866 A (WISTAR INST) 5 March 1998 see the whole document	1,2
E	WO 98 48015 A (CHUGAI RES INST MOLECULAR MED ;JONES MICHAEL H CHUGAI RESEARC (JP)) 29 October 1998 see whole document, particularly the claims. & DATABASE WPI Derwent Publications Ltd., London, GB; AN 98-583658 XP002103211 see abstract	18,22, 23, 27-29, 31,32, 40, 44-50, 58-60, 67-72, 74, 76-78, 85,88, 89,102, 103
E	WO 98 32853 A (GENETICS INST) 30 July 1998 see seq. 7 and 8 see page 6, line 23 - page 8, line 12; claims 20-22 see page 21, line 17 - page 22, line 11	18,21, 22,24, 27-29, 44,45, 47-50, 53,59, 60,62, 67-72, 74, 76-80,82

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	SCANLAN, M.J. ET AL.: "Isoforms of the human PDZ-73 protein exhibit differential tissue expression" BIOCHIMICA ET BIOPHYSICA ACTA, vol. 1445, no. 1, 1999, pages 39-52, XP002104553 also for claims 77-80,82-84,116. see the whole document ---	
T	DRABKIN, H.A. ET AL.: "DEF-3(g16/NY-LU-12), an RNA binding protein from the 3p21.3 homozygous deletion region in SCLC" ONCOGENE, vol. 18, 1999, pages 2589-97, XP002104554 see the whole document -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 98/14679

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 85-111 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-14, 17-36, 39-55, 58-64, 67-117; see additional sheets, pages 3-4.
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-11, 17-33, 39-52, 58-61, 67-117,
all partially

The nucleic acid sequence of Seq.ID 1, fragments or complements thereof, and the corresponding polypeptide(s) encoded thereby, and immunogenic and/or HLA binding fragments thereof, optionally as part of a complex with a HLA molecule, an expression vector comprising said nucleic acid, and optionally a human HLA molecule, a host cell transformed with said vector, and an antibody against said polypeptide(s).

Also a method of diagnosing of a disorder characterised by overexpression of said polypeptide(s) and a method for determining regression, progression or onset of a disease associated with overexpression of said polypeptide(s), using agents that specifically bind to said nucleic acid, said polypeptide(s) or complexes of (fragments of) said polypeptide(s) and a HLA molecule. A kit comprising two polynucleotides for the detection of said nucleic acid
Also pharmaceutical preparations

- which enrich the presence of said polypeptide-HLA complex, optionally comprising an adjuvant, or
- which inhibits the expression of said polypeptide(s), or
- comprising an agent that selectively binds said polypeptide, optionally as a conjugate with a diagnostic or therapeutic compound, or
- comprising said nucleic acid, optionally in an expression vector, optionally in a host cell, or
- comprising said polypeptide(s), optionally in combination with an adjuvant, or
- comprising cytolytic T cells, specific for said polypeptide-HLA complex, or
- comprising an antibody against said polypeptide(s).

Inventions 2-119: claims 1-11, 13, 15, 17-33, 35, 37,
39-52, 54, 56, 58-61, 63, 65, 67-117, all partially (1)

Inventions 2-119: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:2-40, 66, 89-169 (odd numbers), 170, 172, 174, and 176-210, where invention 2 is limited to Seq.ID:2 and corresponding polypeptides encoded thereby, invention 3 is limited to Seq.ID:3 and corresponding polypeptides encoded thereby,....., and invention 119 is limited to Seq.ID:210 and corresponding polypeptides encoded thereby.

Invention 120: claims 1-10, 13, 17-32, 35,
39-51, 54, 58-60, 63, 67-117, all partially

Idem as subject 1 but limited to the DNA sequences seq.ID:211 and 329 and corresponding polypeptides encoded thereby.

Inventions 121-452: claims 1-10,13,16-32,35,38-51, 54,57-60,63,66-117, all partially (1)

Inventions 121-452: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:212-328, and 330-543, where invention 121 is limited to Seq.ID:211 and corresponding polypeptides encoded thereby, invention 122 is limited to Seq.ID:212 and corresponding polypeptides encoded thereby,....., and invention 452 is limited to Seq.ID:543 and corresponding polypeptides encoded thereby.

Invention 453: claims 1-10,12,17-32,34,39-51,53, 58-60,62,67-117, all partially

Idem as subject 1 but limited to the DNA sequences seq.ID:544 and 554 and corresponding polypeptides encoded thereby.

Inventions 454 and 455: claims 1-10,12,17-32,34, 39-51,53,58-60,62,67-117, all partially

Inventions 454 and 455: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:546 and 548, where invention 454 is limited to Seq.ID:546 and corresponding polypeptides encoded thereby, and invention 455 is limited to Seq.ID:548 and corresponding polypeptides encoded thereby.

Invention 456: claims 1-10,12,17-32,34,39-51,53, 58-60,62,67-117, all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:550, 552, 556, 558 and 560 and corresponding polypeptides encoded thereby.

Inventions 457-582: claims 1-10,12-14,17-32,34-36, 39-51,53-55,58-60,62-64,67-117, all partially (1)

Inventions 457-582: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:562-586 (even numbers),

588-683, 686, 687, 689, 691, 692, 692, and 696-706, where invention 457 is limited to Seq.ID:562 and corresponding polypeptides encoded thereby, invention 458 is limited to Seq.ID:564 and corresponding polypeptides encoded thereby,....., and invention 582 is limited to Seq.ID:706 and corresponding polypeptides encoded thereby.

Invention 583: claims 1-10, 14, 17-32, 36, 39-51, 55, 58-60, 64, 67-117, all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:707, 709, 711 and 712 and corresponding polypeptides encoded thereby.

Inventions 584-592: claims 1-117, all partially (1)

Inventions 584-592: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:799-815 (odd numbers), where invention 584 is limited to Seq.ID:799 and corresponding polypeptides encoded thereby, invention 585 is limited to Seq.ID:801 and corresponding polypeptides encoded thereby,....., and invention 592 is limited to Seq.ID:815 and corresponding polypeptides encoded thereby).

For the sake of conciseness, the subject matter of the first invention is explicitly defined, the other subject matters are defined by analogy thereto.

(1) In as far as the claims searched for a group of inventions refer to specific groups of sequences, only those claims which refer to the groups comprising the nucleic acid sequence of a particular invention, and/or its corresponding polypeptide sequence(s), form parts of that invention.

Due to the fact that extensive sequence homologies were found between several groups of sequences during the additional searches, some of the sequences have been grouped, whereby each of these groups comprising two or more such homologous sequences is considered to be one invention.

Claims searched during primary and additional searches: 1-14, 17-36, 39-55, 58-64, 67-117, limited to:

Invention 1, seq.ID.1
Invention 52, seq.ID.111, and 112 (transl.)
Invention 61, seq.ID.129, and 130 (transl.)
Invention 71, seq.ID.149, and 150 (transl.)
Invention 72, seq.ID.151, and 152 (transl.)
Invention 116, seq.ID.206
Invention 120, seq.ID.211 and 329; (related sequences)
Invention 137, seq.ID.228
Invention 139, seq.ID.330

Invention 219, seq.ID.411

Invention 453, seq.ID.544, and 545 (transl.),
and seq.ID.554, and 555 (transl.);
(related sequences)

Invention 454, seq.ID.546, and 547 (transl.)

Invention 455, seq.ID.548, and 548 (transl.)

Invention 456, seq.ID.550, and 551 (transl.),
and seq.ID.552, and 553 (transl.),
and seq.ID.556, and 557 (transl.);

and seq.ID.558, and 559 (transl.);

and seq.ID.560, and 561 (transl.);

(related sequences)

Invention 547 seq.ID.665

Invention 548, seq.ID.666

Invention 554, seq.ID.672

Invention 558, seq.ID.676

Invention 563, seq.ID.681

Invention 566, seq.ID.686

Invention 583, seq.ID.707, and 708 (transl.),

and seq.ID.709, and 710 (transl.),

and seq.ID.711,

and seq.ID.712;

(related sequences).

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